


FORM PTO-1390 U.S. DEPARTMENT OF COMMERCE PATENT AND TRADEMARK OFFICE (REV. 1094)		ATTORNEY'S DOCKET NUMBER L0461/7078
TRANSMITTAL LETTER TO THE UNITED STATES DESIGNATED/ELECTED OFFICE (DO/EO/US) CONCERNING A FILING UNDER 35 U.S.C. 371		09/462929 U.S. APPLICATION NO. (if known) 35 U.S.C. 371
INTERNATIONAL APPLICATION NO. PCT/US98/14679	INTERNATIONAL FILING DATE 15 July 1998 (15.07.98)	PRIORITY DATE CLAIMED 17 July 1997 (17.07.97)
TITLE OF INVENTION CANCER ASSOCIATED NUCLEIC ACIDS AND POLYPEPTIDES		
APPLICANT(S) FOR DO/EO/US OLD, Lloyd J.; SCANLAN, Matthew J.; STOCKERT, Elisabeth; GURE, Ali; CHEN, Yao-Tseng; GOUT, Ivan; O'HARE, Michael; OBATA, Yuichi; PFREUNDSCHUH, Michael; TURECI, Ozlem; SAHIN, Ugur		
Applicant herewith submits to the United States Designated/Elected Office (DO/EO/US) the following items and other information:		
<ol style="list-style-type: none"> 1. <input checked="" type="checkbox"/> This is a FIRST submission of items concerning a filing under 35 U.S.C. 371. 2. <input type="checkbox"/> This is a SECOND or SUBSEQUENT submission of items concerning a filing under 35 U.S.C. 371. 3. <input checked="" type="checkbox"/> This express request to begin national procedures (35 U.S.C. 371(f) at any time rather than delay examination until the expiration of the applicable time limit set in 35 U.S.C. 371(b) and PCT Articles 22 and 39(1). 4. <input checked="" type="checkbox"/> A proper Demand for International Preliminary Examination was made by the 19th month from the earliest claimed priority date. 5. <input checked="" type="checkbox"/> A copy of the International Application as filed (35 U.S.C. 371(c)(2)). <ol style="list-style-type: none"> a. <input type="checkbox"/> is transmitted herewith (required only if not transmitted by the International Bureau). b. <input type="checkbox"/> has been transmitted by the International Bureau. c. <input checked="" type="checkbox"/> is not required, as the application was filed in the United States Receiving Office (RO/US). 6. <input type="checkbox"/> A translation of the International Application into English (35 U.S.C. 371(c)(2)) with verification of translation. 7. <input checked="" type="checkbox"/> Amendments to the claims of the International Application under PCT Article 19 (35 U.S.C. 371(c)(3)). <ol style="list-style-type: none"> a. <input type="checkbox"/> are transmitted herewith (required only if not transmitted by the International Bureau). b. <input type="checkbox"/> have been transmitted by the International Bureau. c. <input type="checkbox"/> have not been made; however, the time limit for making such amendments has NOT expired. d. <input checked="" type="checkbox"/> have not been made and will not be made. 8. <input type="checkbox"/> A translation of the amendments to the claims under PCT Article 19 (35 U.S.C. 371(c)(3)). 9. <input type="checkbox"/> An oath or declaration of the inventor(s) (35 U.S.C. 371(c)(4)). 10. <input type="checkbox"/> A translation of the annexes to the International Preliminary Examination Report under PCT Article 36 (35 U.S.C. 371(C)(5)). 		
Items 11. To 16. Below concern document(s) or information included:		
11. <input type="checkbox"/> An Information Disclosure Statement under 37 CFR 1.97 and 1.98 with references.		
12. <input type="checkbox"/> An assignment document for recording. A separate cover sheet in compliance with 37 CFR 3.28 and 3.31 is included.		
13. <input checked="" type="checkbox"/> A FIRST preliminary amendment. <input type="checkbox"/> A SECOND or SUBSEQUENT preliminary amendment.		
14. <input type="checkbox"/> A substitute specification (submitted as a first Preliminary Amendment).		
15. <input type="checkbox"/> A change of power of attorney and/or address letter.		
16. <input checked="" type="checkbox"/> Other items or information: Mailed via Express Mailing Label No. EL437905460US Post Card		
Express Mail Label No. EL437905460US Dated Filed: January 14, 2000		

002090-6629460

U.S. APPLICATION NO. 09/462929 (If known, see 37 CFR 1.55)		INTERNATIONAL APPLICATION PCT/US98/14679		ATTORNEY'S DOCKET NUMBER L0461/7078	
17. <input checked="" type="checkbox"/> The following fees are submitted:				CALCULATIONS <small>PTO USE ONLY</small>	
BASIC NATIONAL FEE (37 CFR 1.492(a)(1)-(5)): Search Report has been prepared by the EPO or JPO \$840.00 International preliminary examination fee paid to USPTO (37 CFR 1.482) \$670.00 No international preliminary examination fee paid to USPTO (37 CFR 1.482) but international search fee paid to USPTO (37 CFR 1.445(a)(2)).. \$760.00 Neither international preliminary examination fee (37 CFR 1.482) nor international search fee (37 CFR 1.445(a)(2)) paid to USPTO..... \$970.00 International preliminary examination fee paid to USPTO (37 CFR 1.482) and all claims satisfied provisions of PCT Article 33(2)-(4) \$96.00					
ENTER APPROPRIATE BASIC FEE AMOUNT =				\$840.00	
Surcharge of \$130.00 for furnishing the oath or declaration later than <input type="checkbox"/> 20 <input checked="" type="checkbox"/> 30 months from the earliest claimed priority date (37 CFR 1.492(e)).				\$	
CLAIMS	NUMBER FILED	NUMBER EXTRA	RATE		
Total Claims	35-20 =	15	X \$18.00	\$270.00	
Independent Claims	19- 3 =	16	X \$78.00	\$1248.00	
MULTIPLE DEPENDENT CLAIM(S) (if applicable)			+\$260.00	\$260.00	
TOTAL OF ABOVE CALCULATIONS =				\$2618.00	
Reduction by 1/2 for filing by small entity, if applicable. Verified Small Entity Statement must also be filed (Note 37 CFR 1.9, 1.27, 1.28).				\$	
SUBTOTAL =				\$	
Processing fee of \$130.00 for furnishing the English translation later than <input type="checkbox"/> 20 <input type="checkbox"/> 30 months from the earliest claimed priority date (37 CFR 1.492(f)).				\$	
TOTAL NATIONAL FEE =				\$	
Fee for recording the enclosed assignment (37 CFR 1.21(h)). The assignment must be accompanied by an appropriate coversheet (37 CFR 3.28, 3.31). \$40.00 per property +				\$	
TOTAL FEES ENCLOSED =				\$2618.00	
				Amount to be:	
				refunded	\$
				charged	\$
a. <input checked="" type="checkbox"/> A check in the amount of \$ <u>2618.00</u> to cover the above fees is enclosed. b. Please charge by Deposit Account No. _____ In the amount of \$ _____ To cover the above fees. A duplicate copy of this sheet is enclosed c. <input checked="" type="checkbox"/> The commissioner is hereby authorized to charge any additional fees which may be required, or credit any overpayment to Deposit Account No. 23/2825. A duplicate of this sheet is enclosed.					
NOTE: Where an appropriate time limit under 37 CFR 1.494 or 1.495 has not been met, a petition to revive (37 CFR 1.137(a) or (b) must be filed and granted to restore the application to pending status.					
SEND ALL CORRESPONDENCE TO			 SIGNATURE		
John R. Van Amsterdam WOLF, GREENFIELD & SACKS, P.C. 600 Atlantic Avenue Boston, Massachusetts 02210			John R. Van Amsterdam NAME		
			40,212 REGISTRATION NO		

ATTORNEY'S DOCKET NO. L0461/7078

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicant: Old et al.
Serial No: PCT/US98/14679
Filed: July 15, 1998
For: CANCER ASSOCIATED ANTIGENS AND USES THEREFOR
Examiner: Not Assigned
Art Unit: Unknown

Box PCT
ASSISTANT COMMISSIONER FOR PATENTS
WASHINGTON, D.C. 20231

Sir:

PRELIMINARY AMENDMENT

Please amend the application as follows.

In the Specification

Please amend the specification as follows. Please add the following paragraph as the first paragraph of the specification:

--This application is a national stage application under 35 U.S.C. §371 of PCT/US98/14679, filed July 15, 1998, which is a continuation in part of U.S. application serial no. 08/896,164, filed July 17, 1997, U.S. application serial no. 08/948,705, filed October 10, 1997, and U.S. application serial no. 09/102,322, filed June 22, 1998, all of which are now pending. This application also claims priority under 35 U.S.C. §119 to U.S. application serial no. 60/061,599, filed October 10, 1997, and U.S. application serial no. 60/061,765, filed October 10, 1997, both of which are now abandoned. This application also claims priority under 35 U.S.C. §119 to Great Britain application no. 9721697.2, filed October 11, 1997.--

In the Claims

Please delete without prejudice claims 3, 4, 6-17, 19-21, 23-30, 32-39, 41, 43, 45-48, 50-57, 60-66, 68-70, 72, 78, 80, 81, 84, 86-89, 91, 92, 94-98, 100, 101, 103, 104, 106, 107, 109-111, 113-115 and 117.

Please amend the claims as follows:

- 40.(amended) The composition of claim[s] 31[-38], wherein the agent is an antibody.
- 42.(amended) A composition of matter comprising
a conjugate of the agent of claims 31[-41] and 40 and a therapeutic or diagnostic agent.
- 49.(amended) A pharmaceutical composition comprising
an isolated polypeptide comprising a PP Group 1 or a PP Group 2 polypeptide, or an
HLA binding fragment thereof and
a pharmaceutically acceptable carrier.
- 58.(amended) The pharmaceutical composition of claim[s] 49[-57], further comprising an
adjuvant.
- 71.(amended) An expression vector comprising an isolated nucleic acid molecule of claim[s]
59[, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69 or 70] operably linked to a promoter.
- 74.(amended) A host cell transformed or transfected with an expression vector of claims 71,
[72,] or 73.
- 75.(amended) A host cell transformed or transfected with an expression vector of claim 71 [or
claim 72] and further comprising a nucleic acid encoding HLA.
- 76.(amended) An isolated polypeptide encoded by the isolated nucleic acid molecule of claim[s]
59[, 60, 61, 62, 63, 64, 65, or 66].
- 102.(amended) A method for treating a condition characterized by expression in a subject of
abnormal amounts of a protein encoded by a nucleic acid molecule that is a NA Group 1 nucleic
acid molecule, comprising

administering to a subject a pharmaceutical composition of any one of claims 18, [19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30,] 44[, 45, 46, 47, 48,] and 49[, 50, 51, 52, 53, 54, 55, 56, 47, and 58] in an amount effective to prevent, delay the onset of, or inhibit the condition in the subject.

112. (amended) A composition of matter useful in stimulating an immune response to a plurality of [a] proteins encoded by nucleic acid molecules that are NA Group 1 molecules, comprising a plurality of peptides derived from the amino acid sequences of the proteins, wherein the peptides bind to one or more MHC molecules presented on the surface of the cells which express an abnormal amount of the protein.

Remarks

Please enter this amendment prior to calculation of the fees. The amendments to the specification were made to correct typographical errors and reduce claims. Support for the amendment to claim 49 can be found in the claims as filed. No new matter has been added.

Respectfully submitted,



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402 Rec'd PCT/PTO 14 JAN 2000
CANCER ASSOCIATED NUCLEIC ACIDS AND POLYPEPTIDES

Field of the Invention

The invention relates to nucleic acids and encoded polypeptides which are cancer
5 associated antigens expressed in patients afflicted with breast cancer. The invention also relates
to agents which bind the nucleic acids or polypeptides. The nucleic acid molecules,
polypeptides coded for by such molecules and peptides derived therefrom, as well as related
antibodies and cytolytic T lymphocytes, are useful, *inter alia*, in diagnostic and therapeutic
contexts.

Background of the Invention

The mechanism by which T cells recognize foreign materials has been implicated in
cancer. A number of cytolytic T lymphocyte (CTL) clones directed against autologous
melanoma antigens, testicular antigens, and melanocyte differentiation antigens have been
15 described. In many instances, the antigens recognized by these clones have been
characterized.

The use of autologous CTLs for identifying tumor antigens requires that the target cells
which express the antigens can be cultured *in vitro* and that stable lines of autologous CTL
clones which recognize the antigen-expressing cells can be isolated and propagated. While this
20 approach has worked well for melanoma antigens, other tumor types, such as epithelial cancers
including breast and colon cancer, have proved refractory to the approach.

More recently another approach to the problem has been described by Sahin et al. (*Proc.
Natl. Acad. Sci. USA* 92:11810-11813, 1995). According to this approach, autologous antisera
are used to identify immunogenic protein antigens expressed in cancer cells by screening
25 expression libraries constructed from tumor cell cDNA. Antigen-encoding clones so identified
have been found to have elicited an high-titer humoral immune response in the patients from
which the antisera were obtained. Such a high-titer IgG response implies helper T cell
recognition of the detected antigen. These tumor antigens can then be screened for the presence
of MHC/HLA class I and class II motifs and reactivity with CTLs

30 The invention is elaborated upon in the disclosure which follows.

Summary of the Invention

Autologous antibody screening has now been applied to cancer using antisera from cancer patients. Numerous cancer associated antigens have been identified. The invention provides, *inter alia*, isolated nucleic acid molecules, expression vectors containing those molecules and host cells transfected with those molecules. The invention also provides isolated proteins and peptides, antibodies to those proteins and peptides and CTLs which recognize the proteins and peptides. Fragments including functional fragments and variants of the foregoing also are provided. Kits containing the foregoing molecules additionally are provided. The foregoing can be used in the diagnosis, monitoring, research, or treatment of conditions characterized by the expression of one or more cancer associated antigens.

Prior to the present invention, only a handful of cancer associated genes had been identified in the past 20 years. The invention involves the surprising discovery of many genes, some previously known and many previously unknown, which are expressed in individuals who have cancer. These individuals all have serum antibodies against the proteins (or fragments thereof) encoded by these genes. Thus, abnormally expressed genes are recognized by the host's immune system and therefore can form a basis for diagnosis, monitoring and therapy.

The invention involves the use of a single material, a plurality of different materials and even large panels and combinations of materials. For example, a single gene, a single protein encoded by a gene, a single functional fragment thereof, a single antibody thereto, etc. can be used in methods and products of the invention. Likewise, pairs, groups and even panels of these materials can be used for diagnosis, monitoring and therapy. The pairs, groups or panels can involve 2, 3, 4, 5... to as many as 25, 50, 100 or more genes, gene products, fragments thereof or agents that recognize such materials. A plurality of such materials are not only useful in monitoring, typing, characterizing and diagnosing cells abnormally expressing such genes, but a plurality of such materials can be used therapeutically. An example of the use of a plurality of such materials for the prevention, delay of onset, amelioration, etc. of cancer cells, which express or will express such genes prophylactically or acutely. Any and all combinations of the genes, gene products, and materials which recognize the genes and gene products can be tested and identified for use according to the invention. It would be far too lengthy to recite all such combinations; those skilled in the art, particularly in view of the teaching contained herein, will readily be able to determine which combinations are most appropriate for which circumstances.

As will be clear from the following discussion, the invention has *in vivo* and *in vitro* uses,

including for therapeutic, diagnostic, monitoring and research purposes. One aspect of the invention is the ability to fingerprint a cell expressing a number of the genes identified according to the invention. Such fingerprints will be characteristic, for example, of the stage of the cancer, the type of the cancer, or even the effect in animal models of a therapy on a cancer.

5 Cells also can be screened to determine whether such cells abnormally express the genes identified according to the invention.

The invention, in one aspect, is a method of diagnosing a disorder characterized by expression of a cancer associated antigen precursor coded for by a nucleic acid molecule. The method involves the steps of contacting a biological sample isolated from a subject with an agent that specifically binds to the nucleic acid molecule, an expression product thereof, or a fragment of an expression product thereof complexed with an MHC, preferably an HLA, molecule, wherein the nucleic acid molecule is a NA Group 1 nucleic acid molecule, and determining the interaction between the agent and the nucleic acid molecule, the expression product or fragment of the expression product as a determination of the disorder.

15 In one embodiment the agent is selected from the group consisting of (a) a nucleic acid molecule comprising NA Group 1 nucleic acid molecules or a fragment thereof, (b) a nucleic acid molecule comprising NA Group 3 nucleic acid molecules or a fragment thereof, (c) a nucleic acid molecule comprising NA Group 17 nucleic acid molecules or a fragment thereof, (d) an antibody that binds to an expression product, or a fragment thereof, of NA group 1 nucleic acids, (e) an antibody that binds to an expression product, or a fragment thereof, of NA group 3 nucleic acids, (f) an antibody that binds to an expression product, or a fragment thereof, of NA group 17 nucleic acids, (g) and agent that binds to a complex of an MHC, preferably HLA, molecule and a fragment of an expression product of a NA Group 1 nucleic acid, (h) an agent that binds to a complex of an MHC, preferably HLA, molecule and a fragment of an expression product of a NA group 3 nucleic acid, and (I) an agent that binds to a complex of an MHC, preferably HLA, molecule and a fragment of an expression product of a NA Group 17 nucleic acid.

The disorder may be characterized by expression of a plurality of cancer associated antigen precursors and wherein the agent is a plurality of agents, each of which is specific for a different human cancer associated antigen precursor, and wherein said plurality of agents is at least 2, at least 3, at least 4, at least 5, at least 6, at least 7, at least 8, at least 9 or at least 10 such agents.

In each of the above embodiments the agent may be specific for a human cancer associated antigen precursor that is a breast, a gastric, a lung, a prostate, a renal or a colon cancer associated antigen precursor.

In another aspect the invention is a method for determining regression, progression or onset of a condition characterized by expression of abnormal levels of a protein encoded by a nucleic acid molecule that is a NA Group 1 molecule. The method involves the steps of monitoring a sample, from a subject who has or is suspected of having the condition, for a parameter selected from the group consisting of (i) the protein, (ii) a peptide derived from the protein, (iii) an antibody which selectively binds the protein or peptide, and (iv) cytolytic T cells specific for a complex of the peptide derived from the protein and an MHC molecule, as a determination of regression, progression or onset of said condition. In one embodiment the sample is a body fluid, a body effusion or a tissue.

In another embodiment the step of monitoring comprises contacting the sample with a detectable agent selected from the group consisting of (a) an antibody which selectively binds the protein of (i), or the peptide of (ii), (b) a protein or peptide which binds the antibody of (iii), and (c) a cell which presents the complex of the peptide and MHC molecule of (iv). In a preferred embodiment the antibody, the protein, the peptide or the cell is labeled with a radioactive label or an enzyme. The sample in a preferred embodiment is assayed for the peptide.

According to another embodiment the nucleic acid molecule is one of the following: a NA Group 3 molecule, a NA Group 11 molecule, a NA Group 12 molecule, a NA Group 13 molecule, a NA Group 14 molecule, a NA Group 15 molecule, or a NA Group 16 molecule. In yet another embodiment the protein is a plurality of proteins, the parameter is a plurality of parameters, each of the plurality of parameters being specific for a different of the plurality of proteins.

The invention in another aspect is a pharmaceutical preparation for a human subject. The pharmaceutical preparation includes an agent which when administered to the subject enriches selectively the presence of complexes of an HLA molecule and a human cancer associated antigen, and a pharmaceutically acceptable carrier, wherein the human cancer associated antigen is a fragment of a human cancer associated antigen precursor encoded by a nucleic acid molecule which comprises a NA Group 1 molecule. In one embodiment the nucleic acid molecule is a NA Group 3 nucleic acid molecule.

The agent in one embodiment comprises a plurality of agents, each of which enriches selectively in the subject complexes of an HLA molecule and a different human cancer associated antigen. Preferably the plurality is at least two, at least three, at least four or at least 5 different such agents.

5 In another embodiment the agent is selected from the group consisting of (1) an isolated polypeptide comprising the human cancer associated antigen, or a functional variant thereof, (2) an isolated nucleic acid operably linked to a promoter for expressing the isolated polypeptide, or functional variant thereof, (3) a host cell expressing the isolated polypeptide, or functional variant thereof, and (4) isolated complexes of the polypeptide, or functional
10 variant thereof, and an HLA molecule.

The agent may be a cell expressing an isolated polypeptide. In one embodiment the agent is a cell expressing an isolated polypeptide comprising the human cancer associated antigen or a functional variant thereof, and wherein the cell is nonproliferative. In another embodiment the agent is a cell expressing an isolated polypeptide comprising the human cancer
15 associated antigen or a functional variant thereof, and wherein the cell expresses an HLA molecule that binds the polypeptide. The cell can express one or both of the polypeptide and HLA molecule recombinantly. In another preferred embodiment the cell is nonproliferative. In yet another embodiment the agent is at least two, at least three, at least four or at least five different polypeptides, each representing a different human cancer associated antigen or
20 functional variant thereof.

The agent in one embodiment is a PP Group 2 polypeptide. In other embodiments the agent is a PP Group 3 polypeptide or a PP Group 4 polypeptide.

In an embodiment each of the pharmaceutical preparations described herein also includes an adjuvant.

25 According to another aspect the invention, a composition is provided of an isolated agent that binds selectively a PP Group 1 polypeptide. In separate embodiments the agent binds selectively to a polypeptide selected from the following: a PP Group 3 polypeptide, a PP Group 11 polypeptide, a PP Group 12 polypeptide, a PP Group 13 polypeptide, a PP Group 14 polypeptide, a PP Group 15 polypeptide, and a PP Group 16 polypeptide. In other
30 embodiments, the agent is a plurality of different agents that bind selectively at least two, at least three, at least four, or at least five different such polypeptides. In each of the above described embodiments the agent may be an antibody.

In another aspect the invention is a composition of matter .composed of a conjugate of the agent of the above-described compositions of the invention and a therapeutic or diagnostic agent. Preferably the conjugate is of the agent and a therapeutic or diagnostic that is an antineoplastic.

5 The invention in another aspect is a pharmaceutical composition of an isolated nucleic acid molecule selected from the group consisting of: (1) NA Group 1 molecules, and (2) NA Group 2 molecules, and a pharmaceutically acceptable carrier. In one embodiment the isolated nucleic acid molecule comprises a NA Group 3 or NA Group 4 molecule. In another embodiment the isolated nucleic acid molecule comprises at least two isolated nucleic acid
10 molecules coding for two different polypeptides, each polypeptide comprising a different cancer associated antigen.

Preferably the pharmaceutical composition also includes an expression vector with a promoter operably linked to the isolated nucleic acid molecule. In another embodiment the pharmaceutical composition also includes a host cell recombinantly expressing the isolated
15 nucleic acid molecule.

According to another aspect of the invention a pharmaceutical composition is provided. The pharmaceutical composition includes an isolated polypeptide comprising a PP Group 1 or a PP Group 2 polypeptide, and a pharmaceutically acceptable carrier. In one embodiment the isolated polypeptide comprises a PP Group 3 or a PP Group 4 polypeptide.

20 In another embodiment the isolated polypeptide comprises at least two different polypeptides, each comprising a different cancer associated antigen. In separate embodiments the isolated polypeptides are selected from the following: PP Group 11 polypeptides or HLA binding fragments thereof, PP Group 12 polypeptides or HLA binding fragments thereof, PP Group 13 polypeptides or HLA binding fragments thereof, PP Group 14 polypeptides or HLA
25 binding fragments thereof, PP Group 15 polypeptides or HLA binding fragments thereof, or PP Group 16 polypeptides or HLA binding fragments thereof.

In an embodiment each of the pharmaceutical compositions described herein also includes an adjuvant.

Another aspect the invention is an isolated nucleic acid molecule comprising a NA
30 Group 3 molecule. Another aspect the invention is an isolated nucleic acid molecule comprising a NA Group 4 molecule. In separate embodiments the isolated nucleic acid molecules are selected from the following: a Group 11 molecule or a functional fragment

thereof, a Group 12 molecule or a functional fragment thereof, a Group 13 molecule or a functional fragment thereof, a Group 14 molecule or a functional fragment thereof, a Group 15 molecule or a functional fragment thereof, or a Group 16 molecule or a functional fragment thereof.

5 The invention in another aspect is an isolated nucleic acid molecule selected from the group consisting of (a) a fragment of a nucleic acid selected from the group of nucleic acid molecules consisting of SEQ ID numbered below and comprising all nucleic acid sequences among SEQ ID NOs 1-816, of sufficient length to represent a sequence unique within the human genome, and identifying a nucleic acid encoding a human cancer associated antigen precursor, (b) complements of (a), provided that the fragment includes a sequence of
10 contiguous nucleotides which is not identical to any sequence selected from the sequence group consisting of (1) sequences having the GenBank accession numbers of the sequence Group 1, (2) complements of (1), and (3) fragments of (1) and (2).

 In one embodiment the sequence of contiguous nucleotides is selected from the group
15 consisting of: (1) at least two contiguous nucleotides nonidentical to the sequence Group 1, (2) at least three contiguous nucleotides nonidentical to the sequence Group 1, (3) at least four contiguous nucleotides nonidentical to the sequence Group 1, (4) at least five contiguous nucleotides nonidentical to the sequence Group 1, (5) at least six contiguous nucleotides nonidentical to the sequence Group 1, or (6) at least seven contiguous nucleotides nonidentical
20 to the sequence Group 1.

 In another embodiment the fragment has a size selected from the group consisting of at least: 8 nucleotides, 10 nucleotides, 12 nucleotides, 14 nucleotides, 16 nucleotides, 18 nucleotides, 20, nucleotides, 22 nucleotides, 24 nucleotides, 26 nucleotides, 28 nucleotides, 30 nucleotides, 50 nucleotides, 75 nucleotides, 100 nucleotides, 200 nucleotides, 1000 nucleotides
25 and every integer length therebetween.

 In yet another embodiment the molecule encodes a polypeptide which, or a fragment of which, binds a human HLA receptor or a human antibody.

 Another aspect of the invention is an expression vector comprising an isolated nucleic acid molecule of the invention described above operably linked to a promoter.

30 According to one aspect the invention is an expression vector comprising a nucleic acid operably linked to a promoter, wherein the nucleic acid is a NA Group 2 molecule. In another aspect the invention is an expression vector comprising a NA Group 1 or Group 2 molecule

and a nucleic acid encoding an MHC, preferably HLA, molecule.

In yet another aspect the invention is a host cell transformed or transfected with an expression vector of the invention described above.

In another aspect the invention is a host cell transformed or transfected with an expression vector comprising an isolated nucleic acid molecule of the invention described above operably linked to a promoter, or an expression vector comprising a nucleic acid operably linked to a promoter, wherein the nucleic acid is a NA Group 1 or 2 molecule and further comprising a nucleic acid encoding HLA.

According to another aspect of the invention an isolated polypeptide encoded by the isolated nucleic acid molecules the invention, described above, is provided. These include PP Group 1-17 polypeptides. The invention also includes a fragment of the polypeptide which is immunogenic. In one embodiment the fragment, or a portion of the fragment, binds HLA or a human antibody.

The invention includes in another aspect an isolated fragment of a human cancer associated antigen precursor which, or portion of which, binds HLA or a human antibody, wherein the precursor is encoded by a nucleic acid molecule that is a NA Group 1 molecule. In one embodiment the fragment is part of a complex with HLA. In another embodiment the fragment is between 8 and 12 amino acids in length. In another embodiment the invention includes an isolated polypeptide comprising a fragment of the polypeptide of sufficient length to represent a sequence unique within the human genome and identifying a polypeptide that is a human cancer associated antigen precursor.

According to another aspect of the invention a kit for detecting the presence of the expression of a cancer associated antigen precursor is provided. The kit includes a pair of isolated nucleic acid molecules each of which consists essentially of a molecule selected from the group consisting of (a) a 12-32 nucleotide contiguous segment of the nucleotide sequence of any of the NA Group 1 molecules and (b) complements of ("a"), wherein the contiguous segments are nonoverlapping. In one embodiment the pair of isolated nucleic acid molecules is constructed and arranged to selectively amplify an isolated nucleic acid molecule that is a NA Group 3 molecule. Preferably, the pair amplifies a human NA Group 3 molecule.

According to another aspect of the invention a method for treating a subject with a disorder characterized by expression of a human cancer associated antigen precursor is provided. The method includes the step of administering to the subject an amount of an agent,

which enriches selectively in the subject the presence of complexes of an HLA molecule and a human cancer associated antigen, effective to ameliorate the disorder, wherein the human cancer associated antigen is a fragment of a human cancer associated antigen precursor encoded by a nucleic acid molecule selected from the group consisting of (a) a nucleic acid molecule comprising NA group 1 nucleic acid molecules, (b) a nucleic acid molecule comprising NA group 3 nucleic acid molecules, (c) a nucleic acid molecule comprising NA group 17 nucleic acid molecules.

In one embodiment the disorder is characterized by expression of a plurality of human cancer associated antigen precursors and wherein the agent is a plurality of agents, each of which enriches selectively in the subject the presence of complexes of an HLA molecule and a different human cancer associated antigen. Preferably the plurality is at least 2, at least 3, at least 4, or at least 5 such agents.

In another embodiment the agent is an isolated polypeptide selected from the group consisting of PP Group 1, PP Group 2, PP Group 3, PP Group 4, PP Group 5, PP Group 6, PP Group 7, PP Group 8, PP Group 9, PP Group 10, PP Group 11, PP Group 12, PP Group 13, PP Group 14, PP Group 15, PP Group 16 and PP Group 17 polypeptides.

In yet another embodiment the disorder is cancer.

According to another aspect the invention is a method for treating a subject having a condition characterized by expression of a cancer associated antigen precursor in cells of the subject. The method includes the steps of (i) removing an immunoreactive cell containing sample from the subject, (ii) contacting the immunoreactive cell containing sample to the host cell under conditions favoring production of cytolytic T cells against a human cancer associated antigen which is a fragment of the precursor, (iii) introducing the cytolytic T cells to the subject in an amount effective to lyse cells which express the human cancer associated antigen, wherein the host cell is transformed or transfected with an expression vector comprising an isolated nucleic acid molecule operably linked to a promoter, the isolated nucleic acid molecule being selected from the group of nucleic acid molecules consisting of NA Group 1, NA Group 2, NA Group 3, NA Group 4, NA Group 5, NA Group 6, NA Group 7, NA Group 8, NA Group 9, NA Group 10, NA Group 11, NA Group 12, NA Group 13, NA Group 14, NA Group 15, NA Group 16, and NA Group 17.

In one embodiment the host cell recombinantly expresses an HLA molecule which binds the human cancer associated antigen. In another embodiment the host cell endogenously

expresses an HLA molecule which binds the human cancer associated antigen.

The invention includes in another aspect a method for treating a subject having a condition characterized by expression of a cancer associated antigen precursor in cells of the subject. The method includes the steps of (I) identifying a nucleic acid molecule expressed by the cells associated with said condition, wherein said nucleic acid molecule is a NA Group 1 molecule (ii) transfecting a host cell with a nucleic acid selected from the group consisting of (a) the nucleic acid molecule identified, (b) a fragment of the nucleic acid identified which includes a segment coding for a cancer associated antigen, (c) deletions, substitutions or additions to (a) or (b), and (d) degenerates of (a), (b), or (c); (iii) culturing said transfected host cells to express the transfected nucleic acid molecule, and; (iv) introducing an amount of said host cells or an extract thereof to the subject effective to increase an immune response against the cells of the subject associated with the condition. Preferably, the antigen is a human antigen and the subject is a human.

In one embodiment the method also includes the step of (a) identifying an MHC molecule which presents a portion of an expression product of the nucleic acid molecule, wherein the host cell expresses the same MHC molecule as identified in (a) and wherein the host cell presents an MHC binding portion of the expression product of the nucleic acid molecule.

In another embodiment the method also includes the step of treating the host cells to render them non-proliferative.

In yet another embodiment the immune response comprises a B-cell response or a T cell response. Preferably the response is a T-cell response which comprises generation of cytolytic T-cells specific for the host cells presenting the portion of the expression product of the nucleic acid molecule or cells of the subject expressing the human cancer associated antigen.

In another embodiment the nucleic acid molecule is a NA Group 3 molecule.

Another aspect of the invention is a method for treating or diagnosing or monitoring a subject having a condition characterized by expression of an abnormal amount of a protein encoded by a nucleic acid molecule that is a NA Group 1 molecule. The method includes the step of administering to the subject an antibody which specifically binds to the protein or a peptide derived therefrom, the antibody being coupled to a therapeutically useful agent, in an amount effective to treat the condition.

In one embodiment the antibody is a monoclonal antibody. Preferably the monoclonal antibody is a chimeric antibody or a humanized antibody.

In another aspect the invention is a method for treating a condition characterized by expression in a subject of abnormal amounts of a protein encoded by a nucleic acid molecule that is a NA Group 1 nucleic acid molecule. The method involves the step of administering to a subject at least one of the pharmaceutical compositions of the invention described above in an amount effective to prevent, delay the onset of, or inhibit the condition in the subject. In one embodiment the condition is cancer. In another embodiment the method includes the step of first identifying that the subject expresses in a tissue abnormal amounts of the protein.

The invention in another aspect is a method for treating a subject having a condition characterized by expression of abnormal amounts of a protein encoded by a nucleic acid molecule that is a NA Group 1 nucleic acid molecule. The method includes the steps of (i) identifying cells from the subject which express abnormal amounts of the protein; (ii) isolating a sample of the cells; (iii) cultivating the cells, and (iv) introducing the cells to the subject in an amount effective to provoke an immune response against the cells.

In one embodiment the cells express a protein selected from the group consisting of a PP Group 11 protein, a PP Group 12 protein, a PP Group 13 protein, PP Group 14 protein, a PP Group 15 protein and a PP Group 16 protein. In another embodiment the method includes the step of rendering the cells non-proliferative, prior to introducing them to the subject.

In another aspect the invention is a method for treating a pathological cell condition characterized by abnormal expression of a protein encoded by a nucleic acid molecule that is a NA Group 1 nucleic acid molecule. The method includes the step of administering to a subject in need thereof an effective amount of an agent which inhibits the expression or activity of the protein.

In one embodiment the agent is an inhibiting antibody which selectively binds to the protein and wherein the antibody is a monoclonal antibody, a chimeric antibody or a humanized antibody. In another embodiment the agent is an antisense nucleic acid molecule which selectively binds to the nucleic acid molecule which encodes the protein. In yet another important embodiment the nucleic acid molecule is a NA Group 3 nucleic acid molecule.

The invention includes in another aspect a composition of matter useful in stimulating an immune response to a plurality of a protein encoded by nucleic acid molecules that are NA Group 1 molecules. The composition is a plurality of peptides derived from the amino acid

sequences of the proteins, wherein the peptides bind to one or more MHC molecules presented on the surface of the cells which express an abnormal amount of the protein.

In one embodiment at least a portion of the plurality of peptides bind to MHC molecules and elicit a cytolytic response thereto. In another embodiment the composition of matter
5 includes an adjuvant. In another embodiment the adjuvant is a saponin, GM-CSF, or an interleukin.

According to another aspect the invention is an isolated antibody which selectively binds to a complex of: (I) a peptide derived from a protein encoded by a nucleic acid molecule that is a NA Group 1 molecule and (ii) and an MHC molecule to which binds the peptide to form the
10 complex, wherein the isolated antibody does not bind to (I) or (ii) alone.

In one embodiment the antibody is a monoclonal antibody, a chimeric antibody or a humanized antibody.

The invention also involves the use of the genes, gene products, fragments thereof, agents which bind thereto, and so on in the preparation of medicaments. A particular medicament is for
15 treating cancer and a more particular medicament is for treating breast cancer, lung cancer, renal cancer, colon cancer, prostate cancer or gastric cancer.

Detailed Description of the Invention

In the above summary and in the ensuing description, lists of sequences are provided.
20 The lists are meant to embrace each single sequence separately, two or more sequences together where they form a part of the same gene, any combination of two or more sequences which relate to different genes, including and up to the total number on the list, as if each and every combination were separately and specifically enumerated. Likewise, when mentioning fragment size, it is intended that a range embrace the smallest fragment mentioned to the full-length of the
25 sequence (-1 so that it is a fragment), each and every fragment length intended as if specifically enumerated. Thus, if a fragment could be between 10 and 15 in length, it is explicitly meant to mean 10, 11, 12, 13, 14, or 15 in length.

The summary and the claims mention antigen precursors and antigens. As used in the summary and in the claims, a precursor is substantially the full-length protein encoded by the
30 coding region of the isolated DNA and the antigen is a peptide which complexes with MHC, preferably HLA, and which participates in the immune response as part of that complex. Such antigens are typically 9 amino acids long, although this may vary slightly.

As used herein, a subject is a human, non-human primate, cow, horse, pig, sheep, goat, dog, cat or rodent. In all embodiments human cancer antigens and human subjects are preferred.

The present invention in one aspect involves the cloning of cDNAs encoding human cancer associated antigen precursors using autologous antisera of subjects having cancer. The sequences of the clones representing genes identified according to the methods described herein are presented in the attached Sequence Listing, and the predicted amino acid sequences of some clones also are presented. Of the foregoing, it can be seen that some of the clones are considered completely novel as no nucleotide or amino acid homologies to coding regions were found in the databases searched. Other clones are novel but have some homology to sequences deposited in databases (mainly EST sequences). Nevertheless, the entire gene sequence was not previously known. In some cases no function was suspected and in other cases, even if a function was suspected, it was not known that the gene was associated with cancer. In all cases, it was not known or suspected that the gene encoded a cancer antigen which reacted with antibody from autologous sera. Analysis of the clone sequences by comparison to nucleic acid and protein databases determined that still other of the clones surprisingly are closely related to other previously-cloned genes. The sequences of these related genes is also presented in the Sequence Listing. The nature of the foregoing genes as encoding antigens recognized by the immune systems of cancer patients is, of course, unexpected.

The invention thus involves in one aspect cancer associated antigen polypeptides, genes encoding those polypeptides, functional modifications and variants of the foregoing, useful fragments of the foregoing, as well as diagnostics and therapeutics relating thereto.

Homologs and alleles of the cancer associated antigen nucleic acids of the invention can be identified by conventional techniques. Thus, an aspect of the invention is those nucleic acid sequences which code for cancer associated antigen precursors. Because this application contains so many sequences, the following chart is provided to identify the various groups of sequences discussed in the claims and in the summary:

"Nucleic Acid Sequences"

NA Group 1. (a) nucleic acid molecules which hybridize under stringent conditions to a molecule consisting of a nucleic acid sequence selected from the group consisting of nucleic acid sequences among SEQ ID NOs 1-816 and which code for a cancer associated antigen precursor,

(b) deletions, additions and substitutions which code for a respective cancer associated antigen precursor,

(c) nucleic acid molecules that differ from the nucleic acid molecules of (a) or (b) in codon sequence due to the degeneracy of the genetic code, and

(d) complements of (a), (b) or (c).

NA Group 2. Fragments of NA Group 1, which codes for a polypeptide which, or a portion of which, binds an MHC molecule to form a complex recognized by an autologous antibody or lymphocyte.

NA Group 3. The subset of NA Group 1 where the nucleotide sequence is selected from the group consisting of:

(a) previously unknown human nucleic acids coding for a human cancer associated antigen precursor,

(b) deletions, additions and substitutions which code for a respective human cancer associated antigen precursor,

(c) nucleic acid molecules that differ from the nucleic acid molecules of (a) or (b) in codon sequence due to the degeneracy of the genetic code, and

(d) complements of (a), (b) or (c).

NA Group 4. Fragments of NA Group 3, which code for a polypeptide which, or a portion of which, binds to an MHC molecule to form a complex recognized by an autologous antibody or lymphocyte.

NA Group 5. A subset of NA Group 1, wherein the nucleic acid molecule codes for a human breast cancer associated antigen precursor.

NA Group 6. A subset of NA Group 1, wherein the nucleic acid molecule codes for a human colon cancer associated antigen precursor.

NA Group 7. A subset of NA Group 1, wherein the nucleic acid molecule codes for a human gastric cancer associated antigen precursor.

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NA Group 8. A subset of NA Group 1, wherein the nucleic acid molecule codes for a human lung cancer associated antigen precursor.

NA Group 9. A subset of NA Group 1, wherein the nucleic acid molecule codes for a human
5 renal cancer associated antigen precursor.

NA Group 10. A subset of NA Group 1, wherein the nucleic acid molecule codes for a human prostate cancer associated antigen precursor.

10 NA Group 11. A subset of NA Group 3, wherein the nucleic acid molecule codes for a human breast cancer associated antigen precursor.

NA Group 12. A subset of NA Group 3, wherein the nucleic acid molecule codes for a human colon cancer associated antigen precursor.

15 NA Group 13. A subset of NA Group 3, wherein the nucleic acid molecule codes for a human gastric cancer associated antigen precursor.

20 NA Group 14. A subset of NA Group 3, wherein the nucleic acid molecule codes for a human lung cancer associated antigen precursor.

NA Group 15. A subset of NA Group 3, wherein the nucleic acid molecule codes for a human renal cancer associated antigen precursor.

25 NA Group 16. A subset of NA Group 3, wherein the nucleic acid molecule codes for a human prostate cancer associated antigen precursor.

NA Group 17. A subset of NA Group 1, comprising human cancer associated antigens that react with allogenic cancer antisera.

30

Polypeptide Sequences

PP Group 1. Polypeptides encoded by NA Group 1.

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- PP Group 2. Polypeptides encoded by NA Group 2
- PP Group 3. Polypeptides encoded by NA Group 3.
- PP Group 4. Polypeptides encoded by NA Group 4.
- PP Group 5. Polypeptides encoded by NA Group 5.
- 5 PP Group 6. Polypeptides encoded by NA Group 6.
- PP Group 7. Polypeptides encoded by NA Group 7.
- PP Group 8. Polypeptides encoded by NA Group 8.
- PP Group 9. Polypeptides encoded by NA Group 9.
- PP Group 10. Polypeptides encoded by NA Group 10.
- 10 PP Group 11. Polypeptides encoded by NA Group 11.
- PP Group 12. Polypeptides encoded by NA Group 12.
- PP Group 13. Polypeptides encoded by NA Group 13.
- PP Group 14. Polypeptides encoded by NA Group 14.
- PP Group 15. Polypeptides encoded by NA Group 15.
- 15 PP Group 16. Polypeptides encoded by NA Group 16.
- PP Group 17. Polypeptides encoded by NA Group 17.

The term "stringent conditions" as used herein refers to parameters with which the art is familiar. Nucleic acid hybridization parameters may be found in references which compile such methods, e.g. *Molecular Cloning: A Laboratory Manual*, J. Sambrook, et al., eds., Second Edition, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York, 1989, or *Current Protocols in Molecular Biology*, F.M. Ausubel, et al., eds., John Wiley & Sons, Inc., New York. More specifically, stringent conditions, as used herein, refers, for example, to hybridization at 65°C in hybridization buffer (3.5 x SSC, 0.02% Ficoll, 0.02% polyvinyl pyrrolidone, 0.02% Bovine Serum Albumin, 2.5mM NaH₂PO₄(pH7), 0.5% SDS, 2mM EDTA). SSC is 0.15M sodium chloride/0.15M sodium citrate, pH7; SDS is sodium dodecyl sulphate; and EDTA is ethylenediaminetetracetic acid. After hybridization, the membrane upon which the DNA is transferred is washed, for example, in 2 x SSC at room temperature and then at 0.1 - 0.5 x SSC/0.1 x SDS at temperatures up to 68°C.

There are other conditions, reagents, and so forth which can be used, which result in a similar degree of stringency. The skilled artisan will be familiar with such conditions, and thus they are not given here. It will be understood, however, that the skilled artisan will be able to

manipulate the conditions in a manner to permit the clear identification of homologs and alleles of cancer associated antigen nucleic acids of the invention (e.g., by using lower stringency conditions). The skilled artisan also is familiar with the methodology for screening cells and libraries for expression of such molecules which then are routinely isolated, followed by
5 isolation of the pertinent nucleic acid molecule and sequencing.

In general homologs and alleles typically will share at least 40% nucleotide identity and/or at least 50% amino acid identity to the sequences of breast cancer associated antigen nucleic acid and polypeptides, respectively, in some instances will share at least 50% nucleotide identity and/or at least 65% amino acid identity and in still other instances will share at least 60%
10 nucleotide identity and/or at least 75% amino acid identity. The homology can be calculated using various, publicly available software tools developed by NCBI (Bethesda, Maryland) that can be obtained through the internet (<ftp://ncbi.nlm.nih.gov/pub/>). Exemplary tools include the BLAST system available at <http://www.ncbi.nlm.nih.gov>. Pairwise and ClustalW alignments (BLOSUM30 matrix setting) as well as Kyte-Doolittle hydropathic analysis can be obtained
15 using the MacVector sequence analysis software (Oxford Molecular Group). Watson-Crick complements of the foregoing nucleic acids also are embraced by the invention.

In screening for cancer associated antigen genes, a Southern blot may be performed using the foregoing conditions, together with a radioactive probe. After washing the membrane to which the DNA is finally transferred, the membrane can be placed against X-ray film to detect
20 the radioactive signal. In screening for the expression of cancer associated antigen nucleic acids, Northern blot hybridizations using the foregoing conditions (see also the Examples) can be performed on samples taken from breast cancer patients or subjects suspected of having a condition characterized by expression of breast cancer associated antigen genes. Amplification protocols such as polymerase chain reaction using primers which hybridize to the sequences
25 presented also can be used for detection of the cancer associated antigen genes or expression thereof.

The breast cancer associated genes correspond to SEQ ID NOs. 1-40 and 66. The preferred breast cancer associated antigens for the methods of diagnosis disclosed herein are those set forth in SEQ ID NOs:[31, 33 and 34], which were found to react with allogeneic breast
30 cancer antisera. Encoded polypeptides (e.g., proteins), peptides and antisera thereto are also preferred for diagnosis.

The colon cancer associated genes correspond to SEQ ID Nos. 544-586, even numbers

only. The preferred colon cancer associated antigens for the methods of diagnosis disclosed herein are those, which were found to react with allogeneic colon cancer antisera. Encoded polypeptides (e.g., proteins), peptides and antisera thereto are also preferred for diagnosis.

The gastric cancer associated genes correspond to SEQ ID NOs 176-436 and 588-674.

5 The preferred gastric cancer associated antigens for the methods of diagnosis disclosed herein are those, which were found to react with allogeneic gastric cancer antisera. Encoded polypeptides (e.g., proteins), peptides and antisera thereto are also preferred for diagnosis.

The renal cancer associated genes correspond to SEQ ID Nos. 89-169, odd numbers only, and 170, 172, and 174. The preferred renal cancer associated antigens for the methods of
10 diagnosis disclosed herein are those, which were found to react with allogeneic renal cancer antisera. Encoded polypeptides (e.g., proteins), peptides and antisera thereto are also preferred for diagnosis.

The lung cancer associated genes correspond to SEQ ID Nos. 689, 691, 692, 694, 696-707, 709, 711, and 712. The preferred lung cancer associated antigens for the methods of
15 diagnosis disclosed herein are those, which were found to react with allogeneic lung cancer antisera. Encoded polypeptides (e.g., proteins), peptides and antisera thereto are also preferred for diagnosis.

The prostate cancer associated genes correspond to SEQ ID NOs 437-543. The preferred prostate cancer associated antigens for the methods of diagnosis disclosed herein are those,
20 which were found to react with allogeneic prostate cancer antisera. Encoded polypeptides (e.g., proteins), peptides and antisera thereto are also preferred for diagnosis.

The invention also includes degenerate nucleic acids which include alternative codons to those present in the native materials. For example, serine residues are encoded by the codons TCA, AGT, TCC, TCG, TCT and AGC. Each of the six codons is equivalent for the purposes of
25 encoding a serine residue. Thus, it will be apparent to one of ordinary skill in the art that any of the serine-encoding nucleotide triplets may be employed to direct the protein synthesis apparatus, *in vitro* or *in vivo*, to incorporate a serine residue into an elongating breast cancer associated antigen polypeptide. Similarly, nucleotide sequence triplets which encode other amino acid residues include, but are not limited to: CCA, CCC, CCG and CCT (proline codons); CGA, CGC, CGG, CGT, AGA and AGG (arginine codons); ACA, ACC, ACG and ACT (threonine
30 codons); AAC and AAT (asparagine codons); and ATA, ATC and ATT (isoleucine codons). Other amino acid residues may be encoded similarly by multiple nucleotide sequences. Thus,

the invention embraces degenerate nucleic acids that differ from the biologically isolated nucleic acids in codon sequence due to the degeneracy of the genetic code.

The invention also provides isolated unique fragments of cancer associated antigen nucleic acid sequences or complements thereof. A unique fragment is one that is a 'signature' for the larger nucleic acid. It, for example, is long enough to assure that its precise sequence is not found in molecules within the human genome outside of the cancer associated antigen nucleic acids defined above (and human alleles). Those of ordinary skill in the art may apply no more than routine procedures to determine if a fragment is unique within the human genome. Unique fragments, however, exclude fragments completely composed of the nucleotide sequences of any of GenBank accession numbers listed in Table 1 or other previously published sequences as of the filing date of the priority documents for sequences listed in a respective priority document or the filing date of this application for sequences listed for the first time in this application which overlap the sequences of the invention.

A fragment which is completely composed of the sequence described in the foregoing GenBank deposits is one which does not include any of the nucleotides unique to the sequences of the invention. Thus, a unique fragment must contain a nucleotide sequence other than the exact sequence of those in GenBank or fragments thereof. The difference may be an addition, deletion or substitution with respect to the GenBank sequence or it may be a sequence wholly separate from the GenBank sequence.

Unique fragments can be used as probes in Southern and Northern blot assays to identify such nucleic acids, or can be used in amplification assays such as those employing PCR. As known to those skilled in the art, large probes such as 200, 250, 300 or more nucleotides are preferred for certain uses such as Southern and Northern blots, while smaller fragments will be preferred for uses such as PCR. Unique fragments also can be used to produce fusion proteins for generating antibodies or determining binding of the polypeptide fragments, or for generating immunoassay components. Likewise, unique fragments can be employed to produce nonfused fragments of the cancer associated antigen polypeptides, useful, for example, in the preparation of antibodies, and in immunoassays. Unique fragments further can be used as antisense molecules to inhibit the expression of cancer associated antigen nucleic acids and polypeptides, particularly for therapeutic purposes as described in greater detail below.

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As will be recognized by those skilled in the art, the size of the unique fragment will depend upon its conservancy in the genetic code. Thus, some regions of cancer associated antigen sequences and complements thereof will require longer segments to be unique while others will require only short segments, typically between 12 and 32 nucleotides (e.g. 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31 and 32 or more bases long, up to the entire length of the disclosed sequence. As mentioned above, this disclosure intends to embrace each and every fragment of each sequence, beginning at the first nucleotide, the second nucleotide and so on, up to 8 nucleotides short of the end, and ending anywhere from nucleotide number 8, 9, 10 and so on for each sequence, up to the very last nucleotide, (provided the sequence is unique as described above).

Virtually any segment of the polypeptide coding region of novel cancer associated antigen nucleic acids, or complements thereof, that is 18 or more nucleotides in length will be unique. Those skilled in the art are well versed in methods for selecting such sequences, typically on the basis of the ability of the unique fragment to selectively distinguish the sequence of interest from other sequences in the human genome of the fragment to those on known databases typically is all that is necessary, although *in vitro* confirmatory hybridization and sequencing analysis may be performed. Especially preferred include nucleic acids encoding a series of epitopes, known as "polytopes". The epitopes can be arranged in sequential or overlapping fashion (*see, e.g.,* Thomson et al., *Proc. Natl. Acad. Sci. USA* 92:5845-5849, 1995; Gilbert et al., *Nature Biotechnol.* 15:1280-1284, 1997), with or without the natural flanking sequences, and can be separated by unrelated linker sequences if desired. The polytope is processed to generated individual epitopes which are recognized by the immune system for generation of immune responses.

Thus, for example, peptides derived from a polypeptide having an amino acid sequence encoded by one of the nucleic acid disclosed herein, and which are presented by MHC molecules and recognized by CTL or T helper lymphocytes, can be combined with peptides from one or more other cancer associated antigens (e.g. by preparation of hybrid nucleic acids or polypeptides) to form "polytopes". The two or more peptides (or nucleic acids encoding the peptides) can be selected from those described herein, or they can include one or more peptides of previously known cancer associated antigens. Exemplary cancer associated peptide antigens that can be administered to induce or enhance an immune response are derived from tumor associated genes and encoded proteins including MAGE-1, MAGE-2, MAGE-3, MAGE-4, MAGE-5, MAGE-6, MAGE-7,

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MAGE-8, MAGE-9, MAGE-10, MAGE-11, GAGE-1, GAGE-2, GAGE-3, GAGE-4, GAGE-5, GAGE-6, BAGE-1, RAGE-1, LB33/MUM-1, PRAME, NAG, MAGE-Xp2, MAGE-Xp3, MAGE-Xp4, tyrosinase, brain glycogen phosphorylase, Melan-A, and MAGE-C1. See, for example, PCT application publication no. WO96/10577. Other examples will be known to one of ordinary skill in the art (for example, see Coulie, *Stem Cells* 13:393-403, 1995), and can be used in the invention in a like manner as those disclosed herein. One of ordinary skill in the art can prepare polypeptides comprising one or more peptides and one or more of the foregoing cancer associated peptides, or nucleic acids encoding such polypeptides, according to standard procedures of molecular biology.

Thus polytopes are groups of two or more potentially immunogenic or immune response stimulating peptides which can be joined together in various arrangements (e.g. concatenated, overlapping). The polytope (or nucleic acid encoding the polytope) can be administered in a standard immunization protocol, e.g. to animals, to test the effectiveness of the polytope in stimulating, enhancing and/or provoking an immune response.

The peptides can be joined together directly or via the use of flanking sequences to form polytopes, and the use of polytopes as vaccines is well known in the art (see, e.g., Thomson et al., *Proc. Acad. Natl. Acad. Sci USA* 92(13):5845-5849, 1995; Gilbert et al., *Nature Biotechnol.* 15(12):1280-1284, 1997; Thomson et al., *J. Immunol.* 157(2):822-826, 1996; Tam et al., *J. Exp. Med.* 171(1):299-306, 1990). for example, Tam showed that polytopes consisting of both MHC class I and class II binding epitopes successfully generated antibody and protective immunity in a mouse model. Tam also demonstrated that polytopes comprising "strings" of epitopes are processed to yield individual epitopes which are presented by MHC molecules and recognized by CTLs. Thus polytopes containing various numbers and combinations of epitopes can be prepared and tested for recognition by CTLs and for efficacy in increasing an immune response.

It is known that tumors express a set of tumor antigens, of which only certain subsets may be expressed in the tumor of any given patient (for examples of this, see the Examples below). Polytopes can be prepared which correspond to the different combination of epitopes representing the subset of tumor rejection antigens expressed in a particular patient. Polytopes also can be prepared to reflect a broader spectrum of tumor rejection antigens known to be expressed by a tumor type. Polytopes can be introduced to a patient in need of such treatment as polypeptide structures, or via the use of nucleic acid delivery systems known in the art (see, e.g., Allsopp et al., *Eur. J.*

Immunol. 26(8):1951-1959, 1996). Adenovirus, pox virus, Ty-virus like particles, adeno-associated virus, plasmids, bacteria, etc. can be used in such delivery. One can test the polytope delivery systems in mouse models to determine efficacy of the delivery system. The systems also can be tested in human clinical trials.

5 In instances in which a human HLA class I molecule presents tumor rejection antigens derived from cancer associated nucleic acids, the expression vector may also include a nucleic acid sequence coding for the HLA molecule that presents any particular tumor rejection antigen derived from these nucleic acids and polypeptides. Alternatively, the nucleic acid sequence coding for such a HLA molecule can be contained within a separate expression vector. In a situation where the
10 vector contains both coding sequences, the single vector can be used to transfect a cell which does not normally express either one. Where the coding sequences for a cancer associated antigen precursor and the HLA molecule which presents it are contained on separate expression vectors, the expression vectors can be cotransfected. The cancer associated antigen precursor coding sequence may be used alone, when, e.g. the host cell already expresses a HLA molecule which presents a
15 cancer associated antigen derived from precursor molecules. Of course, there is no limit on the particular host cell which can be used. As the vectors which contain the two coding sequences may be used in any antigen-presenting cells if desired, and the gene for cancer associated antigen precursor can be used in host cells which do not express a HLA molecule which presents a cancer associated antigen. Further, cell-free transcription systems may be used in lieu of cells.

20 As mentioned above, the invention embraces antisense oligonucleotides that selectively bind to a nucleic acid molecule encoding a cancer associated antigen polypeptide, to reduce the expression of cancer associated antigens. This is desirable in virtually any medical condition wherein a reduction of expression of cancer associated antigens is desirable, e.g., in the treatment of cancer. This is also useful for *in vitro* or *in vivo* testing of the effects of a reduction of expression of
25 one or more cancer associated antigens.

As used herein, the term "antisense oligonucleotide" or "antisense" describes an oligonucleotide that is an oligoribonucleotide, oligodeoxyribonucleotide, modified oligoribonucleotide, or modified oligodeoxyribonucleotide which hybridizes under physiological conditions to DNA comprising a particular gene or to an mRNA transcript of that gene and, thereby,
30 inhibits the transcription of that gene and/or the translation of that mRNA. The antisense molecules

are designed so as to interfere with transcription or translation of a target gene upon hybridization with the target gene or transcript. Those skilled in the art will recognize that the exact length of the antisense oligonucleotide and its degree of complementarity with its target will depend upon the specific target selected, including the sequence of the target and the particular bases which comprise that sequence. It is preferred that the antisense oligonucleotide be constructed and arranged so as to bind selectively with the target under physiological conditions, i.e., to hybridize substantially more to the target sequence than to any other sequence in the target cell under physiological conditions. Based upon the sequences of nucleic acids encoding breast cancer associated antigen, or upon allelic or homologous genomic and/or cDNA sequences, one of skill in the art can easily choose and synthesize any of a number of appropriate antisense molecules for use in accordance with the present invention. In order to be sufficiently selective and potent for inhibition, such antisense oligonucleotides should comprise at least 10 and, more preferably, at least 15 consecutive bases which are complementary to the target, although in certain cases modified oligonucleotides as short as 7 bases in length have been used successfully as antisense oligonucleotides (Wagner et al., *Nature Biotechnol.* 14:840-844, 1996). Most preferably, the antisense oligonucleotides comprise a complementary sequence of 20-30 bases. Although oligonucleotides may be chosen which are antisense to any region of the gene or mRNA transcripts, in preferred embodiments the antisense oligonucleotides correspond to N-terminal or 5' upstream sites such as translation initiation, transcription initiation or promoter sites. In addition, 3'-untranslated regions may be targeted. Targeting to mRNA splicing sites has also been used in the art but may be less preferred if alternative mRNA splicing occurs. In addition, the antisense is targeted, preferably, to sites in which mRNA secondary structure is not expected (see, e.g., Sainio et al., *Cell Mol. Neurobiol.* 14(5):439-457, 1994) and at which proteins are not expected to bind. Finally, although the listed sequences are cDNA sequences, one of ordinary skill in the art may easily derive the genomic DNA corresponding to the cDNA of a cancer associated antigen. Thus, the present invention also provides for antisense oligonucleotides which are complementary to the genomic DNA corresponding to nucleic acids encoding breast cancer associated antigens. Similarly, antisense to allelic or homologous cDNAs and genomic DNAs are enabled without undue experimentation.

In one set of embodiments, the antisense oligonucleotides of the invention may be composed of "natural" deoxyribonucleotides, ribonucleotides, or any combination thereof. That is, the 5' end

of one native nucleotide and the 3' end of another native nucleotide may be covalently linked, as in natural systems, via a phosphodiester internucleoside linkage. These oligonucleotides may be prepared by art recognized methods which may be carried out manually or by an automated synthesizer. They also may be produced recombinantly by vectors.

5 In preferred embodiments, however, the antisense oligonucleotides of the invention also may include "modified" oligonucleotides. That is, the oligonucleotides may be modified in a number of ways which do not prevent them from hybridizing to their target but which enhance their stability or targeting or which otherwise enhance their therapeutic effectiveness.

The term "modified oligonucleotide" as used herein describes an oligonucleotide in which
10 (1) at least two of its nucleotides are covalently linked via a synthetic internucleoside linkage (i.e., a linkage other than a phosphodiester linkage between the 5' end of one nucleotide and the 3' end of another nucleotide) and/or (2) a chemical group not normally associated with nucleic acids has been covalently attached to the oligonucleotide. Preferred synthetic internucleoside linkages are phosphorothioates, alkylphosphonates, phosphorodithioates, phosphate esters,
15 alkylphosphonothioates, phosphoramidates, carbamates, carbonates, phosphate triesters, acetamides, carboxymethyl esters and peptides.

The term "modified oligonucleotide" also encompasses oligonucleotides with a covalently modified base and/or sugar. For example, modified oligonucleotides include oligonucleotides having backbone sugars which are covalently attached to low molecular weight organic groups other
20 than a hydroxyl group at the 3' position and other than a phosphate group at the 5' position. Thus modified oligonucleotides may include a 2'-O-alkylated ribose group. In addition, modified oligonucleotides may include sugars such as arabinose instead of ribose. The present invention, thus, contemplates pharmaceutical preparations containing modified antisense molecules that are complementary to and hybridizable with, under physiological conditions, nucleic acids encoding
25 breast cancer associated antigen polypeptides, together with pharmaceutically acceptable carriers.

Antisense oligonucleotides may be administered as part of a pharmaceutical composition. Such a pharmaceutical composition may include the antisense oligonucleotides in combination with any standard physiologically and/or pharmaceutically acceptable carriers which are known in the art. The compositions should be sterile and contain a therapeutically effective amount of the antisense
30 oligonucleotides in a unit of weight or volume suitable for administration to a patient. The term

“pharmaceutically acceptable” means a non-toxic material that does not interfere with the effectiveness of the biological activity of the active ingredients. The term “physiologically acceptable” refers to a non-toxic material that is compatible with a biological system such as a cell, cell culture, tissue, or organism. The characteristics of the carrier will depend on the route of administration. Physiologically and pharmaceutically acceptable carriers include diluents, fillers, salts, buffers, stabilizers, solubilizers, and other materials which are well known in the art, as further described below.

As used herein, a “vector” may be any of a number of nucleic acids into which a desired sequence may be inserted by restriction and ligation for transport between different genetic environments or for expression in a host cell. Vectors are typically composed of DNA although RNA vectors are also available. Vectors include, but are not limited to, plasmids, phagemids and virus genomes. A cloning vector is one which is able to replicate in a host cell, and which is further characterized by one or more endonuclease restriction sites at which the vector may be cut in a determinable fashion and into which a desired DNA sequence may be ligated such that the new recombinant vector retains its ability to replicate in the host cell. In the case of plasmids, replication of the desired sequence may occur many times as the plasmid increases in copy number within the host bacterium or just a single time per host before the host reproduces by mitosis. In the case of phage, replication may occur actively during a lytic phase or passively during a lysogenic phase. An expression vector is one into which a desired DNA sequence may be inserted by restriction and ligation such that it is operably joined to regulatory sequences and may be expressed as an RNA transcript. Vectors may further contain one or more marker sequences suitable for use in the identification of cells which have or have not been transformed or transfected with the vector. Markers include, for example, genes encoding proteins which increase or decrease either resistance or sensitivity to antibiotics or other compounds, genes which encode enzymes whose activities are detectable by standard assays known in the art (e.g., β -galactosidase or alkaline phosphatase), and genes which visibly affect the phenotype of transformed or transfected cells, hosts, colonies or plaques (e.g., green fluorescent protein). Preferred vectors are those capable of autonomous replication and expression of the structural gene products present in the DNA segments to which they are operably joined.

As used herein, a coding sequence and regulatory sequences are said to be “operably” joined

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when they are covalently linked in such a way as to place the expression or transcription of the coding sequence under the influence or control of the regulatory sequences. If it is desired that the coding sequences be translated into a functional protein, two DNA sequences are said to be operably joined if induction of a promoter in the 5' regulatory sequences results in the transcription of the coding sequence and if the nature of the linkage between the two DNA sequences does not (1) result in the introduction of a frame-shift mutation, (2) interfere with the ability of the promoter region to direct the transcription of the coding sequences, or (3) interfere with the ability of the corresponding RNA transcript to be translated into a protein. Thus, a promoter region would be operably joined to a coding sequence if the promoter region were capable of effecting transcription of that DNA sequence such that the resulting transcript might be translated into the desired protein or polypeptide.

The precise nature of the regulatory sequences needed for gene expression may vary between species or cell types, but shall in general include, as necessary, 5' non-transcribed and 5' non-translated sequences involved with the initiation of transcription and translation respectively, such as a TATA box, capping sequence, CAAT sequence, and the like. Especially, such 5' non-transcribed regulatory sequences will include a promoter region which includes a promoter sequence for transcriptional control of the operably joined gene. Regulatory sequences may also include enhancer sequences or upstream activator sequences as desired. The vectors of the invention may optionally include 5' leader or signal sequences. The choice and design of an appropriate vector is within the ability and discretion of one of ordinary skill in the art.

Expression vectors containing all the necessary elements for expression are commercially available and known to those skilled in the art. See, e.g., Sambrook et al., *Molecular Cloning: A Laboratory Manual*, Second Edition, Cold Spring Harbor Laboratory Press, 1989. Cells are genetically engineered by the introduction into the cells of heterologous DNA (RNA) encoding a breast cancer associated antigen polypeptide or fragment or variant thereof. That heterologous DNA (RNA) is placed under operable control of transcriptional elements to permit the expression of the heterologous DNA in the host cell.

Preferred systems for mRNA expression in mammalian cells are those such as pRc/CMV (available from Invitrogen, Carlsbad, CA) that contain a selectable marker such as a gene that confers G418 resistance (which facilitates the selection of stably transfected cell lines) and the

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human cytomegalovirus (CMV) enhancer-promoter sequences. Additionally, suitable for expression in primate or canine cell lines is the pCEP4 vector (Invitrogen), which contains an Epstein Barr Virus (EBV) origin of replication, facilitating the maintenance of plasmid as a multicopy extrachromosomal element. Another expression vector is the pEF-BOS plasmid containing the promoter of polypeptide Elongation Factor 1 α , which stimulates efficiently transcription *in vitro*. The plasmid is described by Mishizuma and Nagata (*Nuc. Acids Res.* 18:5322, 1990), and its use in transfection experiments is disclosed by, for example, Demoulin (*Mol. Cell. Biol.* 16:4710-4716, 1996). Still another preferred expression vector is an adenovirus, described by Stratford-Perricaudet, which is defective for E1 and E3 proteins (*J. Clin. Invest.* 90:626-630, 1992). The use of the adenovirus as an Adeno.P1A recombinant for the expression of an antigen is disclosed by Warnier et al., in intradermal injection in mice for immunization against P1A (*Int. J. Cancer*, 67:303-310, 1996). Additional vectors for delivery of nucleic acid are provided below.

The invention also embraces so-called expression kits, which allow the artisan to prepare a desired expression vector or vectors. Such expression kits include at least separate portions of a vector and one or more of the previously discussed breast cancer associated antigen nucleic acid molecules. Other components may be added, as desired, as long as the previously mentioned nucleic acid molecules, which are required, are included. The invention also includes kits for amplification of a breast cancer associated antigen nucleic acid, including at least one pair of amplification primers which hybridize to a breast cancer associated antigen nucleic acid. The primers preferably are 12-32 nucleotides in length and are non-overlapping to prevent formation of "primer-dimers". One of the primers will hybridize to one strand of the breast cancer associated antigen nucleic acid and the second primer will hybridize to the complementary strand of the breast cancer associated antigen nucleic acid, in an arrangement which permits amplification of the breast cancer associated antigen nucleic acid. Selection of appropriate primer pairs is standard in the art. For example, the selection can be made with assistance of a computer program designed for such a purpose, optionally followed by testing the primers for amplification specificity and efficiency.

The invention also permits the construction of cancer associated antigen gene "knock-outs" in cells and in animals, providing materials for studying certain aspects of cancer and immune system responses to cancer.

The invention also provides isolated polypeptides (including whole proteins and partial

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proteins) encoded by the foregoing cancer associated antigen nucleic acids. Such polypeptides are useful, for example, alone or as fusion proteins to generate antibodies, as components of an immunoassay or diagnostic assay or as therapeutics. Cancer associated antigen polypeptides can be isolated from biological samples including tissue or cell homogenates, and can also be expressed
5 recombinantly in a variety of prokaryotic and eukaryotic expression systems by constructing an expression vector appropriate to the expression system, introducing the expression vector into the expression system, and isolating the recombinantly expressed protein. Short polypeptides, including antigenic peptides (such as are presented by MHC molecules on the surface of a cell for immune recognition) also can be synthesized chemically using well-established methods of peptide synthesis.

10 A unique fragment of a cancer associated antigen polypeptide, in general, has the features and characteristics of unique fragments as discussed above in connection with nucleic acids. As will be recognized by those skilled in the art, the size of the unique fragment will depend upon factors such as whether the fragment constitutes a portion of a conserved protein domain. Thus, some regions of breast cancer associated antigens will require longer segments to be unique while others
15 will require only short segments, typically between 5 and 12 amino acids (e.g. 5, 6, 7, 8, 9, 10, 11 or 12 or more, including each integer up to the full length, amino acids long).

Unique fragments of a polypeptide preferably are those fragments which retain a distinct functional capability of the polypeptide. Functional capabilities which can be retained in a unique fragment of a polypeptide include interaction with antibodies, interaction with other polypeptides or
20 fragments thereof, selective binding of nucleic acids or proteins, and enzymatic activity. One important activity is the ability to act as a signature for identifying the polypeptide. Another is the ability to complex with HLA and to provoke in a human an immune response. Those skilled in the art are well versed in methods for selecting unique amino acid sequences, typically on the basis of the ability of the unique fragment to selectively distinguish the sequence of interest from non-family
25 members. A comparison of the sequence of the fragment to those on known databases typically is all that is necessary.

The invention embraces variants of the cancer associated antigen polypeptides described above. As used herein, a "variant" of a cancer associated antigen polypeptide is a polypeptide which contains one or more modifications to the primary amino acid sequence of a cancer associated
30 antigen polypeptide. Modifications which create a cancer associated antigen variant can be made to

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a cancer associated antigen polypeptide 1) to reduce or eliminate an activity of a cancer associated antigen polypeptide; 2) to enhance a property of a cancer associated antigen polypeptide, such as protein stability in an expression system or the stability of protein-protein binding; 3) to provide a novel activity or property to a cancer associated antigen polypeptide, such as addition of an antigenic epitope or addition of a detectable moiety; or 4) to provide equivalent or better binding to an HLA molecule. Modifications to a cancer associated antigen polypeptide are typically made to the nucleic acid which encodes the cancer associated antigen polypeptide, and can include deletions, point mutations, truncations, amino acid substitutions and additions of amino acids or non-amino acid moieties. Alternatively, modifications can be made directly to the polypeptide, such as by cleavage, addition of a linker molecule, addition of a detectable moiety, such as biotin, addition of a fatty acid, and the like. Modifications also embrace fusion proteins comprising all or part of the cancer associated antigen amino acid sequence. One of skill in the art will be familiar with methods for predicting the effect on protein conformation of a change in protein sequence, and can thus "design" a variant cancer associated antigen polypeptide according to known methods. One example of such a method is described by Dahiyat and Mayo in *Science* 278:82-87, 1997, whereby proteins can be designed *de novo*. The method can be applied to a known protein to vary a only a portion of the polypeptide sequence. By applying the computational methods of Dahiyat and Mayo, specific variants of a cancer associated antigen polypeptide can be proposed and tested to determine whether the variant retains a desired conformation.

In general, variants include cancer associated antigen polypeptides which are modified specifically to alter a feature of the polypeptide unrelated to its desired physiological activity. For example, cysteine residues can be substituted or deleted to prevent unwanted disulfide linkages. Similarly, certain amino acids can be changed to enhance expression of a breast cancer associated antigen polypeptide by eliminating proteolysis by proteases in an expression system (e.g., dibasic amino acid residues in yeast expression systems in which KEX2 protease activity is present).

Mutations of a nucleic acid which encode a cancer associated antigen polypeptide preferably preserve the amino acid reading frame of the coding sequence, and preferably do not create regions in the nucleic acid which are likely to hybridize to form secondary structures, such a hairpins or loops, which can be deleterious to expression of the variant polypeptide.

Mutations can be made by selecting an amino acid substitution, or by random mutagenesis of

a selected site in a nucleic acid which encodes the polypeptide. Variant polypeptides are then expressed and tested for one or more activities to determine which mutation provides a variant polypeptide with the desired properties. Further mutations can be made to variants (or to non-variant cancer associated antigen polypeptides) which are silent as to the amino acid sequence of the polypeptide, but which provide preferred codons for translation in a particular host. The preferred codons for translation of a nucleic acid in, e.g., *E. coli*, are well known to those of ordinary skill in the art. Still other mutations can be made to the noncoding sequences of a cancer associated antigen gene or cDNA clone to enhance expression of the polypeptide. The activity of variants of cancer associated antigen polypeptides can be tested by cloning the gene encoding the variant cancer associated antigen polypeptide into a bacterial or mammalian expression vector, introducing the vector into an appropriate host cell, expressing the variant cancer associated antigen polypeptide, and testing for a functional capability of the cancer associated antigen polypeptides as disclosed herein. For example, the variant cancer associated antigen polypeptide can be tested for reaction with autologous or allogeneic sera as disclosed in the Examples. Preparation of other variant polypeptides may favor testing of other activities, as will be known to one of ordinary skill in the art.

The skilled artisan will also realize that conservative amino acid substitutions may be made in cancer associated antigen polypeptides to provide functionally equivalent variants of the foregoing polypeptides, i.e., the variants retain the functional capabilities of the cancer associated antigen polypeptides. As used herein, a "conservative amino acid substitution" refers to an amino acid substitution which does not alter the relative charge or size characteristics of the protein in which the amino acid substitution is made. Variants can be prepared according to methods for altering polypeptide sequence known to one of ordinary skill in the art such as are found in references which compile such methods, e.g. *Molecular Cloning: A Laboratory Manual*, J. Sambrook, et al., eds., Second Edition, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York, 1989, or *Current Protocols in Molecular Biology*, F.M. Ausubel, et al., eds., John Wiley & Sons, Inc., New York. Exemplary functionally equivalent variants of the cancer associated antigen polypeptides include conservative amino acid substitutions of in the amino acid sequences of SEQ ID proteins disclosed herein. Conservative substitutions of amino acids include substitutions made amongst amino acids within the following groups: (a) M, I, L, V; (b) F, Y, W; (c) K, R, H; (d) A, G; (e) S, T; (f) Q, N; and (g) E, D.

For example, upon determining that a peptide derived from a cancer associated antigen polypeptide is presented by an MHC molecule and recognized by CTLs (e.g., as described in the Examples), one can make conservative amino acid substitutions to the amino acid sequence of the peptide, particularly at residues which are thought not to be direct contact points with the MHC molecule. For example, methods for identifying functional variants of HLA class II binding peptides are provided in a published PCT application of Strominger and Wucherpfennig (PCT/US96/03182). Peptides bearing one or more amino acid substitutions also can be tested for concordance with known HLA/MHC motifs prior to synthesis using, e.g. the computer program described by D'Amaro and Drijfhout (D'Amaro et al., *Human Immunol.* 43:13-18, 1995; Drijfhout et al., *Human Immunol.* 43:1-12, 1995). The substituted peptides can then be tested for binding to the MHC molecule and recognition by CTLs when bound to MHC. These variants can be tested for improved stability and are useful, *inter alia*, in vaccine compositions.

Conservative amino-acid substitutions in the amino acid sequence of cancer associated antigen polypeptides to produce functionally equivalent variants of cancer associated antigen polypeptides typically are made by alteration of a nucleic acid encoding a cancer associated antigen polypeptide. Such substitutions can be made by a variety of methods known to one of ordinary skill in the art. For example, amino acid substitutions may be made by PCR-directed mutation, site-directed mutagenesis according to the method of Kunkel (Kunkel, *Proc. Nat. Acad. Sci. U.S.A.* 82: 488-492, 1985), or by chemical synthesis of a gene encoding a cancer associated antigen polypeptide. Where amino acid substitutions are made to a small unique fragment of a cancer associated antigen polypeptide, such as an antigenic epitope recognized by autologous or allogeneic sera or cytolytic T lymphocytes, the substitutions can be made by directly synthesizing the peptide. The activity of functionally equivalent fragments of cancer associated antigen polypeptides can be tested by cloning the gene encoding the altered cancer associated antigen polypeptide into a bacterial or mammalian expression vector, introducing the vector into an appropriate host cell, expressing the altered cancer associated antigen polypeptide, and testing for a functional capability of the cancer associated antigen polypeptides as disclosed herein. Peptides which are chemically synthesized can be tested directly for function, e.g., for binding to antisera recognizing associated antigens.

The invention as described herein has a number of uses, some of which are described elsewhere herein. First, the invention permits isolation of the cancer associated antigen protein

molecules. A variety of methodologies well-known to the skilled practitioner can be utilized to obtain isolated cancer associated antigen molecules. The polypeptide may be purified from cells which naturally produce the polypeptide by chromatographic means or immunological recognition. Alternatively, an expression vector may be introduced into cells to cause production of the polypeptide. In another method, mRNA transcripts may be microinjected or otherwise introduced into cells to cause production of the encoded polypeptide. Translation of mRNA in cell-free extracts such as the reticulocyte lysate system also may be used to produce polypeptide. Those skilled in the art also can readily follow known methods for isolating cancer associated antigen polypeptides. These include, but are not limited to, immunochromatography, HPLC, size-exclusion chromatography, ion-exchange chromatography and immune-affinity chromatography.

The isolation and identification of cancer associated antigen genes also makes it possible for the artisan to diagnose a disorder characterized by expression of cancer associated antigens. These methods involve determining expression of one or more cancer associated antigen nucleic acids, and/or encoded cancer associated antigen polypeptides and/or peptides derived therefrom. In the former situation, such determinations can be carried out via any standard nucleic acid determination assay, including the polymerase chain reaction, or assaying with labeled hybridization probes. In the latter situation, such determinations can be carried out by screening patient antisera for recognition of the polypeptide.

The invention also makes it possible isolate proteins which bind to cancer associated antigens as disclosed herein, including antibodies and cellular binding partners of the cancer associated antigens. Additional uses are described further herein.

The invention also provides, in certain embodiments, "dominant negative" polypeptides derived from cancer associated antigen polypeptides. A dominant negative polypeptide is an inactive variant of a protein, which, by interacting with the cellular machinery, displaces an active protein from its interaction with the cellular machinery or competes with the active protein, thereby reducing the effect of the active protein. For example, a dominant negative receptor which binds a ligand but does not transmit a signal in response to binding of the ligand can reduce the biological effect of expression of the ligand. Likewise, a dominant negative catalytically-inactive kinase which interacts normally with target proteins but does not phosphorylate the target proteins can reduce phosphorylation of the target proteins in response to a cellular signal. Similarly, a dominant

negative transcription factor which binds to a promoter site in the control region of a gene but does not increase gene transcription can reduce the effect of a normal transcription factor by occupying promoter binding sites without increasing transcription.

The end result of the expression of a dominant negative polypeptide in a cell is a reduction in function of active proteins. One of ordinary skill in the art can assess the potential for a dominant negative variant of a protein, and using standard mutagenesis techniques to create one or more dominant negative variant polypeptides. For example, given the teachings contained herein of cancer associated antigens, especially those which are similar to known proteins which have known activities, one of ordinary skill in the art can modify the sequence of the cancer associated antigens by site-specific mutagenesis, scanning mutagenesis, partial gene deletion or truncation, and the like. See, e.g., U.S. Patent No. 5,580,723 and Sambrook et al., *Molecular Cloning: A Laboratory Manual*, Second Edition, Cold Spring Harbor Laboratory Press, 1989. The skilled artisan then can test the population of mutagenized polypeptides for diminution in a selected and/or for retention of such an activity. Other similar methods for creating and testing dominant negative variants of a protein will be apparent to one of ordinary skill in the art.

The invention also involves agents such as polypeptides which bind to cancer associated antigen polypeptides. Such binding agents can be used, for example, in screening assays to detect the presence or absence of cancer associated antigen polypeptides and complexes of cancer associated antigen polypeptides and their binding partners and in purification protocols to isolated cancer associated antigen polypeptides and complexes of cancer associated antigen polypeptides and their binding partners. Such agents also can be used to inhibit the native activity of the cancer associated antigen polypeptides, for example, by binding to such polypeptides.

The invention, therefore, embraces peptide binding agents which, for example, can be antibodies or fragments of antibodies having the ability to selectively bind to cancer associated antigen polypeptides. Antibodies include polyclonal and monoclonal antibodies, prepared according to conventional methodology.

Significantly, as is well-known in the art, only a small portion of an antibody molecule, the paratope, is involved in the binding of the antibody to its epitope (see, in general, Clark, W.R. (1986) *The Experimental Foundations of Modern Immunology* Wiley & Sons, Inc., New York; Roitt, I. (1991) *Essential Immunology*, 7th Ed., Blackwell Scientific Publications, Oxford). The

pFc' and Fc regions, for example, are effectors of the complement cascade but are not involved in antigen binding. An antibody from which the pFc' region has been enzymatically cleaved, or which has been produced without the pFc' region, designated an F(ab')₂ fragment, retains both of the antigen binding sites of an intact antibody. Similarly, an antibody from which the Fc region has been enzymatically cleaved, or which has been produced without the Fc region, designated an Fab fragment, retains one of the antigen binding sites of an intact antibody molecule. Proceeding further, Fab fragments consist of a covalently bound antibody light chain and a portion of the antibody heavy chain denoted Fd. The Fd fragments are the major determinant of antibody specificity (a single Fd fragment may be associated with up to ten different light chains without altering antibody specificity) and Fd fragments retain epitope-binding ability in isolation.

Within the antigen-binding portion of an antibody, as is well-known in the art, there are complementarity determining regions (CDRs), which directly interact with the epitope of the antigen, and framework regions (FRs), which maintain the tertiary structure of the paratope (see, in general, Clark, 1986; Roitt, 1991). In both the heavy chain Fd fragment and the light chain of IgG immunoglobulins, there are four framework regions (FR1 through FR4) separated respectively by three complementarity determining regions (CDR1 through CDR3). The CDRs, and in particular the CDR3 regions, and more particularly the heavy chain CDR3, are largely responsible for antibody specificity.

It is now well-established in the art that the non-CDR regions of a mammalian antibody may be replaced with similar regions of conspecific or heterospecific antibodies while retaining the epitopic specificity of the original antibody. This is most clearly manifested in the development and use of "humanized" antibodies in which non-human CDRs are covalently joined to human FR and/or Fc/pFc' regions to produce a functional antibody. Thus, for example, PCT International Publication Number WO 92/04381 teaches the production and use of humanized murine RSV antibodies in which at least a portion of the murine FR regions have been replaced by FR regions of human origin. Such antibodies, including fragments of intact antibodies with antigen-binding ability, are often referred to as "chimeric" antibodies.

Thus, as will be apparent to one of ordinary skill in the art, the present invention also provides for F(ab')₂, Fab, Fv and Fd fragments; chimeric antibodies in which the Fc and/or FR and/or CDR1 and/or CDR2 and/or light chain CDR3 regions have been replaced by homologous

human or non-human sequences; chimeric F(ab')₂ fragment antibodies in which the FR and/or CDR1 and/or CDR2 and/or light chain CDR3 regions have been replaced by homologous human or non-human sequences; chimeric Fab fragment antibodies in which the FR and/or CDR1 and/or CDR2 and/or light chain CDR3 regions have been replaced by homologous human or non-human sequences; and chimeric Fd fragment antibodies in which the FR and/or CDR1 and/or CDR2 regions have been replaced by homologous human or non-human sequences. The present invention also includes so-called single chain antibodies.

Thus, the invention involves polypeptides of numerous size and type that bind specifically to cancer associated antigen polypeptides, and complexes of both cancer associated antigen polypeptides and their binding partners. These polypeptides may be derived also from sources other than antibody technology. For example, such polypeptide binding agents can be provided by degenerate peptide libraries which can be readily prepared in solution, in immobilized form or as phage display libraries. Combinatorial libraries also can be synthesized of peptides containing one or more amino acids. Libraries further can be synthesized of peptoids and non-peptide synthetic moieties.

Phage display can be particularly effective in identifying binding peptides useful according to the invention. Briefly, one prepares a phage library (using e.g. m13, fd, or lambda phage), displaying inserts from 4 to about 80 amino acid residues using conventional procedures. The inserts may represent, for example, a completely degenerate or biased array. One then can select phage-bearing inserts which bind to the cancer associated antigen polypeptide. This process can be repeated through several cycles of reselection of phage that bind to the cancer associated antigen polypeptide. Repeated rounds lead to enrichment of phage bearing particular sequences. DNA sequence analysis can be conducted to identify the sequences of the expressed polypeptides. The minimal linear portion of the sequence that binds to the cancer associated antigen polypeptide can be determined. One can repeat the procedure using a biased library containing inserts containing part or all of the minimal linear portion plus one or more additional degenerate residues upstream or downstream thereof. Yeast two-hybrid screening methods also may be used to identify polypeptides that bind to the cancer associated antigen polypeptides. Thus, the cancer associated antigen polypeptides of the invention, or a fragment thereof, can be used to screen peptide libraries, including phage display libraries, to identify and select peptide binding partners of the cancer

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associated antigen polypeptides of the invention. Such molecules can be used, as described, for screening assays, for purification protocols, for interfering directly with the functioning of cancer associated antigen and for other purposes that will be apparent to those of ordinary skill in the art.

As detailed herein, the foregoing antibodies and other binding molecules may be used for example to identify tissues expressing protein or to purify protein. Antibodies also may be coupled to specific diagnostic labeling agents for imaging of cells and tissues that express cancer associated antigens or to therapeutically useful agents according to standard coupling procedures. Diagnostic agents include, but are not limited to, barium sulfate, iocetamic acid, iopanoic acid, ipodate calcium, diatrizoate sodium, diatrizoate meglumine, metrizamide, tyropanoate sodium and radiodiagnostics including positron emitters such as fluorine-18 and carbon-11, gamma emitters such as iodine-123, technitium-99m, iodine-131 and indium-111, nuclides for nuclear magnetic resonance such as fluorine and gadolinium. Other diagnostic agents useful in the invention will be apparent to one of ordinary skill in the art. As used herein, "therapeutically useful agents" include any therapeutic molecule which desirably is targeted selectively to a cell expressing one of the cancer antigens disclosed herein, including antineoplastic agents, radioiodinated compounds, toxins, other cytostatic or cytolytic drugs, and so forth. Antineoplastic therapeutics are well known and include: aminogluthethimide, azathioprine, bleomycin sulfate, busulfan, carmustine, chlorambucil, cisplatin, cyclophosphamide, cyclosporine, cytarabidine, dacarbazine, dactinomycin, daunorubicin, doxorubicin, taxol, etoposide, fluorouracil, interferon- α , lomustine, mercaptopurine, methotrexate, mitotane, procarbazine HCl, thioguanine, vinblastine sulfate and vincristine sulfate. Additional antineoplastic agents include those disclosed in Chapter 52, Antineoplastic Agents (Paul Calabresi and Bruce A. Chabner), and the introduction thereto, 1202-1263, of Goodman and Gilman's "The Pharmacological Basis of Therapeutics", Eighth Edition, 1990, McGraw-Hill, Inc. (Health Professions Division). Toxins can be proteins such as, for example, pokeweed anti-viral protein, cholera toxin, pertussis toxin, ricin, gelonin, abrin, diphtheria exotoxin, or *Pseudomonas* exotoxin. Toxin moieties can also be high energy-emitting radionuclides such as cobalt-60.

In the foregoing methods, antibodies prepared according to the invention also preferably are specific for the cancer associated antigen/MHC complexes described herein.

When "disorder" is used herein, it refers to any pathological condition where the cancer associated antigens are expressed. An example of such a disorder is cancer, breast, colon, gastric,

renal, prostate and lung cancers as particular examples.

Samples of tissue and/or cells for use in the various methods described herein can be obtained through standard methods such as tissue biopsy, including punch biopsy and cell scraping, and collection of blood or other bodily fluids by aspiration or other methods.

5 In certain embodiments of the invention, an immunoreactive cell sample is removed from a subject. By "immunoreactive cell" is meant a cell which can mature into an immune cell (such as a B cell, a helper T cell, or a cytolytic T cell) upon appropriate stimulation. Thus immunoreactive cells include CD34⁺ hematopoietic stem cells, immature T cells and immature B cells. When it is desired to produce cytolytic T cells which recognize a cancer associated antigen, the
10 immunoreactive cell is contacted with a cell which expresses a cancer associated antigen under conditions favoring production, differentiation and/or selection of cytolytic T cells; the differentiation of the T cell precursor into a cytolytic T cell upon exposure to antigen is similar to clonal selection of the immune system.

15 Some therapeutic approaches based upon the disclosure are premised on a response by a subject's immune system, leading to lysis of antigen presenting cells, such as breast cancer cells which present one or more cancer associated antigens. One such approach is the administration of autologous CTLs specific to a cancer associated antigen/MHC complex to a subject with abnormal cells of the phenotype at issue. It is within the ability of one of ordinary skill in the art to develop such CTLs *in vitro*. An example of a method for T cell differentiation is presented in International
20 Application number PCT/US96/05607. Generally, a sample of cells taken from a subject, such as blood cells, are contacted with a cell presenting the complex and capable of provoking CTLs to proliferate. The target cell can be a transfectant, such as a COS cell of the type described herein. These transfectants present the desired complex of their surface and, when combined with a CTL of interest, stimulate its proliferation. COS cells, such as those used herein are widely available, as are
25 other suitable host cells. Specific production of a CTL clone is described herein, and is well known in the art. The clonally expanded autologous CTLs then are administered to the subject.

Another method for selecting antigen-specific CTL clones has recently been described (Altman et al., *Science* 274:94-96, 1996; Dunbar et al., *Curr. Biol.* 8:413-416, 1998), in which fluorogenic tetramers of MHC class I molecule/peptide complexes are used to detect specific CTL
30 clones. Briefly, soluble MHC class I molecules are folded *in vitro* in the presence of β_2 -

microglobulin and a peptide antigen which binds the class I molecule. After purification, the MHC/peptide complex is purified and labeled with biotin. Tetramers are formed by mixing the biotinylated peptide-MHC complex with labeled avidin (e.g. phycoerythrin) at a molar ratio of 4:1. Tetramers are then contacted with a source of CTLs such as peripheral blood or lymph node. The
5 tetramers bind CTLs which recognize the peptide antigen/MHC class I complex. Cells bound by the tetramers can be sorted by fluorescence activated cell sorting to isolate the reactive CTLs. The isolated CTLs then can be expanded *in vitro* for use as described herein.

To detail a therapeutic methodology, referred to as adoptive transfer (Greenberg, *J. Immunol.* 136(5): 1917, 1986; Riddel et al., *Science* 257: 238, 1992; Lynch et al, *Eur. J. Immunol.* 21: 1403-
10 1410, 1991; Kast et al., *Cell* 59: 603-614, 1989), cells presenting the desired complex are combined with CTLs leading to proliferation of the CTLs specific thereto. The proliferated CTLs are then administered to a subject with a cellular abnormality which is characterized by certain of the abnormal cells presenting the particular complex. The CTLs then lyse the abnormal cells, thereby achieving the desired therapeutic goal.

The foregoing therapy assumes that at least some of the subject's abnormal cells present the relevant HLA cancer associated antigen complex. This can be determined very easily, as the art is very familiar with methods for identifying cells which present a particular HLA molecule, as well as how to identify cells expressing DNA of the pertinent sequences, in this case a cancer associated antigen sequence. Once cells presenting the relevant complex are identified via the foregoing
15 screening methodology, they can be combined with a sample from a patient, where the sample contains CTLs. If the complex presenting cells are lysed by the mixed CTL sample, then it can be assumed that a cancer associated antigen is being presented, and the subject is an appropriate candidate for the therapeutic approaches set forth *supra*.
20

Adoptive transfer is not the only form of therapy that is available in accordance with the
25 invention. CTLs can also be provoked *in vivo*, using a number of approaches. One approach is the use of non-proliferative cells expressing the complex. The cells used in this approach may be those that normally express the complex, such as irradiated tumor cells or cells transfected with one or both of the genes necessary for presentation of the complex (i.e. the antigenic peptide and the presenting HLA molecule). Chen et al. (*Proc. Natl. Acad. Sci. USA* 88: 110-114, 1991) exemplifies
30 this approach, showing the use of transfected cells expressing HPVE7 peptides in a therapeutic

regime. Various cell types may be used. Similarly, vectors carrying one or both of the genes of interest may be used. Viral or bacterial vectors are especially preferred. For example, nucleic acids which encode a breast cancer associated antigen polypeptide or peptide may be operably linked to promoter and enhancer sequences which direct expression of the cancer associated antigen polypeptide or peptide in certain tissues or cell types. The nucleic acid may be incorporated into an expression vector. Expression vectors may be unmodified extrachromosomal nucleic acids, plasmids or viral genomes constructed or modified to enable insertion of exogenous nucleic acids, such as those encoding cancer associated antigen, as described elsewhere herein. Nucleic acids encoding a cancer associated antigen also may be inserted into a retroviral genome, thereby facilitating integration of the nucleic acid into the genome of the target tissue or cell type. In these systems, the gene of interest is carried by a microorganism, e.g., a Vaccinia virus, retrovirus or adenovirus, and the materials de facto "infect" host cells. The cells which result present the complex of interest, and are recognized by autologous CTLs, which then proliferate.

A similar effect can be achieved by combining the cancer associated antigen or a stimulatory fragment thereof with an adjuvant to facilitate incorporation into antigen presenting cells *in vivo*. The breast cancer associated antigen polypeptide is processed to yield the peptide partner of the HLA molecule while a cancer associated antigen peptide may be presented without the need for further processing. Generally, subjects can receive an intradermal injection of an effective amount of the cancer associated antigen. Initial doses can be followed by booster doses, following immunization protocols standard in the art. Preferred cancer associated antigens include those found to react with allogeneic cancer antisera, such as the nucleic acids (and encoded polypeptides and peptides) of SEQ ID NO:31,33 and 34 and others, for example, shown in the examples below.

The invention involves the use of various materials disclosed herein to "immunize" subjects or as "vaccines". As used herein, "immunization" or "vaccination" means increasing or activating an immune response against an antigen. It does not require elimination or eradication of a condition but rather contemplates the clinically favorable enhancement of an immune response toward an antigen. Generally accepted animal models can be used for testing of immunization against breast cancer using a cancer associated antigen nucleic acid. For example, cancer cells can be introduced into a mouse to create a tumor, and one or more cancer associated antigen nucleic acids can be delivered by the methods described herein. The effect on the cancer cells (e.g., reduction of tumor

size) can be assessed as a measure of the effectiveness of the cancer associated antigen nucleic acid immunization. Of course, testing of the foregoing animal model using more conventional methods for immunization include the administration of one or more cancer associated antigen polypeptides or peptides derived therefrom, optionally combined with one or more adjuvants and/or cytokines to boost the immune response. Methods for immunization, including formulation of a vaccine composition and selection of doses, route of administration and the schedule of administration (e.g. primary and one or more booster doses), are well known in the art. The tests also can be performed in humans, where the end point is to test for the presence of enhanced levels of circulating CTLs against cells bearing the antigen, to test for levels of circulating antibodies against the antigen, to test for the presence of cells expressing the antigen and so forth.

As part of the immunization compositions, one or more cancer associated antigens or stimulatory fragments thereof are administered with one or more adjuvants to induce an immune response or to increase an immune response. An adjuvant is a substance incorporated into or administered with antigen which potentiates the immune response. Adjuvants may enhance the immunological response by providing a reservoir of antigen (extracellularly or within macrophages), activating macrophages and stimulating specific sets of lymphocytes. Adjuvants of many kinds are well known in the art. Specific examples of adjuvants include monophosphoryl lipid A (MPL, SmithKline Beecham), a congener obtained after purification and acid hydrolysis of *Salmonella minnesota* Re 595 lipopolysaccharide; saponins including QS21 (SmithKline Beecham), a pure QA-21 saponin purified from *Quillja saponaria* extract; DQS21, described in PCT application WO96/33739 (SmithKline Beecham); QS-7, QS-17, QS-18, and QS-L1 (So et al., *Mol. Cells* 7:178-186, 1997); incomplete Freund's adjuvant; complete Freund's adjuvant; montanide; and various water-in-oil emulsions prepared from biodegradable oils such as squalene and/or tocopherol. Preferably, the peptides are administered mixed with a combination of DQS21/MPL. The ratio of DQS21 to MPL typically will be about 1:10 to 10:1, preferably about 1:5 to 5:1 and more preferably about 1:1. Typically for human administration, DQS21 and MPL will be present in a vaccine formulation in the range of about 1 µg to about 100 µg. Other adjuvants are known in the art and can be used in the invention (see, e.g. Goding, *Monoclonal Antibodies: Principles and Practice*, 2nd Ed., 1986). Methods for the preparation of mixtures or emulsions of peptide and adjuvant are well known to those of skill in the art of vaccination.

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Other agents which stimulate the immune response of the subject can also be administered to the subject. For example, other cytokines are also useful in vaccination protocols as a result of their lymphocyte regulatory properties. Many other cytokines useful for such purposes will be known to one of ordinary skill in the art, including interleukin-12 (IL-12) which has been shown to enhance the protective effects of vaccines (*see, e.g., Science* 268: 1432-1434, 1995), GM-CSF and IL-18. Thus cytokines can be administered in conjunction with antigens and adjuvants to increase the immune response to the antigens.

There are a number of immune response potentiating compounds that can be used in vaccination protocols. These include costimulatory molecules provided in either protein or nucleic acid form. Such costimulatory molecules include the B7-1 and B7-2 (CD80 and CD86 respectively) molecules which are expressed on dendritic cells (DC) and interact with the CD28 molecule expressed on the T cell. This interaction provides costimulation (signal 2) to an antigen/MHC/TCR stimulated (signal 1) T cell, increasing T cell proliferation and effector function. B7 also interacts with CTLA4 (CD152) on T cells and studies involving CTLA4 and B7 ligands indicate that the B7-CTLA4 interaction can enhance antitumor immunity and CTL proliferation, Zheng P., et al. *PNAS* 95 (11) 6284-6289 (1998).

B7 typically is not expressed on tumor cells so they are not efficient antigen presenting cells (APCs) for T cells. Induction of B7 expression would enable the tumor cells to stimulate more efficiently CTL proliferation and effector function. A combination of B7/IL-6/IL-12 costimulation has been shown to induce IFN-gamma and a Th1 cytokine profile in the T cell population leading to further enhanced T cell activity, Gajewski et al., *J. Immunol*, 154:5637-5648 (1995). Tumor cell transfection with B7 has been discussed in relation to *in vitro* CTL expansion for adoptive transfer immunotherapy by Wang et al., *J Immunol*, 19:1-8 (1986). Other delivery mechanisms for the B7 molecule would include nucleic acid (naked DNA) immunization Kim J., et al. *Nat Biotechnol.*, 15:7:641-646 (1997) and recombinant viruses such as adeno and pox (Wendtner et al., *Gene Ther*, 4:7:726-735 (1997)). These systems are all amenable to the construction and use of expression cassettes for the coexpression of B7 with other molecules of choice such as the antigens or fragment(s) of antigens discussed herein (including polytopes) or cytokines. These delivery systems can be used for induction of the appropriate molecules *in vitro* and for *in vivo* vaccination situations. The use of anti-CD28 antibodies to directly stimulate T cells *in vitro* and *in vivo* could also be

considered.

Lymphocyte function associated antigen-3 (LFA-3) is expressed on APCs and some tumor cells and interacts with CD2 expressed on T cells. This interaction induces T cell IL-2 and IFN-gamma production and can thus complement but not substitute, the B7/CD28 costimulatory interaction, Parra et al., *J. Immunol.*, 158:637-642 (1997), Fenton et al., *J. Immunother*, 21:2:95-108 (1989).

Lymphocyte function associated antigen-1 (LFA-1) is expressed on leukocytes and interacts with ICAM-1 expressed on APCs and some tumor cells. This interaction induces T cell IL-2 and IFN-gamma production and can thus complement but not substitute, the B7/CD28 costimulatory interaction, Fenton et al., *J. Immunother*, 21:2:95-108 (1998). LFA-1 is thus a further example of a costimulatory molecule that could be provided in a vaccination protocol in the various ways discussed above for B7.

Complete CTL activation and effector function requires Th cell help through the interaction between the Th cell CD40L (CD40 ligand) molecule and the CD40 molecule expressed by DCS, Ridge et al., *Nature*, 393:474 (1998), Bennett et al., *Nature*, 393:478 (1998), Schoenberger et al., *Nature*, 393:480 (1998). This mechanism of this costimulatory signal is likely to involve upregulation of B7 and associated IL-6/IL-12 production by the DC (APC). The CD40-CD40L interaction thus complements the signal 1 (antigen/MHC-TCR) and signal 2 (B7-CD28) interactions.

The use of anti-CD40 antibodies to stimulate DC cells directly, would be expected to enhance a response to tumor antigens which are normally encountered outside of a inflammatory context or are presented by non-professional APCs (tumor cells). In these situations Th help and B7 costimulation signals are not provided. This mechanism might be used in the context of antigen pulsed DC based therapies or in situations where Th epitopes have not been defined within known TRA precursors.

A cancer associated antigen polypeptide, or a fragment thereof, also can be used to isolate their native binding partners. Isolation of such binding partners may be performed according to well-known methods. For example, isolated cancer associated antigen polypeptides can be attached to a substrate (e.g., chromatographic media, such as polystyrene beads, or a filter), and then a solution suspected of containing the binding partner may be applied to the substrate. If a binding partner which can interact with cancer associated antigen polypeptides is present in the solution,

then it will bind to the substrate-bound cancer associated antigen polypeptide. The binding partner then may be isolated.

It will also be recognized that the invention embraces the use of the cancer associated antigen cDNA sequences in expression vectors, as well as to transfect host cells and cell lines, be these
5 prokaryotic (e.g., *E. coli*), or eukaryotic (e.g., dendritic cells, B cells, CHO cells, COS cells, yeast expression systems and recombinant baculovirus expression in insect cells). Especially useful are mammalian cells such as human, mouse, hamster, pig, goat, primate, etc. They may be of a wide variety of tissue types, and include primary cells and cell lines. Specific examples include keratinocytes, peripheral blood leukocytes, bone marrow stem cells and embryonic stem cells. The
10 expression vectors require that the pertinent sequence, i.e., those nucleic acids described *supra*, be operably linked to a promoter.

The invention also contemplates delivery of nucleic acids, polypeptides or peptides for vaccination. Delivery of polypeptides and peptides can be accomplished according to standard vaccination protocols which are well known in the art. In another embodiment, the delivery of
15 nucleic acid is accomplished by *ex vivo* methods, i.e. by removing a cell from a subject, genetically engineering the cell to include a breast cancer associated antigen, and reintroducing the engineered cell into the subject. One example of such a procedure is outlined in U.S. Patent 5,399,346 and in exhibits submitted in the file history of that patent, all of which are publicly available documents. In general, it involves introduction *in vitro* of a functional copy of a gene into a cell(s) of a subject, and
20 returning the genetically engineered cell(s) to the subject. The functional copy of the gene is under operable control of regulatory elements which permit expression of the gene in the genetically engineered cell(s). Numerous transfection and transduction techniques as well as appropriate expression vectors are well known to those of ordinary skill in the art, some of which are described in PCT application WO95/00654. *In vivo* nucleic acid delivery using vectors such as viruses and
25 targeted liposomes also is contemplated according to the invention.

In preferred embodiments, a virus vector for delivering a nucleic acid encoding a cancer associated antigen is selected from the group consisting of adenoviruses, adeno-associated viruses, poxviruses including vaccinia viruses and attenuated poxviruses, Semliki Forest virus, Venezuelan equine encephalitis virus, retroviruses, Sindbis virus, and Ty virus-like particle. Examples of
30 viruses and virus-like particles which have been used to deliver exogenous nucleic acids include:

replication-defective adenoviruses (e.g., Xiang et al., *Virology* 219:220-227, 1996; Eloit et al., *J. Virol* 7:5375-5381, 1997; Chengalvala et al., *Vaccine* 15:335-339, 1997), a modified retrovirus (Townsend et al., *J. Virol.* 71:3365-3374, 1997), a nonreplicating retrovirus (Irwin et al., *J. Virol.* 68:5036-5044, 1994), a replication defective Semliki Forest virus (Zhao et al., *Proc. Natl. Acad. Sci. USA* 92:3009-3013, 1995), canarypox virus and highly attenuated vaccinia virus derivative (Paoletti, *Proc. Natl. Acad. Sci. USA* 93:11349-11353, 1996), non-replicative vaccinia virus (Moss, *Proc. Natl. Acad. Sci. USA* 93:11341-11348, 1996), replicative vaccinia virus (Moss, *Dev. Biol. Stand.* 82:55-63, 1994), Venezuelan equine encephalitis virus (Davis et al., *J. Virol.* 70:3781-3787, 1996), Sindbis virus (Pugachev et al., *Virology* 212:587-594, 1995), and Ty virus-like particle (Allsopp et al., *Eur J. Immunol* 26:1951-1959, 1996). In preferred embodiments, the virus vector is an adenovirus.

Another preferred virus for certain applications is the adeno-associated virus, a double-stranded DNA virus. The adeno-associated virus is capable of infecting a wide range of cell types and species and can be engineered to be replication-deficient. It further has advantages, such as heat and lipid solvent stability, high transduction frequencies in cells of diverse lineages, including hematopoietic cells, and lack of superinfection inhibition thus allowing multiple series of transductions. The adeno-associated virus can integrate into human cellular DNA in a site-specific manner, thereby minimizing the possibility of insertional mutagenesis and variability of inserted gene expression. In addition, wild-type adeno-associated virus infections have been followed in tissue culture for greater than 100 passages in the absence of selective pressure, implying that the adeno-associated virus genomic integration is a relatively stable event. The adeno-associated virus can also function in an extrachromosomal fashion.

In general, other preferred viral vectors are based on non-cytopathic eukaryotic viruses in which non-essential genes have been replaced with the gene of interest. Non-cytopathic viruses include retroviruses, the life cycle of which involves reverse transcription of genomic viral RNA into DNA with subsequent proviral integration into host cellular DNA. Adenoviruses and retroviruses have been approved for human gene therapy trials. In general, the retroviruses are replication-deficient (i.e., capable of directing synthesis of the desired proteins, but incapable of manufacturing an infectious particle). Such genetically altered retroviral expression vectors have general utility for the high-efficiency transduction of genes *in vivo*. Standard protocols for

producing replication-deficient retroviruses (including the steps of incorporation of exogenous genetic material into a plasmid, transfection of a packaging cell lined with plasmid, production of recombinant retroviruses by the packaging cell line, collection of viral particles from tissue culture media, and infection of the target cells with viral particles) are provided in Kriegler, M., "Gene Transfer and Expression, A Laboratory Manual," W.H. Freeman C.O., New York (1990) and Murry, E.J. Ed. "Methods in Molecular Biology," vol. 7, Humana Press, Inc., Clifton, New Jersey (1991).

Preferably the foregoing nucleic acid delivery vectors: (1) contain exogenous genetic material that can be transcribed and translated in a mammalian cell and that can induce an immune response in a host, and (2) contain on a surface a ligand that selectively binds to a receptor on the surface of a target cell, such as a mammalian cell, and thereby gains entry to the target cell.

Various techniques may be employed for introducing nucleic acids of the invention into cells, depending on whether the nucleic acids are introduced *in vitro* or *in vivo* in a host. Such techniques include transfection of nucleic acid-CaPO₄ precipitates, transfection of nucleic acids associated with DEAE, transfection or infection with the foregoing viruses including the nucleic acid of interest, liposome mediated transfection, and the like. For certain uses, it is preferred to target the nucleic acid to particular cells. In such instances, a vehicle used for delivering a nucleic acid of the invention into a cell (e.g., a retrovirus, or other virus; a liposome) can have a targeting molecule attached thereto. For example, a molecule such as an antibody specific for a surface membrane protein on the target cell or a ligand for a receptor on the target cell can be bound to or incorporated within the nucleic acid delivery vehicle. Preferred antibodies include antibodies which selectively bind a cancer associated antigen, alone or as a complex with a MHC molecule.

Especially preferred are monoclonal antibodies. Where liposomes are employed to deliver the nucleic acids of the invention, proteins which bind to a surface membrane protein associated with endocytosis may be incorporated into the liposome formulation for targeting and/or to facilitate uptake. Such proteins include capsid proteins or fragments thereof tropic for a particular cell type, antibodies for proteins which undergo internalization in cycling, proteins that target intracellular localization and enhance intracellular half life, and the like. Polymeric delivery systems also have been used successfully to deliver nucleic acids into cells, as is known by those skilled in the art. Such systems even permit oral delivery of nucleic acids.

When administered, the therapeutic compositions of the present invention can be

administered in pharmaceutically acceptable preparations. Such preparations may routinely contain pharmaceutically acceptable concentrations of salt, buffering agents, preservatives, compatible carriers, supplementary immune potentiating agents such as adjuvants and cytokines and optionally other therapeutic agents.

5 The therapeutics of the invention can be administered by any conventional route, including injection or by gradual infusion over time. The administration may, for example, be oral, intravenous, intraperitoneal, intramuscular, intracavity, subcutaneous, or transdermal. When antibodies are used therapeutically, a preferred route of administration is by pulmonary aerosol. Techniques for preparing aerosol delivery systems containing antibodies are well known to those of
10 skill in the art. Generally, such systems should utilize components which will not significantly impair the biological properties of the antibodies, such as the paratope binding capacity (see, for example, Sciarra and Cutie, "Aerosols," in Remington's Pharmaceutical Sciences, 18th edition, 1990, pp 1694-1712; incorporated by reference). Those of skill in the art can readily determine the various parameters and conditions for producing antibody aerosols without resort to undue
15 experimentation. When using antisense preparations of the invention, slow intravenous administration is preferred.

20 The compositions of the invention are administered in effective amounts. An "effective amount" is that amount of a cancer associated antigen composition that alone, or together with further doses, produces the desired response, e.g. increases an immune response to the cancer associated antigen. In the case of treating a particular disease or condition characterized by expression of one or more cancer associated antigens, such as cancer, the desired response is inhibiting the progression of the disease. This may involve only slowing the progression of the disease temporarily, although more preferably, it involves halting the progression of the disease permanently. This can be monitored by routine methods or can be monitored according to
25 diagnostic methods of the invention discussed herein. The desired response to treatment of the disease or condition also can be delaying the onset or even preventing the onset of the disease or condition.

Such amounts will depend, of course, on the particular condition being treated, the severity of the condition, the individual patient parameters including age, physical condition, size and
30 weight, the duration of the treatment, the nature of concurrent therapy (if any), the specific route of

administration and like factors within the knowledge and expertise of the health practitioner. These factors are well known to those of ordinary skill in the art and can be addressed with no more than routine experimentation. It is generally preferred that a maximum dose of the individual components or combinations thereof be used, that is, the highest safe dose according to sound medical judgment. It will be understood by those of ordinary skill in the art, however, that a patient may insist upon a lower dose or tolerable dose for medical reasons, psychological reasons or for virtually any other reasons.

The pharmaceutical compositions used in the foregoing methods preferably are sterile and contain an effective amount of breast cancer associated antigen or nucleic acid encoding cancer associated antigen for producing the desired response in a unit of weight or volume suitable for administration to a patient. The response can, for example, be measured by determining the immune response following administration of the cancer associated antigen composition via a reporter system as described herein, by measuring downstream effects such as gene expression, or by measuring the physiological effects of the breast cancer associated antigen composition, such as regression of a tumor or decrease of disease symptoms. Other assays will be known to one of ordinary skill in the art and can be employed for measuring the level of the response.

The doses of cancer associated antigen compositions (e.g., polypeptide, peptide, antibody, cell or nucleic acid) administered to a subject can be chosen in accordance with different parameters, in particular in accordance with the mode of administration used and the state of the subject. Other factors include the desired period of treatment. In the event that a response in a subject is insufficient at the initial doses applied, higher doses (or effectively higher doses by a different, more localized delivery route) may be employed to the extent that patient tolerance permits.

In general, for treatments for eliciting or increasing an immune response, doses of cancer associated antigen are formulated and administered in doses between 1 ng and 1 mg, and preferably between 10 ng and 100 μ g, according to any standard procedure in the art. Where nucleic acids encoding cancer associated antigen or variants thereof are employed, doses of between 1 ng and 0.1 mg generally will be formulated and administered according to standard procedures. Other protocols for the administration of cancer associated antigen compositions will be known to one of ordinary skill in the art, in which the dose amount, schedule of injections, sites of injections, mode of administration (e.g., intra-tumoral) and the like vary from the foregoing. Administration of cancer

associated antigen compositions to mammals other than humans, e.g. for testing purposes or veterinary therapeutic purposes, is carried out under substantially the same conditions as described above.

As part of the immunization compositions, the peptide antigens are administered with one or more adjuvants to induce an immune response or to increase an immune response. An adjuvant is a substance incorporated into or administered with antigen which potentiates the immune response. Adjuvants may enhance the immunological response by providing a reservoir of antigen (extracellularly or within macrophages), activating macrophages and stimulating specific sets of lymphocytes. Adjuvants of many kinds are well known in the art. Specific examples of adjuvants include monophosphoryl lipid A (MPL, SmithKline Beecham), a congener obtained after purification and acid hydrolysis of *Salmonella minnesota* Re 595 lipopolysaccharide; saponins including QS21 (SmithKline Beecham), a pure QA-21 saponin purified from *Quillja saponaria* extract; DQS21, described in PCT application WO96/33739 (SmithKline Beecham); QS-7, QS-17, QS-18, and QS-L1 (So et al., *Mol. Cells* 7:178-186, 1997); incomplete Freund's adjuvant; complete Freund's adjuvant; montanide; and various water-in-oil emulsions prepared from biodegradable oils such as squalene and/or tocopherol. Other adjuvants are known in the art and can be used in the invention (see, e.g. Goding, *Monoclonal Antibodies: Principles and Practice*, 2nd Ed., 1986). Methods for the preparation of mixtures or emulsions of peptide and adjuvant are well known to those of skill in the art of vaccination.

Where cancer associated antigen peptides are used for vaccination, modes of administration which effectively deliver the cancer associated antigen and adjuvant, such that an immune response to the antigen is increased, can be used. For administration of a cancer associated antigen peptide in adjuvant, preferred methods include intradermal, intravenous, intramuscular and subcutaneous administration. Although these are preferred embodiments, the invention is not limited by the particular modes of administration disclosed herein. Standard references in the art (e.g., *Remington's Pharmaceutical Sciences*, 18th edition, 1990) provide modes of administration and formulations for delivery of immunogens with adjuvant or in a non-adjuvant carrier.

When administered, the pharmaceutical preparations of the invention are applied in pharmaceutically-acceptable amounts and in pharmaceutically-acceptable compositions. The term "pharmaceutically acceptable" means a non-toxic material that does not interfere with the

effectiveness of the biological activity of the active ingredients. Such preparations may routinely contain salts, buffering agents, preservatives, compatible carriers, and optionally other therapeutic agents. When used in medicine, the salts should be pharmaceutically acceptable, but non-pharmaceutically acceptable salts may conveniently be used to prepare pharmaceutically-acceptable salts thereof and are not excluded from the scope of the invention. Such pharmacologically and pharmaceutically-acceptable salts include, but are not limited to, those prepared from the following acids: hydrochloric, hydrobromic, sulfuric, nitric, phosphoric, maleic, acetic, salicylic, citric, formic, malonic, succinic, and the like. Also, pharmaceutically-acceptable salts can be prepared as alkaline metal or alkaline earth salts, such as sodium, potassium or calcium salts.

A breast cancer associated antigen composition may be combined, if desired, with a pharmaceutically-acceptable carrier. The term "pharmaceutically-acceptable carrier" as used herein means one or more compatible solid or liquid fillers, diluents or encapsulating substances which are suitable for administration into a human. The term "carrier" denotes an organic or inorganic ingredient, natural or synthetic, with which the active ingredient is combined to facilitate the application. The components of the pharmaceutical compositions also are capable of being co-mingled with the molecules of the present invention, and with each other, in a manner such that there is no interaction which would substantially impair the desired pharmaceutical efficacy.

The pharmaceutical compositions may contain suitable buffering agents, including: acetic acid in a salt; citric acid in a salt; boric acid in a salt; and phosphoric acid in a salt.

The pharmaceutical compositions also may contain, optionally, suitable preservatives, such as: benzalkonium chloride; chlorobutanol; parabens and thimerosal.

The pharmaceutical compositions may conveniently be presented in unit dosage form and may be prepared by any of the methods well-known in the art of pharmacy. All methods include the step of bringing the active agent into association with a carrier which constitutes one or more accessory ingredients. In general, the compositions are prepared by uniformly and intimately bringing the active compound into association with a liquid carrier, a finely divided solid carrier, or both, and then, if necessary, shaping the product.

Compositions suitable for oral administration may be presented as discrete units, such as

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capsules, tablets, lozenges, each containing a predetermined amount of the active compound. Other compositions include suspensions in aqueous liquids or non-aqueous liquids such as a syrup, elixir or an emulsion.

Compositions suitable for parenteral administration conveniently comprise a sterile aqueous or non-aqueous preparation of breast cancer associated antigen polypeptides or nucleic acids, which is preferably isotonic with the blood of the recipient. This preparation may be formulated according to known methods using suitable dispersing or wetting agents and suspending agents. The sterile injectable preparation also may be a sterile injectable solution or suspension in a non-toxic parenterally-acceptable diluent or solvent, for example, as a solution in 1,3-butane diol. Among the acceptable vehicles and solvents that may be employed are water, Ringer's solution, and isotonic sodium chloride solution. In addition, sterile, fixed oils are conventionally employed as a solvent or suspending medium. For this purpose any bland fixed oil may be employed including synthetic mono-or di-glycerides. In addition, fatty acids such as oleic acid may be used in the preparation of injectables. Carrier formulation suitable for oral, subcutaneous, intravenous, intramuscular, etc. administrations can be found in *Remington's Pharmaceutical Sciences*, Mack Publishing Co., Easton, PA.

Examples

Example 1: Preparation of breast cancer cDNA expression libraries

Step 1: Purification of total RNA from tumors.

Total RNA was isolated from tumor samples using the guanidium thiocyanate-phenol-chloroform extraction protocol described by Chomczynski and Sacci (*Anal. Biochem.* 162:156-159, 1987).

Step 2: Purification of mRNA.

A Dynabeads mRNA isolation kit (Dynal, Cat.No. 610.01) was used to isolate mRNA from the pool of total RNA isolated in step 1 above according to the manufacturer's instructions.

Step 3: cDNA synthesis.

cDNA synthesis was performed using a ZAP-cDNA synthesis Kit (Stratagene, La Jolla CA; Cat. No. 200400) according to the manufacturer's protocol. A specific linker-primer which contains a XbaI cloning site was designed and used in this protocol, to facilitate subcloning into TriplEx

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vector. The sequence of the primer was:

GAGAGAGAGAGAGAGAGAGAAGTCGACTCTAGATTTTTTTTTTTTTTTTTTTT-Xba 1 site

Step 4: Ligation into the TriplEx vector arms.

5 The cDNAs generated in step 3 above were ligated into TriplEx vector arms (Clontech, Palo Alto, CA; Cat. No. 6162-1); the arms were predigested with EcoR I/Xba I.

Step 5: Packaging into phages with Gigapack III kit.

The ligation mix (TriplEx/cDNA) from step 4 was packed into phages using the Gigapack III Gold Cloning Kit (Stratagene, Cat. N.200450) according to the protocol supplied with the kit.

10 Step 6: Titering and amplification of generated libraries was performed according to the Stratagene protocols.

The foregoing protocol was used to prepare several libraries from tumor sample of different patients. Some libraries were prepared using the UNI-ZAP XR vector system (Stratagene) according to the manufacturer's protocol, and some using the TriplEx system as described above.

Table 2

UNI-ZAP Libraries		
Code for tumors	Titer of the library	Histopathological diagnosis
HBR173	1.8 x 10 ⁶ pfu	Ductal Carcinoma, Grade III
HBR184	3.5 x 10 ⁶ pfu	Invasive Ductal Carcinoma, Grade II
TriplEx libraries		
Code for tumors	Titer of the library	Histopathological diagnosis
HBR173	2.3 x 10 ⁶ pfu	Ductal Carcinoma, Grade III
HBR184	1.1 x 10 ⁶ pfu	Invasive Ductal Carcinoma, Grade II
HBR257	2.5 x 10 ⁶ pfu	Invasive Ductal Carcinoma, Grade II
HBR297	4.0 x 10 ⁶ pfu	Ductal Carcinoma, Grade II
HBR248	1.0 x 10 ⁶ pfu	Invasive Ductal Carcinoma with Vascular Permeation, Grade III

HBR271	2.5 x 10 ⁶ pfu	Medullary Carcinoma
HBR263	10.0 x 10 ⁶ pfu	Inv. Pleiomorphic Lobular Carcinoma, Grade II

All libraries were screened with the exception of HBR173 (no autologous serum). No
 5 serum-positive clones were found by screening HBR271 library.

Example 2: Immunoscreening

Sera was obtained from donors undergoing routine diagnostic and therapeutic procedures. It was stored at - 70°C prior to absorption. Sera, at a dilution of 1:10 in Tris buffered saline (TBS, pH
 10 7.5), was sequentially passed through Sepharose 4B columns which had been coupled to lysates from *E. coli* Y1090 and bacteriophage infected *E. coli* BNN97 (5 Prime 3 Prime, Inc. Boulder, Co.). Final serum dilutions were prepared in 0.2% non-fat dried milk/TBS (NFDM) and stored at 4°C. Library screening was performed as described by Sahin et al. (*Proc. Natl. Acad. Sci. USA* 92:11810-11813, 1995) with following modifications. Recombinant phage at a concentration of 4 x
 15 10³ per 15 cm plate were amplified for 6 hours and transferred to nitrocellulose membranes for an additional 15 hours at 37°C. Membranes were then blocked with 5% NFDM. As an alternative to generation of IgG subtracted libraries, membranes were pre-screened in a 1:2000 dilution of peroxidase conjugated, Fc fragment specific, goat anti-human IgG (Jackson Immunoresearch Laboratories Inc., West Grove, PA) for 1 hour at room temperature. Color was developed with 3,3'-
 20 diaminobenzidine tetrahydrochloride and IgG encoding clones were scored. Membranes were then incubated in a 1:100 dilution of absorbed autologous sera for 15 hours at room temperature. Following serum exposure, filters were incubated in a 1:3000 dilution of alkaline phosphatase conjugated, Fc fragment specific, goat anti-human IgG (Jackson Immunoresearch Laboratories Inc.) for 1 hour at room temperature and processed for 4-nitro blue tetrazolium
 25 chloride/5-bromo-4-chloro- 3-indolyl-phosphate color development. Serum positive clones were subcloned and retested for serum reactivity as above except nitrocellulose transfer was decreased to 3 hours. For the determination of allogeneic serum reactivity, plates containing an equal number of serum positive clones and negative control plaques were similarly processed less the IgG prescreening steps. A minimum of 5 x 10⁵ recombinants were screened per cDNA library, a number

which approximates a point at which the likelihood of repeat isolations of previously identified clones outweigh the prospect of identifying new clones.

Example 3: DNA Sequencing

- 5 Phage cDNA clones were converted to pBKCMV phagemid forms by in vivo excision. Plasmid DNA was purified on Qiaprep spin columns (Qiagen Inc. Chatsworth, CA) and subjected to EcoRI/XbaI restriction enzyme digestion. Clones representing different cDNA inserts were sequenced at Cornell University DNA services (Ithaca, NY) using an ABI Prism (Perkin Elmer) automated DNA sequencer. The sequences of the clones were compared with sequences in
- 10 GenBank and HGI databases to detect homologous nucleic acid and/or protein sequences. The following table lists exemplary related sequences.

Table 3: Sequences Related to Breast Cancer Associated Antigen Clones

Clone	Nucleotide Homology	Clone	Nucleotide Homology	Clone	Nucleotide Homology
LONY-Br-1	L34543	LONY-Br-23	AA262134, U74628	LONY-Br-44	D15057
LONY-Br-2	S75417	LONY-Br-24	AA282633	LONY-Br-45	AB000815
LONY-Br-3	J05211	LONY-Br-25	M62324	LONY-Br-46	L04733
LONY-Br-4	X15187	LONY-Br-26	M99389	LONY-Br-47	X88791
LONY-Br-5	X62083	LONY-Br-27	X79389	LONY-Br-48	AF000430
LONY-Br-6	J04965	LONY-Br-28	D44466	LONY-Br-49	none
LONY-Br-7	D63784	LONY-Br-29	M33197	LONY-Br-50	AA226732
LONY-Br-8	U11292	LONY-Br-30	M17886	LONY-Br-51	AA046574
LONY-Br-9	HSB06D102	LONY-Br-31	L38941	LONY-Br-52	none
LONY-Br-10	none	LONY-Br-32	X17644	LONY-Br-53	AB002307
LONY-Br-11	none	LONY-Br-33	X75342	92	AA127328
LONY-Br-12	AA430998	LONY-Br-33	X75342	101	AA167314
LONY-Br-13	D83032	LONY-Br-34	U43368	102	AA508139
LONY-Br-14	AA034417	LONY-Br-35	X15882	107	none
LONY-Br-15	AA167070	LONY-Br-37	AA121558	109	AA220229

LONY-Br-16	none	LONY-Br-38	AA211771	110	W67775
LONY-Br-17	AA161103	LONY-Br-39	AA367417	111	AA280070
LONY-Br-19	R13835	LONY-Br-40	AA188052	112	AF004292
LONY-Br-20	HUMORF003	LONY-Br-41	THC83518	131	none
LONY-Br-21	S74572	LONY-Br-42	none	143	AA481578
LONY-Br-22	AA070233	LONY-Br-43	HU35246	162	AA481578

Example 4: Reverse transcriptase (RT) PCR and Rapid Amplification of cDNA Ends (RACE)

The mRNA expression pattern of selected cDNA clones was determined by RT-PCR using a panel of normal tissue RNA. This test panel consisted of lung, testis, small intestine, colon, breast, liver, and placenta, and was purchased from Clontech Laboratories Inc. (Palo Alto, CA). Colon tumor RNA was also included in this panel and was prepared as described above. As a control for genomic DNA contamination, all cDNA synthesis reactions were set up in duplicate with the additional sample lacking reverse transcriptase. Gene specific PCR primers were designed to amplify 5' fragments of 300-400 bp and were purchased commercially (Gibco BRL, Grand Island, NY). PCR reactions were undertaken at an annealing temperature of 68°C using a Perkin Elmer thermal cycler. In certain cases, RT-PCR products were subcloned into the pCR2.1 plasmid vector (Invitrogen) and multiple clones were subjected to DNA sequencing as described. 5' and 3' RACE reactions were undertaken using gene specific and adapter primers in conjunction with Marathon Ready normal colon cDNA and KlenTaq polymerase (Clontech) as per manufacturers protocol. Products were then subcloned into the pCR2.1 plasmid vector (Invitrogen) and screened by PCR with internal primers for presence of the desired insert. Multiple RACE clones were subjected to DNA sequencing as described.

Example 5: Northern blot analysis

Northern blots containing the transfer yields of 2 µg poly A⁺ RNA from a panel of normal tissues were obtained commercially (Clontech). Random primed ³²P labeled probes consisting of 300-600 bp PCR products from 5 prime coding sequences of serum positive cDNA clones were hybridized for 1.5 hours in Expresshyb (Clontech) at 68°C and washed at high stringency (2 times,

30 min. each, 0.1X SSC/0.1% SDS at 68°C). Resultant blots were used to expose Biomax MS autoradiography film (Eastman Kodak Co., Rochester, NY).

Table 4: Breast Cancer Associated Antigen Clone mRNA sizes

Clone	Size (kb)	Clone	Size (kb)	Clone	Size (kb)
LONY-Br-1	1.8	LONY-Br-17	1.0	LONY-Br-33	2.6
LONY-Br-2	2.9	LONY-Br-19	1.5	LONY-Br-34	2.1
LONY-Br-3	4.8	LONY-Br-20	2.4	LONY-Br-35	1.9
LONY-Br-4	1.2	LONY-Br-21	2.4	LONY-Br-36	0.8
LONY-Br-5	0.9	LONY-Br-22	1.6	LONY-Br-37	1.0
LONY-Br-6	1.4	LONY-Br-23	1.3	LONY-Br-38	2.2
LONY-Br-7	1.3	LONY-Br-24	3.9	LONY-Br-39	1.9
LONY-Br-8	0.9	LONY-Br-25	1.9	LONY-Br-40	3.4
LONY-Br-9	6.0	LONY-Br-26	1.5	LONY-Br-41	3.9
LONY-Br-10	3.6	LONY-Br-27	1.2	LONY-Br-42	0.6
LONY-Br-11	4.6	LONY-Br-28	0.5	LONY-Br-43	1.4
LONY-Br-12	2.2	LONY-Br-29	0.6	LONY-Br-44	0.7
LONY-Br-13	1.2	LONY-Br-30	0.8	LONY-Br-45	3.0
LONY-Br-14	0.8	LONY-Br-31	0.4	LONY-Br-46	3.7
LONY-Br-15	0.9	LONY-Br-32	2.2	LONY-Br-47	0.5
LONY-Br-16	2.5	LONY-Br-33	2.6	LONY-Br-48	1.6

Example 6: Isolation of gastric and prostate clones

A stomach cancer cDNA library was established, using standard techniques, then the library was screened, using the SEREX methodology described supra, and set forth by Sahin et al., *Proc. Natl. Acad. Sci. USA* 92: 11810 (1995), and by Chen et al., *Proc. Natl. Acad. Sci. USA* 94: 1914 (1997), incorporated by reference in their entirety.

To be specific, total RNA was isolated by homogenizing tumor samples in 4M guanidium thiocyanate/0.5% sodium N-lauryl sarcosine/ and 25 mM EDTA followed by centrifugation in 5.7 M CsCl/25 mM sodium acetate/10 uM EDTA at 320,000 rpm. Total mRNA was removed by passing the sample over an oligo-dT cellulose column. The cDNA libraries were then constructed

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by taking 5 ug of mRNA, using standard methodologies to reverse transcribe the material.

Libraries were prepared from four different stomach cancer patients, referred to as "SM", "CK" and "SS" and "KM" respectively. A total of 2.5×10^6 , 1.1×10^6 , and 1.7×10^6 cDNA clones were obtained from the "SM", "CK" and "SS" individuals. Additional libraries were prepared from prostate cancer patient "OT".

The cDNA was used to construct a lambda phage library, and 500 phages were plated onto XL1-Blue MRF E. coli, and incubated for eight hours at 37°C. A nitrocellulose membrane was then placed on the plate, followed by overnight incubation. The membrane was then washed, four times, without TBS which contained 0.05% Tween, and was then immersed in TBS containing 5% non-fat dried milk. After one hour, the membrane was incubated with conjugates of peroxidase-goat anti human IgG specific for Fc portions of human antibody (1:2000, diluted in TBS with 1% BSA. The incubation was carried out for one hour, at room temperature, and the membrane was then washed three times with TBS. Those clones which produced antibodies were visualized with 0.06%, 3,3'diamino benzidine tetrachloride, and 0.015% H_2O_2 , in 50 mM Tris (pH 7.5). Any clones which produced immunoglobulin were marked, and then the membrane was washed, two further times, with TBS that contained 0.05% Tween, and then twice with "neat" TBS.

The membranes were then incubated in 1:100 diluted patient serum, overnight, at 4°C. The patient serum had been pretreated. Specifically, 5 ml samples were diluted to 10 ml with TBS containing 1% bovine serum albumin, and 0.02% Na_3N . The serum had been treated to remove antibodies to bacteriophage, by passing it through a 5 ml Sepharose column, to which a lysate of E. coli Y1090 had been attached, followed by passage over a second column which had E. coli lysate and lysate of E. coli infected with lambda bacteriophage. The screening was carried out five times. The samples were then diluted to 50 ml, and kept at -80°C, until used as described herein.

Following the overnight incubation with the membrane, the membrane was washed twice with TBS/0.05% Tween 20, and then once with TBS. A further incubation was carried out, using the protocols discussed supra, for the POD labelled antibodies.

The positive clones were then sequenced, using standard techniques. Following comparison of the sequences to information available in data banks, a total of 36 clones were resolved into known and unknown genes. In the table that follows, the "+" and "-" signs are essentially used to compare signals to each other. All were positive. Table 5, which follows, summarizes some of this

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work isolation and sequencing of "SM" clones. Specifically, with reference to the first page of the table, previously identified human proteins and the nucleotide sequences, set forth in SEQ ID NOS:588-626 are known. The four molecules which follow in SEQ ID NOS:627-634 (gelsolin, zinc finger protein family, variant zinc finger motif protein goliath and homeodomain proteins), have not been identified in humans previously, although there are related molecules found in other species. Finally, with reference to Table 5, the last four moieties, i.e., prepro- α collagen, heterogeneous ribonucleoprotein D, nucleosome assembly protein 2, and NY-ESO-2/Ulsn NRP/V1 small nuclear ribonucleoprotein, are also known. Nucleotide sequences are set forth at SEQ ID NOS:635-642. The nucleic acid molecules having the nucleotide sequences set forth at SEQ ID NOS:643-670 represent molecules for which no related sequences were found. SEQ ID NO:671 combines the sequences of SEQ ID NOS:627-630, inclusive. SEQ ID NO:672 combines SEQ ID NOS:643-656, SEQ ID NO:673 combines SEQ ID NOS:657, 659 and 662, while SEQ ID NO:674 combines SEQ ID NOS: 658, 660, 661 and 663.

SEREX analysis of clones from libraries derived from patients "CK", "SS", "KM" (all gastric cancer) and patient "OT" (prostate cancer) was carried out as described above. The nucleotide sequences of clones derived from gastric cancer patients are presented as SEQ ID NOS:176-436. The nucleotide sequences of clones derived from prostate cancer patient "OT" are presented as SEQ ID Nos:437-543.

Example 7: Isolation and analysis of colon clones

Colon tumor samples were obtained as surgical samples, and were frozen at -80°C until ready for use.

Total RNA was then isolated from the samples, using the guanidium thiocyanate method of Chirgwin, et al., *Biochemistry* 18: 5294-5299 (1979), incorporated by reference. The total RNA thus obtained was then purified to isolate all poly A⁺ RNA, using commercially available products designed for this purpose.

The poly A⁺ RNA was then converted into cDNA, and ligated into λ ZAP, a commercially available expression vector, according to the manufacturer's suggested protocol.

Three cDNA libraries were constructed in this way, using colorectal carcinoma samples.

A fourth library, also from colorectal carcinoma, was prepared, albeit in a different way. The

fourth library was an IgG subtraction library, prepared by using a subtraction partner, generated by PCR amplification of a cDNA clone which encoded an IgG molecule. *See, e.g., Ace et al, Endocrinology* 134: 1305-1309 (1994), and incorporated by reference in its entirety. IgG subtraction is done to eliminate any false, positive signals resulting from interaction of cDNA clones which encode IgG, with the IgG then interacting with the anti-human IgG used in the SEREX assay, as described herein. PCR products were biotinylated, and hybridized with denatured second strand cDNA, at 68°C for 18 hours. Biotinylated hybrid molecules were coupled to streptavidin, and then removed by phenol chloroform extraction. Any remaining cDNA was also ligated into λ ZAP. All libraries were amplified, prior to immunoscreening.

Immunoscreening was carried out using sera obtained from patients undergoing routine diagnostic and therapeutic procedures. The sera were stored at -70°C prior to use. Upon thawing, the sera were diluted at 1:10 in Tris buffered saline (pH 7.5), and were then passed through Sepharose 4B columns. First, the sera were passed through columns which had *E. coli* Y1090 lysates coupled thereto, and then lysates from bacteriophage infected *E. coli* BNN97 lysates. Final serum dilutions were then prepared in 0.2% non-fat dried milk/Tris buffered saline.

The method of Sahin et al., *Proc. Natl. Acad. Sci. USA* 92:11810-11813 (1995), and U.S. Patent No. 5,698,396, both of which are incorporated by reference, was used, with some modifications. Specifically, recombinant phages at a concentration of 4×10^3 phages per 15 cm plate (pfus), were amplified for six hours, after which they were transferred to nitrocellulose membranes for 15 hours. The membranes then were blocked with 5% nonfat dried milk.

As an alternative to the IgG subtraction procedure discussed above, membranes were prescreened in a 1:2000 dilution of peroxidase conjugated, Fc fragment specific goat anti-human IgG, for one hour, at room temperature. Color was developed using 3,3'-diaminobenzidine tetrahydrochloride, which permitted scoring of IgG encoding clones.

Membranes were then incubated in 1:100 dilutions of autologous sera, which had been pretreated with the Sepharose 4B columns, as described *supra*. The filters were then incubated, in a 1:3000 dilution of alkaline phosphatase conjugated Fc fragment specific, goat anti-human IgG, for one hour, at room temperature. The indicator system 4-nitroblue tetrazolium chloride/5-bromo-4-chloro-3-indolyl-phosphate was then added, and color development assessed. Any positive clones were subcloned, and retested, except the time on the nitrocellulose membrane was reduced to three

hours.

Positive clones were isolated and sequenced according to standard procedures. The nucleotide sequences of the clones are set forth in the even numbered sequences from SEQ ID Nos:544-586. The odd numbered sequences from SEQ ID Nos:545-587 represent the translated amino acid sequences of the colon nucleic acid clones. Analysis of probes for SEQ ID NOS:544 and 546 confirmed their universal expression.

The foregoing results reflect SEREX isolation of colon cancer clones using autologous serum. The positive clones were then rescreened, using allogeneic serum, following the same method discussed supra, in example 2, except IgG prescreening was omitted. The allogeneic sera was obtained from sixteen normal blood donors, and twenty nine patients who had been diagnosed with colorectal cancer.

The analysis with the two types of serum revealed that fourteen reacted with a subset of sera from normal and cancer patients, twenty-eight only with autologous sera, and six with both allogeneic and autologous sera. Over 60% of the allogeneic serum samples tested reacted with at least one of these positive clones. About 20% reacted with two or more.

In view of the results described above, further experiments were carried out using serum samples from patients with other forms of cancer, i.e., renal cancer (13 samples), lung cancer (23 samples), and breast cancer (10 samples). The results are set forth in Table 6 which follows:

Table 6: Allogeneic serotyping using colon cancer clones

Clone Number	Normal Sera	Colon Cancer	Renal Cancer	Lung Cancer	Breast Cancer
NY-Co-8	0/16	8/29	1/13	0/23	0/10
NY-Co-9	0/16	5/29	1/13	1/23	0/10
NY-Co-13	0/16	5/29	0/13	0/23	0/10
NY-Co-16	0/16	3/29	0/13	0/23	0/10
NY-Co-20	0/16	4/29	0/13	0/23	0/10
NY-Co-38	0/16	4/29	3/13	0/23	1/10

Of the six clones which were identified as being reactive with autologous and allogeneic

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cancer serum, and not with normal serum, two were found to be identical to previously identified molecules (NY-Co-. Four others were found to have little or no homology to known sequences and thus are preferred allogeneic-reactive colon cancer clones. These nucleic acids and their polypeptide translations are presented as SEQ ID NOS: 544-551: SEQ ID NO: 544/545 (NY-CO-8), SEQ ID NO: 546/547 (NY-CO-9), SEQ ID NO: 548/549 (NY-CO-16) and SEQ ID NO: 550/551 (NY-CO-38). . Of twenty seven allogeneic colon cancer serum samples tested, 67% reacted with at least one of these antigens.

The expression pattern of mRNA corresponding to SEQ ID NOS:544, 546 and 550, as well as other sequences identified via the preceding examples was determined. To do this, RT-PCR was carried out on a panel of RNA samples, taken from normal tissue. The panel contained RNA of lung, testis, small intestine, colon, breast, liver and placenta tissues. The RNA was purchased from a commercial source. RNA from a colon tumor sample was also included. All samples were set up for duplicate runs, so that genomic DNA contamination could be accounted for. In the controls, no reverse transcriptase was used.

Primers were designed which were specific for the cDNA, which would amplify 5'-fragments, from 300-400 base pairs in length. The PCR reactions were undertaken at an annealing temperature of 68°C. Where appropriate, 5' and 3'-RACE reactions were undertaken, using gene specific primers, and adapter primers, together with commercially available reagents. Specifically, SEQ ID NOS: 546 and 550 were tested using RACE. The resulting products were subcloned into vector pCR 2.1, screened via PCR using internal primers, and then sequenced.

SEQ ID NOS:544 and 546 were found to be amplified in all tissues tested. SEQ ID NO:550 was found in colon tumor, colon metastasis, gastric cancer, renal cancer and colon cancer cell lines Colo 204 and HT29, as well as in normal colon, small intestine, brain, stomach, testis, pancreas, liver, lung, heart, fetal brain, mammary gland, bladder, adrenal gland tissues. It is was not found in normal uterine, skeletal muscle, peripheral blood lymphocytes, placental, spleen thymus, or esophagus tissue, nor in lung cancer.

The analysis also identified differential expression of a splice variant of SEQ ID NO:550, i.e., SEQ ID NO:552. When the two sequences were compared, it was found that SEQ ID NO:550 encodes a putative protein of 652 amino acids (SEQ ID NO:551), and molecular weight of 73,337 daltons. SEQ ID NO:552, in contrast, lacks an internal 74 base pairs, corresponding to

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nucleotides 1307-1380 of SEQ ID NO:550. The deletion results in formation of a stop codon at the splice function, and a putative protein of 403 amino acids (SEQ ID NO:553), and molecular weight 45,839. The missing segment results in the putative protein lacking a PEST protein degradation sequence, thereby suggesting a longer half life for this protein.

5 In additional experiments, primers designed not to differentiate between SEQ ID NOS: 550 and 552 resulted in almost universal amplification (placenta being the only exception). In contrast, when primers specific for SEQ ID NO:552 were used differences were seen in normal pancreatic, liver, lung, heart, fetal brain, mammary gland, bladder, and adrenal gland tissue, where there was no expression of SEQ ID NO:552 found.

10 Northern blotting was also carried out for SEQ ID NOS: 544, 546, 550 and 552. These experiments employed the same commercially available RNA libraries discussed above were used.

Samples (2 ug) of polyA⁺ RNA were analyzed from these samples, using random, ³²P labelled probes 300-360 nucleotides in length, obtained from PCR products. These probes were hybridized to the RNA, for 1.5 hours, at 68°C, followed by two washes at 0.1xSSC, 0.1% SDS, 15 68°C, for 30 minutes each time.

SEQ ID NOS:544 and 546 were again found to be universally expressed.

Further screening identified additional isoforms of SEQ ID NOS:544 and 550. These are set forth as SEQ ID NOS: 554, 556, 558 and 560. The isoform represented by SEQ ID NO:554 (translated as SEQ ID NO:555) is a naturally occurring splice variant of SEQ ID NO:544, found 20 in normal colon. SEQ ID NO:556 (translated as SEQ ID NO:557), which is an isoform of SEQ ID NO:550 (translated as SEQ ID NO:551), was found in brain tissue, primarily spinal chord and medulla. SEQ ID NO:558 (translated as SEQ ID NO:559), was found in normal kidney and in colon tumors, metastasized colon cancer, renal cancer, gastric cancer, and in colon cancer cell line Colo 205. It was not found in any normal tissue other than kidney.

25 The nucleic acid molecule whose nucleotide sequence set forth as SEQ ID NO:560 (translated as SEQ ID NO:561), is a further isoform of SEQ ID NO:552. It is similar to SEQ ID NO:558, except it contains a long nucleotide insert encoding a longer COOH terminus. It was expressed in normal bladder and kidney cells, and renal cancer cells. It was not expressed in colon cancer cells.

30 It is reported above that fourteen clones reacted with subsets of serum from both normal

and cancer patients, while twenty eight reacted with autologous sera only. These clones were sequenced, in accordance with standard, art recognized methods. Of the clones which reacted only with autologous sera, nine appear to be previously unidentified sequences. These are set forth as SEQ ID NOS: 562, 564, 566, 568, 570, 572, 574, 576 and 578. SEQ ID NO:562 (translated as SEQ ID NO:563) is 1445 nucleotides long, and shows some similarity to known sequences for myosin and tropomyosin. SEQ ID NO:564 (translated as SEQ ID NO:565), which is 1226 nucleotides long, contains a TPR motif. The sequence set forth in SEQ ID NO:566 (translated as SEQ ID NO:567) is 1857 nucleotides long, and shows similarity to cyclophilins. The nucleotide sequence set forth in SEQ ID NO:568 (translated as SEQ ID NO:569) is 1537 nucleotides long, and shows similarity to murine gene 22A3, which has unknown function, but resembles an unconventional form of myosin, as well as an EST for heat shock inducible mRNA. As for the molecule set forth in SEQ ID NO:570 (translated as SEQ ID NO:571), it appears to resemble a nucleic targeting signal protein. SEQ ID NO: 572 (translated as SEQ ID NO:573) is 604 nucleotides long, and may encode a lysosomal protein. The molecule set forth in SEQ ID NO:574 (translated as SEQ ID NO:575) is 742 nucleotides long, and encodes a protein with an SH3 domain and which shows some similarity to GRB2 and human neutrophil oxidase factor. The molecule set forth in SEQ ID NO:576 (translated as SEQ ID NO:577) is 1087 nucleotides long, and encodes a protein which contains coiled core domains. The molecule set forth in SEQ ID NO:578 (translated as SEQ ID NO:579) is 2569 nucleotides long, shows some similarity with *Drosophila* homeotic material tudor protein, and has a DY(F)GN repeat.

Additional sequences were identified which were expressed in both normal sera and cancer cells. The sequence set forth in SEQ ID NO:580 (translated as SEQ ID NO:581), e.g., is 2077 nucleotides long, and was expressed by both colorectal cancer and normal cells. Analysis of the sequence showed that it possesses a nuclear targeting sequence. The molecule set forth in SEQ ID NO:582 (translated as SEQ ID NO:583) is 3309 nucleotides long, was expressed by colorectal cancer and normal cells, and is similar to heat shock protein 110 family members. The molecule presented in SEQ ID NO:584 (translated as SEQ ID NO:585) was expressed in a colon to lung metastasis, as well as by normal tissue. It is 2918 nucleotides in length. Analysis shows that it contains 2 zinc finger domains. The nucleotide sequence of SEQ ID NO:586 (translated as SEQ ID NO:587) was also expressed in a colon to lung metastasis, is 1898 nucleotides long, and is

also expressed by normal tissue. Specifically, the reactivity of the molecules was as follows:

Table 7

5	SEQ ID NO:	Normal Sera Reactivity	Tumor Sera Reactivity
	580	2/16	2/16
	582	2/16	3/16
10	584	2/16	2/16
	586	2/8	1/16

A more extensive set of RT-PCR experiments were carried out to study the expression pattern of SEQ ID NOS: 550, 552, 558 and 560. The results follow.

Table 8: RT-PCR analysis of colon SEREX clones

	<u>normal tissue</u>	<u>SEQ ID NO.:550</u>	<u>SEQ ID NO.:552</u>	<u>SEQ ID NO.:558</u>	<u>SEQ ID NO.:560</u>
20	kidney	+	Negative	Negative	Negative
	colon	+	Negative	Negative	Negative
	small		Negative	Negative	Negative
	intest.	+	Negative	Negative	Negative
	brain	+	Negative	Negative	Negative
25	stomach	+	Negative	Negative	Negative
	testis	+	Negative	Negative	Negative
	pancreas	+	Negative	Negative	Negative
	lung	+	Negative	Negative	Negative
	liver	+	Negative	Negative	Negative
30	heart	+	Negative	Negative	Negative
	fetal		Negative	Negative	Negative
	brain	+	Negative	Negative	Negative
	mammary		Negative	Negative	Negative
	gland	+	Negative	Negative	Negative
35	bladder	+	Negative	Negative	Negative
	adrenal		Negative	Negative	Negative
	gland	+	Negative	Negative	Negative
	uterus	Negative	Negative	Negative	Negative
	skeletal		Negative	Negative	Negative
40	muscle	Negative	Negative	Negative	Negative
	PBL	Negative	Negative	Negative	Negative
	placenta	Negative	Negative	Negative	Negative

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spleen	Negative	Negative	Negative	Negative
thymus	Negative	Negative	Negative	Negative
esophagus	Negative	Negative	Negative	Negative

Tumor Tissue

5	renal cancer (4)	+ (2/4)	+ (2/4)	+ (2/4)	+ (2/4)
	colon primary tumors (10)	+ (10/10)	+ (10/10)	+(10/10)	Negative
10	colon mets (4)	+ (4/4)	+ (4/4)	+ (4/4)	Negative
	breast cancer (6)	+ (3/6)	Negative	Negative	Negative
	lung cancer (6)	+ (6/6)	Negative	Negative	Negative
15	gastric cancer (1)	+	+	+	Not tested
	<u>colon cancer cell lines</u>				
	colo 205	+	+	+	Negative
	HT29	+	+	Negative	Negative
20	HCT15	Negative	Negative	Negative	Negative

Example 8: Isolation and analysis of additional clones

For the establishment of a cDNA library from human tissue total RNA was obtained from 0.5 g of a renal clear cell carcinoma and established according to the method of Chomzynski as described above. The mRNA was extracted from total RNA with oligo-dT-cellulose. The synthesis of the first strand cDNA was accomplished by the method described by Gubler and Hoffmann, *Gene* 25: 263 (1983) using RNase H and DNA polymerase I. For adaptation of the cDNA Klenow enzyme, adaptors with EcoRI restriction enzyme sites were ligated to the cDNA ends using T4 DNA ligase (Ferretti L and Sgamerella V, *Nucl. Acids Res.* 9: 3695 (1981)). Following restriction enzymatic digestion with the enzyme XhoI, cDNA molecules of different length were separated using Sephacryl 400 and transfected into λ ZAPII phage vectors (Short JM et al., *Nucleic Acids Res.* 16: 7583 (1988)). The recombinant phage DNA was packaged into phages after ligation with packaging extracts and used for the transfection of *E. coli* bacteria. The titration of the library resulted in 1.8×10^6 recombinant primary clones. The total cDNA library was transfected in *E. coli* and amplified. The titer of the cDNA library after amplification was 10^{11} plaque forming units per ml (pfu/ml). These transfected cells were used in experiments which follow.

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In accordance with the invention as described above, identification of immunogenic material was achieved by using human sera which has been completely depleted of antibodies directed against antigens derived from native and lytic λ phage-transfected *E. coli* bacteria. To this end, the serum was absorbed, as follows.

5 *E. coli* bacteria of the strain XL1-blue were cultured in 50 ml LB medium overnight. After achieving an optical density of $OD_{600} = 1.0$, the bacteria were pelleted by centrifugation, resuspended in 5 ml phosphate buffered saline (PBS), and lysed by sonication. The bacterial lysate was bound onto a matrix of activated Sepharose, which was then put into a column and used for the absorption of the human serum. The serum was run over this column 10 times.

10 A culture of *E. coli* XL1 blue bacteria in the exponential growth phase was pelleted by centrifugation, transfected in 0.01 M magnesium sulfate with 10^6 λ ZAPII phages without a recombinant insert and incubated in 5 ml LB medium for four hours. The lysate of the transfected bacteria was used in the same manner as the untransfected bacteria, with the human serum described supra being passed through the column an addition ten times.

15 To complete the depletion of the serum, interfering antibodies from lytically transfected *E. coli* bacteria were cultured on agar plates and their proteins were blotted onto nitrocellulose membranes after 10 hours of culture at 37°C. Following this, the serum which had been preabsorbed according to the above steps was transferred to the blotted nitrocellulose membrane, and the absorption procedure was repeated five times. The serum, which was processed in
20 accordance with the invention, was totally depleted of antibodies directed against antigens derived from *E. coli* and phages.

In this, a renal cancer-specific antigen was identified via the following steps. Bacteria of the strain XL1 blue were transfected with recombinant phages derived from the described cDNA library and plated at a density of $4-5 \times 10^3$ plaque forming units (pfu) per plate in LB-medium with
25 isopropylthiogalactopyranoside ("IPTG"). After 12 hours of incubation at 37°C, nitrocellulose membranes were put on top of the cultures and culture plates were incubated for another four hours. This was followed by incubation of the nitrocellulose membrane for one hour in Tris-buffered saline (PBS) with 5% milk powder. After washing the nitrocellulose membranes three times in TBS, the stripped human serum secured following Example 2 was diluted 1:1000 in TBS/0.5% (w/v) milk
30 power and incubated overnight with gentle shaking. After the incubation with the nitrocellulose

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membrane the serum was removed and kept for additional testing. Following incubation with serum, the nitrocellulose membranes were washed three times in TBS, and incubated with a polyclonal alkaline phosphatase-conjugated goat anti-human IgG serum for one hour. Following this, the nitrocellulose membranes were washed repeatedly with TBS/0.01% (v/v Tween 20). The reaction was developed using nitroblue tetrazolium chloride and bromochloro-indoyl-phosphate in TBS. The binding of human antibodies to the expressed protein became visible by a blue ring-formed color deposit on the nitro-cellulose membrane. The efficient preabsorption of the serum made it possible to develop the membrane at 37°C over several hours without compromising the quality of the test because of background reactivity caused by antibodies against *E. coli* and phage antigens.

Positive clones were localized on the agar plates, transferred into transfection buffer, and used for a second round of transfection and subcloning. A total of 1.8×10^6 recombinant clones were subjected to screening and five different positive-reacting clones were identified.

Positive clones, i.e., those which had bound antibodies derived from the processed human serum, were subcloned to monoclonality by repeated rounds of transfection and testing of reactivity with the processed human serum. P-bluescript phagemids with the respective cDNA inserts were cloned by *in vivo* excision (Hay B and Short JM, *Strategies* 5: 16-19, 1992) from the λ ZAPII phage vectors and used for the transfection of *E. coli* SOLR bacteria. Plasmids were isolated from the bacteria after alkaline lysis with NaOH in a modification of the method of Birnboim HC and Doly J. *J. Nucl. Acids Res.* 7: 1513 (1979). The recombinant plasmid DNA was sequenced according to standard methods using M13-forward and M13-reverse oligonucleotides. The DNA sequence obtained and the resulting amino acid sequence were compared with nucleic acid and protein data banks (Gene Bank, EMBL, Swiss Prot). The sequencing of the cDNA inserts was continued using internal oligonucleotides. Analysis showed no homology with any sequences deposited in the data banks. The full length cDNA clone, referred to as SK313, was cloned with the RACE method (Frohman MA, Dush MK, Martin GR, *Proc. Natl. Acad. Sci. USA* 85: 8998 (1988)), and had a carbonic anhydrase domain at the 5' end.

As a continuation of these experiments, RNA was isolated from a spectrum of malignant and normal human tissues and Northern blots were performed with labeled SK313 (also referred to as clone HOM-RCC-313). The Northern blot analysis demonstrated that the mRNA of clone HOM-

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RCC-313 was overexpressed in 4 out of 19 renal cell carcinomas compared to normal kidneys. Very weak expression was found only in colonic mucosal tissue and in normal kidney. Expression in other tissues was not observed.

To determine the incidence of antibodies against antigens which are identified above, allogeneic sera from healthy individuals and tumor patients were analyzed. To this end, the sera were processed as described above and depleted from antibodies against antigens derived from *E. coli* and phages. For the detection of antigen-specific antibodies, phages derived from reactive clones were mixed with non-reactive phages derived from the same cDNA library at a ratio of 1:10 and tested as described above for reactivity with antibodies in the human test serum. The serum which had been used for the identification of the antigen was used as a positive control. The non-reactive phages served as a negative control. A serum sample was positive for antigen reactive antibodies, if the expected percentage of the phage plaques showed a positive reaction. In the case of the renal cell carcinoma antigen represented by clone HOM-RCC-313, the analysis of a spectrum of human sera showed that only sera from renal cell carcinoma patients contained reactive antibodies. Sera from healthy controls and patients with other tumors did not contain such antibodies.

The cDNA for clone HOM-RCC-313 was excised from the plasmid DNA by digestion with the restriction enzyme EcoR1, was separated by agarose gel electrophoresis, followed by extraction from the gel. This was then used to create a vector which expresses a fusion protein with the bacterial protein anthranilate synthetase. A relevant fragment in the exact open reading frame was cloned into pATH plasmid vectors (Koerner et al., *Meth. Enzymol.* 194: 477 (1991)). Induction of protein expression was obtained after transformation of the plasmids into *E. coli* of strain BL21 as described (Spindler et al., *J. Virol.* 49: 132 (1984)). Expressed fusion proteins were separated by SDS gel electrophoresis, excised from the gel, eluted and freeze dried. Rabbits were immunized by subcutaneous injection with 100 µg of the lyophilisate combined with Freund's adjuvant according to standard procedures. Immunization was repeated three times at two-week intervals using incomplete Freund's adjuvant. The rabbit was bled and antiserum was obtained. The obtained antiserum was depleted from antibodies reactive with *E. coli* and phages as described above and tested for reactivity against the renal carcinoma antigen as described for the human serum. Reactivity was detected at dilutions of 1: >100,000.

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Additional clones were identified from pancreatic cancer tumor specimen using the SEREX method of Sahin et al., (1995). A cDNA library was prepared and reacted with high titer IgG in sera of pancreatic carcinoma patients. A total of 8×10^5 clones were screened with autologous serum, and 4.5×10^3 clones were screened with three different allogeneic sera. Twenty three clones, representing seven different transcripts were found. Four were previously unknown, unisolated genes. Of the remaining three, glycolytic enzyme aldolase A was found (SEQ ID Nos:799 and 800). Another molecule was "known" in that it was homologous to the rat eIF-5 gene (SEQ ID Nos:801 and 802), which is a eukaryotic translation initiation factor. The human eIF-5 gene was not previously known.

When hepatocellular carcinoma libraries were studied in the same way, a total of 1.5×10^6 clones were screened, and 98 positives were found. A total of 59 of these were sequenced, and corresponded to at least 20 different transcripts. Nine of these were assayed with allogeneic sera from hepatocellular cancer (HCC) patients and normal patients. High titered antibody was restricted to HCC patients. The majority of isolated sequences did not correspond to known molecules. Three which did were human albumin (SEQ ID Nos:803 and 804), senescence marker protein SMP30 (SEQ ID NOs:805 and 806), and C3VS (SEQ ID NOs:807 and 808). The latter was overexpressed in 2 of 4 hepatocarcinoma tissues, as compared to normal. Expression of SMP30 was found to vary highly.

The methodology was combined with subtractive cDNA techniques when assaying leukemia cells (T-ALL). An antigen was found which was identical to a broadly expressed, DNA repair enzyme.

Further assays identified the known molecule galectin-9 (SEQ ID NOs:809 and 810), as being highly expressed on human macrophages and dendritic cells. Expression is upregulated during differentiation of monocytes to macrophages. Highest levels were found on monocyte derived, dendritic cells.

Fusion proteins "LD1-mFc" and "LD2-mFc" were constructed to help analyze galectin-9. These consist of murine IgG heavy chain fragments, and a lectin domain (LD1, or LD2), as the N-terminus. Analysis indicated that the C-terminal lectin domain binds to the surface ligands, while the cell surface ligands recognized by the C-terminal lectin domain of galectin-9 was expressed only in a small, subpopulation of dendritic cells.

Further analysis of ovarian cancer cells (500,000 clones, using the SEREX method described

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above), identified previously known antigens MAGE-4 (SEQ ID Nos:811 and 812) and restin (SEQ ID Nos:813 and 814), and six other newly identified molecules.

Further experiments were carried out which involved restin. A variation of restin is known, i.e., "CLIP170", which was reported to mediate binding of endosomes to microlubules. It was found that both resin and CLIP 170 are highly expressed in dendritic cells, and are involved in the formation and transport of macropinosomes, a feature of professional antigen presenting cells. Expression of restin was induced after 48 hours of culture of monocytes in GM-CSF/IL-4 supplemented medium. Highest levels were found in immature dendritic cells. When microlubile systems, which are essential for the activity of restin/CLIP-170 were disrupted, macropinocytosis was lost completely.

Further work with the methodology disclosed herein on glioma identified a clone encoding nm23-H2 protein (SEQ ID Nos:815 and 816). This clone corresponds to subunit B of nucleoside diphosphate kinase, which is implicated in tumor metastasis control. It is also known as PuF, a transcriptional factor, for c-myc proto-oncogenes. Antibodies against the protein were found in 1 of 18 sera of brain malignancy patients, 3 of 20 melanoma patients, and 2 of 20 sera from healthy patients. When expression studies were carried out using RT-PCR, 25 of 28 brain tumor, and 4 or 5 meningioma tumor samples were found to express the gene.

Example 9: Isolation and analysis of lung cancer clones

A cDNA library was constructed from a case of moderately differentiated adenocarcinoma of the lung, obtained from the Department of Pathology at The New York Hospital. The library was constructed in a λ ZAP Express vector using a cDNA library kit (Stratagene, La Jolla, CA).

The cDNA library was screened with autologous patient's serum as described previously [Sahin, U. et al., *Proc Natl Acad Sci USA* 92:11810-3 (1995); Chen, Y.T. et al. *Proc Natl Acad Sci USA*. 94:1914-8 (1997)]. Briefly, the serum was diluted 1:10, pre-absorbed with transfected *E. coli* lysate, and a 1:10 dilution of the absorbed serum (final dilution of serum 1:100) was incubated overnight at room temperature with the nitrocellulose membranes containing the phage plaques. After washing, the filters were incubated with alkaline phosphatase-conjugated goat anti-human Fc γ secondary antibodies and the reactive phage plaques were visualized by incubating with 5-bromo-4-chloro-3-indolyl-phosphate and nitroblue tetrazolium. Phagemid clones encoding human

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immunoglobulin sequences were subsequently eliminated during the secondary screening.

The reactive clones were subcloned, purified, and *in vitro* excised to pBK-CMV plasmid forms (Stratagene). Plasmid DNA was prepared using Wizard Miniprep DNA Purification System (Promega, Madison, WI). The inserted DNA was evaluated by EcoRI-XbaI restriction mapping, and clones representing different cDNA inserts were sequenced. The sequencing reactions were performed by DNA Services at Cornell University (Ithaca, NY) using ABI PRISM (Perkin Elmer) automated sequencers.

To evaluate the mRNA expression pattern of the cloned cDNA in normal and malignant tissues, gene-specific oligonucleotide primers for PCR were designed to amplify cDNA segments of 300-400bp in length, with the estimated primer melting temperature in the range of 65-70°C. All primers were commercially synthesized (Operon Technologies, Alameda, CA). RT-PCR were performed using 35 amplification cycles in a thermal cycler (Perkin Elmer) at an annealing temperature of 60°C.

Genomic DNA were extracted from cell lines and frozen tumor tissue. Following restriction enzyme digestion, the DNA was separated on a 0.7% agarose gel, blotted onto nitrocellulose filters, and hybridized to an ^{32}P -labeled DNA probe at high stringency (65°C, aqueous buffer). Washing of the blot was also under high stringency conditions, with a final wash in 0.2XSSC with 0.2% SDS at 65°C.

To identify the 5' end of the mRNA transcripts, RACE (rapid amplification of cDNA ends) methodology was utilized using the Marathon cDNA amplification kit (Clontech) and adaptor-ligated testicular cDNA as the substrate. The PCR products, after separation by agarose gel electrophoresis, were cloned into the direct PCR cloning vector pGEM-T (Promega).

Single-strand conformation polymorphism (SSCP) analysis was performed to analyze cDNA from various tissues, using previously described protocols [Dracopoli, C.D. et al., New York: John Wiley and Sons, Inc. (1997)]. Briefly, PCR was performed with 5 μl RT product in a final volume of 25 μl , with 2 μCi of $\alpha^{32}\text{P}$ -dCTP (~3000 Ci/mmol, New England Nuclear) per reaction. The PCR conditions was as described for RT-PCR above. After the PCR, 1 μl of the mixture was diluted with 5 μl of denaturing buffer (95% formamide, 20 mM EDTA, 0.05% bromophenol blue, 0.05% xylene cyanol), heat-denatured at 98°C for 2 min, and electrophoresed through an 8% polyacrylamide gel with 10% glycerol. As controls, aliquots of the same samples were diluted with a standard non-

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denaturing DNA loading dye and electrophoresed in parallel. The electrophoresis was performed at room temperature at a constant power of 10-12 watts. The gel was then dried and autoradiography performed for 15-24 hours with an intensifying screen.

5 Identification of Immunoreactive cDNA clones

A cDNA expression library of 1.42×10^7 primary clones was prepared from Lu15, a specimen of moderately differentiated adenocarcinoma of the lung and 8×10^5 phage plaques were immunoscreened with absorbed autologous patient serum at 1:100 dilution. Excluding false-positive clones encoding immunoglobulin gene fragments, 20 positive clones were identified. These clones were purified and sequence analyzed. Comparisons of the sequences showed that these clones represented cDNAs from 12 distinct genes, designated NY-LU-1 through NY-LU-12 (Table 9). A homology search through the GenBank/EMBO databases revealed that 4 of the 12 genes corresponded to previously known molecules, and 8 others were unknown genes, with sequence identity limited only to short segments of known genes or to expressed sequence tags (ESTs).

Table 9: NY-LU clones

Gene Designation	Gene/Sequence Identity [Accession Number]	cDNA	Comments
NY-LU-1	Aldolase A (N and H type) [X06352]	Lu-15/24, 72, 83, 158, 219, 241	Human fructose, 1,6 diphosphate aldolase A. Expressed in muscle (M type), but also in most other tissues (N and H types). Levels increased in most lung cancers; released into blood upon trauma and in several cancers.
NY-LU-2	hASNA-1 [U60276]	Lu-15/26, 66	Human homolog of the ATP-binding ars A component of the bacterial arsenite transporter. Previously cloned by SEREX from a testicular library (Chen et al., unpolished). Ubiquitously expressed.
NY-LU-3	Annexin IX [L19605]	LU-15/64	Homosapiens 56K autoantigen. Antibodies to Annexin IX are found in multiple autoimmune diseases. ubiquitously expressed.

NY-LU-4	Rip-1 [U55766]	Lu-15/65	Human HIV Rev-interacting protein. Expressed in B cells, monocytes and rhabdomyoma cells.
NY-LU-5	Unknown [W61291, W92962, etc.]	Lu-15/80	Expressed ubiquitously (by RT-PCR).
NY-LU-6	Unknown [none]	Lu-15/85	Sequence contains no ORF, expressed ubiquitously (by RT-PCR).
NY-LU-7	Unknown [W23466, AA167732, etc.]	Lu-15/135,217	Expressed in neuron, pregnant uterus, lung ca., parathyroid tumors, etc.
NY-LU-8	Unknown [Z78323, N39225, etc.]	Lu-15/139	Expressed in fetal heart, retin, multiple sclerosis, etc.
NY-LU-9	Unknown [W26569, AA036884, etc.]	Lu-15/145	Expressed in retina, pregnant uterus, fetal liver-spleen, etc.
NY-LU-10	Unknown [M29204, etc.]	Lu-15/154	Expressed in colon, pancreas, pregnant uterus, fibroblasts, etc.
NY-LU-11	Unknown [W23466, AA057400, etc.]	Lu-15/270	Expressed in retina, pregnant uterus, fetal heart, fetal liver-spleen, parathyroid tumors, etc.
NY-LU-12	g16	Lu-15/251	Located at the 3p21 TSG locus (see text)

Of the 4 known genes, aldolase A (NY-LU-1; SEQ ID NOs:689 and 690) was most frequently isolated, representing 6 of 20 primary positive clones in the entire screening. NY-LU-2 (SEQ ID NO:691), represented by two isolates, was the human homolog of the ATP-binding arsA component of the bacterial arsenite transporter, a gene which has been shown to be ubiquitously expressed in various tissues [Kurdi-Haidar, B. et al., *Genomics* 36:486-91 (1996)]. NY-LU-3 (SEQ ID Nos:692 and 693) encodes annexin XI, which is a 56KD ubiquitously expressed antigen to which autoantibodies have been described in sera from patients with various autoimmune diseases [Misaki, Y. et al., *J Biol Chem* 269:4240-6 (1994); Misaki, Y. et al., *J Rheumatol.* 22:97-102 (1995)]. The last gene in this group, NY-LU-4 (SEQ ID NOs:694 and 695), codes for the human HIV Rev interacting protein Rip-1, which has been shown to be expressed in the monocyte cell line U937, the rhabdomyoma cell line RD, as well as in adherent monocytes and primary lymphocytes [Refaeli, Y.

et al., *Proc Natl Acad Sci USA* 92:3621-5 (1995)].

Of the eight unknown genes, 6 (NY-LU-5, 7, 8, 9, 10, 11; SEQ ID Nos:696, 698, 699, 700, 701 and 702/703, respectively) shared sequence identify with reported expressed sequence tags (EST) , likely representing cDNA products derived from the same genes. These ESTs were derived from various somatic tissues unrelated to lung, e.g., neuron, pregnant uterus, colon, endothelial cells, etc., suggesting that these genes are widely expressed in human tissues (Table 9), making them unlikely candidates for vaccine-based tumor immunotherapy. These clones were not further investigated. The only novel gene in this group, NY-LU-6 (SEQ ID NO:697), showed no sequence identity to deposited sequences in the public databases. The tissue expression pattern of this gene was evaluated by RT-PCR analysis using gene-specific primers and a normal tissue RNA panel consisting of lung, colon, kidney, liver, brain and testis. Results showed universal expression in these tissues, and this clone was not further analyzed.

NY-LU-12 is on *TSG* locus of chromosome 3p21.

The last gene in the unknown gene group, NY-LU-12, was represented by the immunoreactive clone Lu15-251. This clone, 1081bp in length, contained an uninterrupted open reading frame (ORF) of 952 bp, followed by a 129bp 3'untranslated region. No translation initiation codon was identified, indicating that this was a partial cDNA clone.

A sequence homology search revealed that this gene shared up to 30% homology with two different human proteins at its C-terminus (Fig. 1), LUCA15 and DXS8237E (GenBank accession numbers U23946, and P98175) and also shared homology to S1-1, the rat counterpart of DXS8237E [Inoue, A. et al., *Nucleic Acids Res.* 24:2990-7 (1996)]. LUCA15 was subsequently proven to be a gene immediately centromeric to NY-LU-12 on the *TSG* locus on chromosome 3p21 (see below and [Wei, M.H. et al., *Cancer Res.* 56: 2487-92 (1996)]). Our analysis of LUCA15 revealed the presence of a nuclear localization signal in the putative LUCA15 protein. DXS8237E, was located on chromosome Xp11.23 [Coleman, M.P. et al., *Genomics* 31:135-8 (1996)] and its rat homolog, S1-1, has been shown to be an RNA-binding protein [Inoue, A. et al., *Nucleic Acids Res.* 24:2990-7 (1996)].

Of particular interest, however, was that a short segment (92bp) at the 5' end of NY-LU-12 was identical to a previously identified gene, g16 (GenBank accession number U50839), which was

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mapped to chromosome 3p21.3 and was interrupted in the small cell lung cancer line NCI-H740.

To compare NY-LU-12 with g16, the full-length NY-LU-12 cDNA sequence was obtained from normal testicular mRNA through a combination of 5'RACE and direct PCR cloning strategies. The predominant cDNA form (SEQ ID No:707), excluding the poly A tail, is of 3591bp in length.

5 An open-reading-frame of 1123 amino acid residues (SEQ ID No:708) was identified (nt. 102-3470), with 101bp of 5' untranslated and 129bp of the 3' untranslated region. The nucleotide and amino acid sequences are shown in Fig. 2.

Comparison with the g16 sequence verified that these two are identical genes and mapped NY-LU-12 to *TSG* locus on 3p21. However, the reported g16 sequence, 2433 bp in length, lacks the
10 5' end 110 bases which include the translational initiation codon at nucleotide 102, and also the 3' end 980 nucleotides of NY-LU-12. In addition, 74bp DNA segment (nt. 1587-1659 of NY-LU-12) was absent in the reported g16 sequence. Oligonucleotide primers flanking this 74 bp region were designed and used to amplify RNA from 1 normal lung, 5 lung cancer cell lines, and 6 lung cancer specimens. Two RT-PCR products were seen in every specimen, corresponding to the sizes of the
15 two cDNA variants. It was thus concluded that this variation represents an alternate splicing event which occurs in both normal and cancerous lung tissues. Of interest, however, was the difference in the putative translational products resulting from this additional 74bp exon. In the absence of this exon, the open-reading-frame of NY-LU-12 would end in the termination codon at nt.1736, as reported for g16, with a total length of 520 amino acid residues (in contrast to 1123 residues in the
20 longer transcript). Moreover, this shorter form would not encode the C-terminal portion of the NY-LU-12 protein, the segment responsible for the immunoreactivity of Lu15-251 to the autologous patient serum.

Additional cDNA variants of NY-LU-12

25 In the process of 5'RACE cloning of the full-length NY-LU-12, three minor forms of cDNA products were identified which varied in their transcriptional initiation site and in their exon usage in the 5' segment of this gene. These variants will be described as transcripts B, C, and D (SEQ ID Nos:709, 711 and 712). Fig. 3 shows the comparison of these transcripts to the predominant cDNA form (transcript A, see Fig. 2).

30 Transcript B (Fig. 3A, bottom) contains an additional exon of 208 base pairs, inserted at

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nucleotide 145 of the NY-LU-12 sequence. The original ORF of NY-LU-12 is disrupted due to this inserted sequence, and the AUG initiation codon used by transcript A is thus unlikely to be used by this transcript. A new potential translational initiation site, however, is found within this new exon and would continue the translation into the ORF of transcript A. The final product would be a protein of 1177 amino acids (SEQ ID NO:710), with the 69 residues at the N-terminus different from transcript A. Interestingly, this new exon encodes for a signal peptide not present in the transcript A (Fig. 3A, bottom), and it is possible that these two products are localized to different subcellular compartments.

Similar to transcript B, transcripts C and D both contained additional exon(s) not present in transcript A. Transcript C contained two extra exons in tandem and a length of 364bp, only one of which (137bp) was present in transcript D, Figure 3B. These extra exon(s), inserted at the same alternate splicing site as transcript B, disrupted the original ORF, and the only long ORF would initiate at nucleotide position 498 of NY-LU-12 (959 of transcript C, 635 of transcript D). Considering the long untranslated region at the 5' end, it is doubtful whether transcripts C and D are indeed translated *in vivo*.

Correlating with this variation of NY-LU-12 mRNA, Northern blot analysis showed several RNA species in normal tissues, ranging approximately from 3 to 4.4 Kb. The intensity of individual bands also appear to vary among different tissues, suggesting post-transcriptional tissue specific regulation of NY-LU-12 mRNA.

Features of NY-LU-12 and its putative gene product

Analysis of the NY-LU-12 amino acid sequence showed 20 inexact 6 amino acid repeats with a consensus sequence of D(F/Y)RGR(D/E) close to the N-terminus (Fig. 2). These repeats were separated by 4 to 6 amino acid intervals, which showed no apparent sequence homology among each other. This feature in primary sequence is distinctive among known proteins. Hydrophilicity plot revealed that this region, although hydrophilic in general, has regular hydrophobic turns, and these cycles of hydrophilicity changes correspond to the hexapeptide repeats. Although the significance of this characteristic is unclear at present, this segment of sequence is highly rich in arginine and aspartic acid, a feature shared by RNA binding proteins. Similar motifs, rich in arginine and aspartic acid residues, were found in other RNA-binding proteins [Witte, M.M.

et al., *Proc Natl Acad Sci USA* 94: 1212-7 (1997); Wilson, R. et al., *Nature* 368:32-8 (1994); Seraphin, B. et al., *Nature* 337:84-7 (1989); Takagaki, Y. et al., *Proc Natl Acad Sci USA* 89:1403-7 (1992)], e.g., RNA [Seraphin, B. et al., *Nature* 337:84-7 (1989)] hnRNA 3' end cleavage stimulation factor [Takagaki, Y. et al., *Proc Natl Acad Sci USA* 89:1403-7 (1992)], etc., indicating that NY-LU-12 is likely to be an RNA-binding protein. Consistent with this, PROSITE analysis of the putative NY-LU-12 protein identified a bipartite nuclear localization signal between amino acids 1016-1032 and a 4-residue nuclear localization pattern (PRKR) at amino acid 604-607 (Fig. 2), suggesting that NY-LU-12 is a nuclear protein. Analysis for post-translational modification sites showed potential sites for tyrosine sulfation, amidation, as well as phosphorylation sites for protein kinase A, C, casein kinase II, and tyrosine kinase. A PEST region, peptide sequences consistently found among unstable proteins with short half lives, was identified at amino acids 897-928 (Fig. 2), implying NY-LU-12 as an unstable protein.

Southern blot analysis of NY-LU-12 in normal and tumor tissues

To investigate the status of NY-LU-12 in normal and tumor cells, Southern blot analysis was performed on 9 lung cancer cell lines (3 adenocarcinoma, 2 squamous, and 3 large cell anaplastic), Lu15 tumor DNA, and a colon cancer cell line HT29 (Fig. 4). (HT29 was included due to the finding of an EST identified in the GenBank, accession number AA079461, which appeared to be a fusion sequence between semaphorin IV gene and NY-LU-12.) Using a 1.1Kb cDNA probe (nucleotide 1095-2140) and HindIII digested DNA, the results showed that one of the two hybridizing bands was absent in NCI-H740, confirming that NY-LU-12 was partially deleted in this cell line. The breakpoint of this deletion, by using primers from different regions, was further defined to be between nucleotides 1433 and 1777 of NY-LU-12, with the 3' sequences homozygously deleted. Besides NCI-H740, however, no evidence of homozygous deletion was seen in any other tumor cell line sample or in LU15. The similar band intensities and identical sizes of the DNA signals in all specimens also argued against the possibility of a heterozygous deletion or translocation of this gene, at least in the region analyzed. No change was found in HT29, suggesting that the semaphorin IV/NY-LU-12 fusion sequence in the GenBank probably represents a cloning artifact.

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SSCP and sequence analysis of NY-LU-12 in Lu15 tumor DNA.

The mapping of NY-LU-12 to the lung cancer *TSG* locus raised the possibility that an altered protein product due to mutational event may be the basis for the autologous immune recognition. This possibility was explored using DNA sequencing and single-strand confirmational polymorphism (SSCP) analysis.

The DNA sequence contained in the immunoreactive clone Lu15-251 (nucleotide 2518-3599 of NY-LU-12) was obtained from the normal counterpart by RT-PCR cloning using autologous normal lung tissue, and no mutations were found when compared to Lu15-251.

RT-PCR SSCP was then used to analyze the entire NY-LU-12 gene, comparing Lu15 tumor tissue and autologous normal lung tissue. To encompass the whole sequence, 10 sets of primer pairs were designed, each amplifying a range of 205 to 603 bps. For products >400bps, a restriction enzyme digestion step was added prior to the electrophoresis step to further reduce the fragment sizes and increase the assay sensitivity. Results showed no reproducible changes between normal and tumor tissues, and thus no evidence of mutation in Lu15 tumor cDNA. A representative set of SSCP analysis is shown in Fig. 5.

Serological response to NY-LU-12 in lung cancer patient

The frequency of anti-NY-LU-12 response was examined among normal adult and patient sera using the phage plaque assay identical to the original immunoscreening procedure. Of 21 absorbed sera from allogeneic lung cancer patients, one (Lu22) reacted strongly with the Lu15-251 plaque at 1:1000 dilution, and another (Lu7) also reacted at 1:1000, but only weakly. Nineteen other lung cancer patient sera were non-reactive, nor were the sera from 16 healthy donors, 15 colon cancer, 5 breast cancer, 1 renal cancer, 1 prostate cancer, 1 esophageal cancer, and 1 melanoma patients.

Example 10: Expression analysis of additional cancer associated nucleic acids

The clone RING 3 was isolated from breast SEREX analysis as LONY-Br-5 (see above). The gene was identified as homologous to the "bromodomain testis" gene (BRDT; GenBank accession number AF019085). Analysis of related genes identified BRDT as a gene expressed only in testis, which was then investigated by RT-PCR analysis as described above.

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The primers used to perform RT-PCR had the following sequences:

BRDT F1: CAAGAAAGGCACTCAACAG (bp 543-563 of BRDT)

BRDT R1: TTCACTACTTGCTTTAACTGC (bp 776-797 of BRDT)

The meiotic protein H1T (Histone 1 Testis; GenBank accession number M60094) was
5 identified through a literature search for meiotic proteins (testis specific expression).

The primers used to perform RT-PCR had the following sequences:

H1F1: TGCCGAACCTCTCTGTGTC (bp 116-135 of H1T)

H1R1: GCTTCGTGTAGATTTAGGAATC (bp 344-366 of H1T)

10 Table 10: RT-PCR analysis

	<u>Normal Tissue</u>	<u>BRDT</u>	<u>H1T</u>
	mammary gland	-	-
	liver	-	-
15	small intestine	-	-
	brain	-	+/- (very weak)
	lung	-	-
	fetal brain	-	-
	placenta	+	+
20	kidney	-	-
	skeletal muscle	-	-
	pancreas	-	-
	adrenal gland	-	-
	heart	-	-
25	thymus	-	-
	uterus	-	-
	prostate	-	+/- (very weak)
	spleen	-	-
	Testis	+	+

30

	<u>Tumor Tissue</u>	<u>BRDT</u>	<u>H1T</u>
	Colon	0/6	0/6
35	Breast	0/6	6/6+
	Melanoma	0/12	3/12+
	Lung	8/26+	4/26+
	Renal	0/2	0/2
	Ovary	0/2	0/2
40	Esophageal	0/1	0/1

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Gastric	0/1	0/1
Bladder	0/2	0/2

Lung cancer specific expression of BRDT was observed (see table above). BRDT was expressed only in normal testis and possibly in placenta. The expression analysis of H1T revealed that all breast tumor samples (6 of 6) and ~30% lung cancers and melanoma tissue samples expressed H1T. H1T was expressed in normal testis and possibly in placenta and brain.

Example 11: allogeneic serotyping

To confirm the cancer associated expression of SEREX clones, allogenic sera screening of gastric cancer patients' sera was conducted. Sera from normal patients (gastritis) was used as a control for expression of the clones in non-gastric cancer. The screening procedure used was as described above for the SEREX screening, except for the absorption of anti-bacterial and anti-bacteriophage antibodies. The modifications were as follows.

Serum from a stomach cancer patient or a normal individual was diluted to 1:10 in TBS (Tris buffered saline; final volume 5 ml) and passed through a column (BIO-RAD Poly-Prep Chromatography Column, Hercules, CA, USA) containing 0.5 ml Sepharose-4B cross linked to E. coli Y1090 lysate and 0.5 ml Sepharose-4B cross linked to E. coli BNN97 (5 Prime 3 Prime, Inc, Boulder, CO, USA). After repeating the column chromatography 10 times, serum was then diluted to 1:100 in TBS containing 1% BSA and 0.02% sodium azide. To remove antibodies to bacteria and bacteriophages further, 10 ml absorbed serum was incubated overnight with a 82 mm nitrocellulose membrane on which XL-1 Blue MRF' bacteria and lambda ZAP Express phages (Stratagene, La Jolla, CA USA) were immobilized. The serum was stored at - 80°C until use. For allogeneic typing, an equal numbers of positive phage and negative phage were mixed and plated and processed by the standard SEREX screening procedure.

The results of the allogenic screening experiments follow:

Table 11: Allogenic Sera Screening of SEREX Sequences from Gastric Patients

Sequence		Isolated in Serex Patients	Allogenic Serotyping Gastric Cancer Sera	Allogenic Serotyping Normal Sera
Gene/Clone	Number			
RPB-J H-2K binding factor		SM1	6/12	6/16
Telomeric repeat binding protein		SM1	1/12	0/16
Ser/Thr protein kinase		SM1	1/12	0/16
SRY interacting protein-1		SM1	2/12	1/16
Sterol carrier protein X		SM1	2/12	0/16
Archain		SM1	1/12	1/16
HEM-1		SM1	2/12	1/16
Id-1 helix-loop-helix protein		SM1	1/12	0/16
helix-loop-helix transcription factor		SM1	1/12	0/16
Follistatin related precursor protein		SM1,CK, KM	6/12	0/16
Translation initiation factor eIF-4gamma		SM1,SS1, KM	5/12	2/16
M phase phosphoprotein I		SM1,SS1	8/12	5/16
Lysal tRNA synthase		SM1	1/12	0/16
Gelsolin		SM1	4/12	0/16
Zinc finger protein		SM1	1/12	1/16
Goliath		SM1	2/12	1/16
zhx-1		SM1	1/12	1/16
SG24		SM1,SS1, KM	5/12	0/16
SG132		SM1	3/12	0/16
S553		SM1	7/12	7/16
S134		SM1	3/12	0/16
S328		SM1	2/12	1/16
S365		SM1, KM	2/12	0/16

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FKBP25		KM, SS1	5/12	0/16
Pros-27		KM, CK	3/12	1/16
BS4		KM	1/12	1/16
GnRH-II		KM	1/12	0/16
CTBP		KM	1/12	0/16
ETF		KM	3/12	1/16
KIAA0438		KM	1/12	5/16
KIAA0367		KM	4/12	3/16
APK1		KM	2/12	0/16
IPP		KM	1/12	0/16
Tropomyosin		KM	1/12	0/16
p63		KM	1/12	0/16
KIAA0181		KM	1/12	0/16
KIAA0349		KM	1/12	0/16
RPB1		KM	5/12	9/15
PPIM		KM	1/12	-
EB virus		KM	3/12	-
G.KM073		KM	6/12	-
G.KM403		KM	1/12	-
KM192		KM	1/12	-
KM294		KM	1/12	-
KM362		KM	1/12	-
KM031		KM	1/12	-
KM081		KM	3/12	-
KM201		KM	1/12	-
KM1496		KM	1/12	-
KM334		KM	1/12	-
KM313		KM	1/12	-
E-cad/Y		CK	1/12	0/16
IPBP		SS1	1/4	-
OS-9		SS1	1/4	-

Kinesin light chain		SS1	1/4	-
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The screening results shown above confirm the association of the SEREX clones with cancer. There is a higher correlation of cancer and the expression of certain clones, in particular, follistatin related precursor protein, the translation initiation factor eIF-4gamma, the unknown sequence SG24, the FK506-binding protein 25, and the unknown sequence G.KM073. These clones are well suited to serve as diagnostic indicators of disease and as targets for therapeutics (e.g., vaccine compositions) development.

10 **Example 12: Preparation of recombinant cancer associated antigens**

To facilitate screening of patients' sera for antibodies reactive with cancer associated antigens, for example by ELISA, recombinant proteins are prepared according to standard procedures. In one method, the clones encoding cancer associated antigens are subcloned into a baculovirus expression vector, and the recombinant expression vectors are introduced into appropriate insect cells. Baculovirus/insect cloning systems are preferred because post-translational modifications are carried out in the insect cells. Another preferred eukaryotic system is the *Drosophila* Expression System from Invitrogen. Clones which express high amounts of the recombinant protein are selected and used to produce the recombinant proteins. The recombinant proteins are tested for antibody recognition using serum from the patient which was used to isolated the particular clone, or in the case of cancer associated antigens recognized by allogeneic sera, e.g. certain breast cancer and gastric cancer associated antigens, by the sera from any of the patients used to isolate the clones or sera which recognize the clones' gene products.

Alternatively, the cancer associated antigen clones are inserted into a prokaryotic expression vector for production of recombinant proteins in bacteria. Other systems, including yeast expression systems and mammalian cell culture systems also can be used.

Example 13: Preparation of antibodies to cancer associated antigens

The recombinant cancer associated antigens produced as in Example 12 above are used to generate polyclonal antisera and monoclonal antibodies according to standard procedures. The antisera and antibodies so produced are tested for correct recognition of the cancer associated

antigens by using the antisera/antibodies in assays of cell extracts of patients known to express the particular cancer associated antigen (e.g. an ELISA assay). These antibodies can be used for experimental purposes (e.g. localization of the cancer associated antigens, immunoprecipitations, Western blots, etc.) as well as diagnostic purposes (e.g., testing extracts of tissue biopsies, testing for the presence of cancer associated antigens).

Example 14: Expression of cancer associated antigens in cancers of similar and different origin.

The expression of one or more of the cancer associated antigens is tested in a range of tumor samples to determine which, if any, other malignancies should be diagnosed and/or treated by the methods described herein. Tumor cell lines and tumor samples are tested for cancer associated antigen expression, preferably by RT-PCR according to standard procedures. Northern blots also are used to test the expression of the cancer associated antigens. Antibody based assays, such as ELISA and western blot, also can be used to determine protein expression. A preferred method of testing expression of cancer associated antigens (in other cancers and in additional same type cancer patients) is allogeneic serotyping using a modified SEREX protocol (as described above for gastric clones).

In all of the foregoing, extracts from the tumors of patients who provided sera for the initial isolation of the cancer associated antigens are used as positive controls. The cells containing recombinant expression vectors described in the Examples above also can be used as positive controls.

The results generated from the foregoing experiments provide panels of multiple cancer associated nucleic acids and/or polypeptides for use in diagnostic (e.g. determining the existence of cancer, determining the prognosis of a patient undergoing therapy, etc.) and therapeutic methods (e.g., vaccine composition, etc.).

Example 15: HLA typing of patients positive for cancer associated antigen

To determine which HLA molecules present peptides derived from the cancer associated antigens, cells of the patients which express the cancer associated antigens are HLA typed.

Peripheral blood lymphocytes are taken from the patient and typed for HLA class I or class II, as

well as for the particular subtype of class I or class II. Tumor biopsy samples also can be used for typing. HLA typing can be carried out by any of the standard methods in the art of clinical immunology, such as by recognition by specific monoclonal antibodies, or by HLA allele-specific PCR (e.g. as described in WO97/31126).

5

Example 16: Characterization of breast cancer associated antigen peptides presented by MHC class I and class II molecules.

Antigens which provoke an antibody response in a subject may also provoke a cell-mediated immune response. Cells process proteins into peptides for presentation on MHC class I or class II molecules on the cell surface for immune surveillance. Peptides presented by certain MHC/HLA molecules generally conform to motifs. These motifs are known in some cases, and can be used to screen the breast cancer associated antigens for the presence of potential class I and/or class II peptides. Summaries of class I and class II motifs have been published (e.g., Rammensee et al., *Immunogenetics* 41:178-228, 1995). Based on the results of experiments such as those described in Example 15, the HLA types which present the individual breast cancer associated antigens are known. Motifs of peptides presented by these HLA molecules thus are preferentially searched.

One also can search for class I and class II motifs using computer algorithms. For example, computer programs for predicting potential CTL epitopes based on known class I motifs has been described (see, e.g., Parker et al, *J. Immunol.* 152:163, 1994; D'Amaro et al., *Human Immunol.* 43:13-18, 1995; Drijfhout et al., *Human Immunol.* 43:1-12, 1995). HLA binding predictions can conveniently be made using an algorithm available via the Internet on the National Institutes of Health World Wide Web site at URL <http://bimas.dcrt.nih.gov>. Methods for determining HLA class II peptides and making substitutions thereto are also known (e.g. Strominger and Wuchterpfennig (PCT/US96/03182)).

The lung cancer SEREX clone polypeptides NY-LU-12 and NY-LU-12B (variant B), SEQ ID NOs: 708 and 710, were subjected to the HLA binding peptide analysis described above, using the NIH website, to identify HLA binding peptides for several common HLA molecules (HLA-A1, A2, A3, A24, B7, B44, and B52). The results are listed below in Table 12.

Table 12: Identification of HLA binding peptides in lung SEREX clones

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		amino acids of	
HLA	peptide	NY-LU-12 protein	SEQ ID NO
5	A1 NVEE-HSFSY	67 - 75	713
	PVDP-NILDY	287 - 295	714
	DTDY-RSMEY	398 - 406	715
10	A2 SLLE-DAIGC	506 - 514	716
	TLMI-QDKEV	521 - 529	717
	YVSSLDWFYC	533 - 542	718
	VIVEVLEPYV	671 - 680	719
	KLTD-WNKLA	948 - 956	720
	QLSDLHKQNL	975 - 984	721
	KQSEQELAYL	991 - 1000	722
	KLVDKEDIDT	1042 - 1051	723
15	VMFA-RYKEL	1114 - 1122	724
20	A3 QMFG-YGQSK	417 - 425	725
	GMPVKNLQLK	481 - 490	726
	GLPE-EEEIK	823 - 831	727
	LLCRRQFPNK	958 - 967	728
25	A24 EYRD-VDHRL	405 - 413	729
	GYVC-VEFSL	499 - 507	730
	DYGY-VCVEF	497 - 505	731
	WYCKRCKANI	540 - 549	732
	TYPQPQKTSI	574 - 583	733
	IYRSTPPEVI	663 - 672	734
	HYYQ-GKKYF	754 - 762	735
	VYVP-QDPGL	816 - 824	736
30	B7 WNRDYPPPPL	26 - 35	737
35	MPPV-DPNIL	285 - 293	738
	TARD-AQRDL	432 - 440	739
	GPSEEKPSRL	448 - 457	740
	TPPEVIVEVL	667 - 676	741
	RVMFARYKEL	1113 - 1122	742
40	B44 REMG-SCMEF	272 - 280	743
	EEQSSDAGLF	376 - 385	744
	KEYN-TGYDY	490 - 498	745
	TEAKQELITY	566 - 575	746
	VEALRVVKIL	710 - 719	747
	GEYG-GDSY	906 - 914	748
	LERREREGKF	1000 - 1009	749

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5	B44	SEAWSSNEKF	59 - 68	787
		REMG-SCMEF	326 - 334	788
		EEQSSDAGLF	430 - 439	789
		KEYN-TGYDY	544 - 552	790
		TEAKQELITY	620 - 629	791
		VEALRVVKIL	764 - 773	792
		GEYG-GDSY	960 - 968	793
		LERREREGKF	1054 - 1063	794
10	B52	RQDGESKTIM	704 - 713	795
		TPPEVIVEVL	721 - 730	796
		YGFIDLDHV	755 - 764	797
		RQFP-NKEVL	1016 - 1024	798

15 Likewise, other clones identified herein can be analyzed for the presence of candidate HLA binding peptides using no more than routine experimentation.

Example 17: Identification of the portion of a cancer associated polypeptide encoding an antigen

20 To determine if the cancer associated antigens isolated as described above can provoke a cytolytic T lymphocyte response, the following method is performed. CTL clones are generated by stimulating the peripheral blood lymphocytes (PBLs) of a patient with autologous normal cells transfected with one of the clones encoding a cancer associated antigen polypeptide or with irradiated PBLs loaded with synthetic peptides corresponding to the putative protein and matching

25 the consensus for the appropriate HLA class I molecule (as described above) to localize an antigenic peptide within the cancer associated antigen clone (*see, e.g., Knuth et al., Proc. Natl. Acad. Sci. USA* 81:3511-3515, 1984; van der Bruggen et al., *Eur. J. Immunol.* 24:3038-3043, 1994). These CTL clones are screened for specificity against COS cells transfected with the cancer associated antigen clone and autologous HLA alleles as described by Brichard et al. (*Eur. J. Immunol.* 26:224-230,

30 1996). CTL recognition of a cancer associated antigen is determined by measuring release of TNF from the cytolytic T lymphocyte or by ⁵¹Cr release assay (Herin et al., *Int. J. Cancer* 39:390-396, 1987). If a CTL clone specifically recognizes a transfected COS cell, then shorter fragments of the cancer associated antigen clone transfected in that COS cell are tested to identify the region of the gene that encodes the peptide. Fragments of the cancer associated antigen clone are prepared by

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exonuclease III digestion or other standard molecular biology methods. Synthetic peptides are prepared to confirm the exact sequence of the antigen.

Optionally, shorter fragments of cancer associated antigen cDNAs are generated by PCR. Shorter fragments are used to provoke TNF release or ^{51}Cr release as above.

5 Synthetic peptides corresponding to portions of the shortest fragment of the cancer associated antigen clone which provokes TNF release are prepared. Progressively shorter peptides are synthesized to determine the optimal cancer associated antigen tumor rejection antigen peptides for a given HLA molecule.

10 A similar method is performed to determine if the cancer associated antigen contains one or more HLA class II peptides recognized by CTLs. One can search the sequence of the cancer associated antigen polypeptides for HLA class II motifs as described above. In contrast to class I peptides, class II peptides are presented by a limited number of cell types. Thus for these experiments, dendritic cells or B cell clones which express HLA class II molecules preferably are used.

15 EQUIVALENTS

Those skilled in the art will recognize, or be able to ascertain using no more than routine experimentation, many equivalents to the specific embodiments of the invention described herein. Such equivalents are intended to be encompassed by the following claims.

20 All references disclosed herein are incorporated by reference in their entirety.

We claim:

TABLE 1

SEQ ID NO. 1:

- 5 U72994, AC004022, Z68323, AE001160, L34078, AF064863, AC002132, U60440, X66494, N21242, AA678312, W86762, R01605, AA782843, AA275156, W41927, AA874648, AA571241, AA562747, W10480, AA451301, AA866631, AA466667, AA999057, AI029140.

10 SEQ ID NO. 2:

AC004022, U72994, AC002420, AC004125, AA690961, W41927, AA874648, AC004022, U72994, AC002420, AC004125, AA690961, W41927, AA874648.

15

SEQ ID NO. 3:

- X98371, AL009008, L31790, Z83220, X92946, AC003975, AF008916, U80460, X75544, X66732, X95275, X52177, X07976, AC004451, Z74307, AB000878, AL009179, AF038667, 20 Z78544, Z48008, U23486, J05096, AB000882, Z30213, L11593, U18530, L27325, AC005191, M99579, AA130270, AA158245, AA903098, AI018453, AA436455, AA980593, AA172479, AA637487, AA116588, AA426854, AA050404, AA390025, AI006618, AI048382, C85944, AA673480, AI006510, AA823338, AA413694, W35075, AA015033, AA413584, W29693, AA637069, AA619839, AA125149, AA039004, AA674696, AA871138, AA414747, 25 AA198099, C91478, F071359, AA925957, AA820054, H16496, AI043756, AA892435, AA893551, AA818669, AA892785, AA944026, D33919, N96570, F19798, AI045451, AA800662, D65187, AA944025, AA925731, AA892314, AA945449.

30 SEQ ID NO. 4:

AA900930, AA925665.

35 SEQ ID NO. 5:

- U58105, Z81485, Z54236, Z48584, U61375, M55267, M59856, X51942, U77302, Z48621, AF032455, Z11866, AB013392, L32792, AA871997, AA084083, AA130829, AA083063, AA666290, N38894, D54459, T28921, AA806015, AA512059, AI043087, AI042894, 40 AA968324, AA238493, AA237462, AI042885, AI046424, AI035670, AA269430, AA250621, AI035540, AA260613, AA106870, AA238658, AA106134, AI042683, AA105958, AA144007, AA986558, AA457910, AA389400, AA673056, AA153254, AA754678, AI021109, AA390813, C36687, T41571, AI011183, AI013356, AI011739, AI030260, AA924384, C44421.

45

SEQ ID NO. 6:

AF036717, U91327, AF036718, U56248, Z48795, Z99290, M30697, U58204, M24417, AF022983, M33581, AC004619, H64641, AA477478, AA369676, AA088359, AA057574,

AA683066, AA446279, AA332363, T09328, R80982, AA069486, AA410842, C18527,
AA293033, H12730, AA287344, AA029631, R83063, AA061290, AA185993, AA880204,
AA499308, AA183172, AA242360, AA792388, AA175587, AA277140, AA880395,
AA899046, AA859550, C35363, C35702, C32682, F14140, T18049, C83149, T45787,
5 AA924623, D47525, Z30723, AA897884, AA042465, AI009871, AA875198, C83016.

SEQ ID NO. 7:

10 X74116, AL022148, AC004548, AC000352, Z11664, Z78065, Z74028, AE000163, AE000750,
X74229, D90700, R59414, AA176708, W02568, AA354664, R43017, AA973553, F10008,
D61827, AA826300, Z41398, T77572, R40189, H85823, W86541, T17276, AA679337,
X83357, AA184845, AA416260, AA475603, AA388692, AA764445, AA388689, AA219880,
AA290020, AA388507, AA387267, C86741, AA414436, AA451259, AA413796, AA930916,
15 AA793690, AA619447, AA062257, AA522026, AA816247, AA892032, AA817702, H33461,
AA925507, AA849449, AI029236, AA247069, AA697975, AA882508, AA893258, AA698410,
AA891755, AA698227, AA892782, AA899328, T04373, AA567522, AA698408, AA202615,
AA141016, AA697974, AA697998, C61176, D69691, AI030205, AA586054.

20

SEQ ID NO. 8:

U08218, L38909, Y11095, AC002431, Z23069, S77418, U39060, L38580, AF053367, Z36506,
M18102, J03624, AA102264, AA730686, H47968, AA357170, AA130974, C06054,
25 AA626429, F00559, AA604528, AA383348, AA040127, N84965, D54884, D54883, R94309,
AA373184, AA128091, W68194, H58283, R76347, AA343938, AA305144, AI049611,
AA384516, AA720553, N57395, R97387, D52674, AA169408, H66293, AA456362, T74258,
AA730145, AA101952, N86388, AA355003, AA307640, AA385679, AA354542, N99075,
N83528, H87678, R84494, R35720, AA670111, AA186452, W32370, D55392, W05161,
30 AA641280, AA120503, C77063, AA146393, AA620177, AA509478, C77481, AA427148,
AA474531, W83304, AA207424, AA763436, AA958473, AA799243, AA493061, AA967792,
AA145256, AA089338, AA756259, AA789767, AA980112, AA866640, AA914516,
AA821675, AA466770, AA015387, AA816036, AA246546, AA941789, AA955779,
AA997768, AA997534, T43805, AA956150, T18836, T23333, AA525666, T18787, AA800483,
35 C64685, AA851367, C91730, AA143899, T23399.

SEQ ID NO. 9:

40 AP000056, U43491, Z74919, L81498, Z94054, AC002503, L81499, AA740188, AA630241,
AA974724, AA806907, N88859, N98242, H12649, R06485, R06511, AA546258, C76846,
AA208416, AA959219, AA276381, W10055, AA462844, AA444278, W13447, W97802,
AA542324, AA137880, AA269331, AA175695, W59029, AA003372, AA146233, AI045761,
C93154, C94084, C94208, D68027, C12780, AA687005, AA080598, C12876, C12390,
45 AA848674, AA924440, T15031, AA451569, H35524.

SEQ ID NO. 10:

U25640, AA127328, H24207, H08275, AA283063, AA826096, AA417382, AA464874, W05562, AA453370, N51211, AA495859, R33871, H00927, AA623997, AA220442, AA178568, AA605493, AA394557, AA956116, AA999037, AA818246.

5

SEQ ID NO. 11:

AB001740, AF039956, AA581972, AA594539, AA236870, AA464410, AA237069, AA694199, AI038896, AA167314, AA577381, AA430117, N23143, R53610, W37647, 10 AA724229, AA313202, AA860618, W16866, AA134966, AA255556, AA305224, R50528, AA844913, W32042, W37383, AA908394, W93357, W31353, R55254, N79251, AA456077, AA477700, AA477701, AA989005, AA455580, N32722, N22935, R50622, AA135047, R51941, T34020, T30416, T32309, AA883332, W93445, AA166984, AA026749, T08224, AA255572, W03768, AA033670, W31880, AA772832, AA230974, AA511207, W82274, 15 AA230365, AA671085, AA511230, AA606681, AA023735, AA444535, W98518, W14718, W85455, AA980318, AA137525, AA035840, AA692158, AA007919, W48013, AA444534, AA981497, AA002566, W48089, W99869, AA960396, AA960580, AA145259, AA145683, AA388960, AA389941, AA266272, AA145124, AA267212, AA959753, AA407991, A175818, AA943997, AA899476, AA899756, AA943998, AA955446, AA012783, AA924956, 20 AA892219, AA955331, AI012225, AA891436.

SEQ ID NO. 12:

25 U72994, AC004022, AF043493, U43252, U43251, U81830, U58105, U68242, Z93242, AL009029, M29872, U12980, M81118, M30471, Z56258, AF012943, AC004080, AC002563, AF024533, AF002991, Z63771, AP000042, AF064863, U80017, AC004087, Z55235, L05920, AA508139, N90748, AA450240, AA948158, AA828938, AA165115, AI003312, AA436633, AA419100, AA743442, AA961990, AA885286, AA861312, T84801, AI040166, AA494115, 30 AA652324, AA181105, AA095541, R59256, AA503712, AA700364, AA603821, T60326, AA779097, AI023884, AA603785, H79111, W39526, AA506607, W94361, N66078, R01605, H22694, W86762, W99303, AA745640, AA678312, AA431870, W41927, AA874648, C92734, C23102, C53080, C91168, D65098, C32959, C50029, M80125, C34452, C83862, C24659, T21473, AA874720, C06696, W43071, AI043300, C53907.

35

SEQ ID NO. 13:

X94232, U90437, AC003052, U59809, AC004001, M95396, Z67884, X77486, U70051, 40 X14805, AF022976, Z83823, X77485, J04171, AF036007, U05768, U88315, Z98048, AF036009, AC005179, U41277, U32517, AE001138, D64060, M84387, H29022, AA814221, N26314, AA935912, AA873506, AA608576, AA453605, AA232674, Z38725, AA772022, AA025212, AA318330, R48115, AA234084, H18508, N64543, AA970508, R36933, AA306944, H49559, AA325555, H85834, H89988, AA343974, AA648643, H65664, T62713, 45 H16554, N21122, AA351037, AA484621, AA221492, AA259314, C76383, C76336, AA607924, C76394, AA408562, AA921258, AI006352, W41405, AA153317, AA015435, AA027405, AA794066, AA498038, AA184222, AI011068, AA859614, AA899776, AA955080, AA799674, AA849652, AI009788, AA900928, AI007950, AA109392, AA753592, U92780, AA957632, AA567950, AI009495.

SEQ ID NO. 14:

AC000075, U66140, R14195, AA220229, T31199, R19104, R19148, Z46126, AA417619,
5 Z45284, H14105, R84666, AA090321, AA350108, W52840, R48497, R13097, T66255,
W44467, AA247676, AA198489, AA388175, AA261453, AA237111, AA790730, AA162394,
AA816498, AI013729, AA684961, AA979759.

10 SEQ ID NO. 15:

AF069301, D10651, U11419, U11287, M91562, U90278, U72724, X57855, X79424, M16512,
M64542, Z14152, AF016667, L01488, Z75955, AF024504, M13968, W67775, AA934587,
AA617696, AA913577, AA628682, W74527, AA969876, AA995606, AA622402, AA027090,
15 AA620556, AA085733, AA187157, AI031865, AA972318, AA897169, W79046, AA531124,
AA733183, T90909, Z25096, AA721771, AA115089, T49643, R00622, N93780, R00626,
AA365494, T71475, N74066, AA027130, T83325, AA115569, AA658299, T55344, T83700,
AA426250, AA393863, AA282967, R08138, AI000112, AA807574, AA077926, AA397527,
W87761, AA243026, R56368, H16371, AA958697, AA003997, AA008542, AA036229,
20 AA397074, AA250467, AA260498, AA968175, AA253686, AA727785, AI019478, AA474978,
AA543461, AA990281, AA245791, AA617042, AA015355, AA983015, AA982200,
AA120064, AA462778, AA242574, AA986993, AA986911, AA882490, AA223057,
AA543989, W65528, AA848318, AA874979, AA800547, AA945302, AA140994, AA991110,
AA851120.

25 SEQ ID NO. 16:

Z68106, X14199, M14872, Z63497, M31670, AC002123, Z63498, AA280070, AA215687,
30 H93207, AA070367, W95534, AA682436, AA741066, AA173269, AA641255, AA215688,
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AI002587, W95419, AA357042, AA761253, AA197191, T54480, AA133029, AA378991,
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002090-02629460

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5 SEQ ID NO. 29:

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SEQ ID NO. 32:

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SEQ ID NO. 109:

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SEQ ID NO. 121:

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SEQ ID NO. 125:

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SEQ ID NO. 127:

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002090-02629460

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SEQ ID NO. 131:

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SEQ ID NO. 135:

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SEQ ID NO. 141:

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SEQ ID NO. 143:

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AA084609, AI050760, AA808998, AA503258, AA613138, AA603156, AA513293, R97934,
AA610233, AA654874, AA501867, AA604831, N22058, AA492114, T50676, AA757426,
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AA159978, AA534204.

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SEQ ID NO. 145:

Z69030, L42375, U37352, D26445, U38192, U38191, U37770, U38190, U37353, U59418,
L76702.

45

SEQ ID NO. 147:

L07872, L34544, L34543, X17459, S63463, M81871, L08904, U60093, U60094, L07873,
L07874.

002090-6669460

SEQ ID NO. 149:

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5 AA732931, AA610556, AA973899, AA598896, AA531553, AA826535, AI000209, AA290836,
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SEQ ID NO. 151:

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15

SEQ ID NO. 153:

U28918, U17714, X82021, Z98048, D17265, D17092, Z82022, L04270.

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SEQ ID NO. 155:

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AI046716, AA237153, W15784, AA547132, AA231089, AA170968, D46090, C61892,
35 C64408, D34777, D35175, D35914, D37381, AA559708, D37143, C60784, AI008855,
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SEQ ID NO. 157:

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SEQ ID NO. 159:

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02866, H35041, AA944944, AA597316, D26977, D68334, AA685934, W88345, AA964819.

SEQ ID NO. 161:

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SEQ ID NO. 163:

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X15183, AF028832, D87666, J04633, L33676, X07270, U94395, M27024, M30627, X16857, X07265, M36830, M30626, AA669137, AA725103, AA890496, AA314095, AA554815, AA313331, AA730100, AA214035, AA876412, AA121630, AA314010, AA927532, AA968674, AA679253, N66271, AA558907, AA309988, AA587079, AA075436, AA160964, 25 AA205657, AA214083, AA130903, AA917032, AA149623, AA857523, AA889843, AA305037, AA491055, W73240, AA255644, W73295, AA765431, AA178947, N66409, AA074895, AA306976, AA075052, AA075387, AA130892, AA857443, AA405942, AA629891, AA152004, AA129550, W56527, AA513807, AA703828, AA223171, C75280, AA889155, AA854676, AA773063, AA774999, AA152392, AA307057, AA316954, 30 AA657352, AA522607, AA188113, AA026444, AI003623, AA312717, AA312400, T64299, AA178992, AA228992, AI042136, AA457613, AI032857, AA164461, AA625127, AA807763, AA130815, AA054695, AA937097, W93534, N67875, AA526896, W52802, AA527942, N34251, W28646, AA668543, AA496091, W52511, AA070581, AA306826, AA120908, AA699607, AA086423, N72134, AA630369, AA564649, AA046806, AA666249, AA306893, 35 AA225404, AA127417, AA854951.

SEQ ID NO. 165:

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AA239037, AA672620, AA915168, AA863498, AA123378.

SEQ ID NO. 167:

Y11251, AF030234, AF043945, L40407.

SEQ ID NO. 169:

U33822, X61838, AA572230, AA589570, AA929790, AA104830, C81582, AA271190, AA290278, AA543616, AI043207, AA107832, AA958460, AI020992, AA795905, AA277468, AA475069, AA111610, AA389139, AA154163.

SEQ ID NO. 170:

D32050, D16969, AC004423, S81497.

SEQ ID NO. 172:

D86982, L07131, M14544, AA296228, AA318436, AA296234, H88394, W26642, AF038251, AA394101, N35855, N56791, N35444, AA147382, AA647547, AA939939, AA895989, AA122437, AA277698, W75741, AI036117, AA980469, AA033178, AI006694, AA980625, AA033190, AA175922, AA172918, AA895209, AA028700, AA416048, AA175247, AA217057, AI045760, R64866, D40836, D41873, AA509279, D40089, AA114361, AA751642, AA848690, AA800525, AA802510, C24001, AA841755, AA882663, D40069, AA433358, D40199, AA958134, AA072494, AI008727, AA618978, AA848687, C21884, AA113662, AA945653, AA660093, C58446, AA908068, AA532100, AA264560, AA426658, AA097169, AA751535.

SEQ ID NO. 174:

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SEQ ID NO: 177

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SEQ ID NO: 178

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- 5 AA637983, AA020137, AA097337, AA117759, W17615, AA285526, AA111347, AA208823, AA879750, AA413058, W33316, AA161891, W41259, AA511152, AA027481, AA020252, AA033106, AA965045, D41048, AI031042, D48020, AA925258, D40853, AA945674, C19585, AI013412, T15040, AA541011, AA990782, AA851306, AA540938, T23386, AA783863, AA979035, AA951002, AA438957, AA979006, AA978995, AA800046, AA556128, C27411,
- 10 D15562, T20348, AA966363, AA949269, AA785774, AA728671, D16092, N37869, D48782.

SEQ ID NO: 179

- 15 Z50194, U44088, U92983, U12200, AC004147, X82200, Z81527, M63469, Z35494, AC003018, AL021408, M92281, AA576961, AA088194, AA258396, D79238, N27861, AA857168, N35619, N40634, N73008, N21585, AA332511, D56582, D12298, AA641278, Z21892, H92531, AA113084, N76094, N31261, AA227469, AI038845, AA520982, R16910, AA380178, AA238335, AA255056, AA981576, W35008, AA238181, AA739268, AA061742,
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SEQ ID NO: 180

- 25 D87072, U52191, L25270, L29564, L29563, D83144, U73169, AC003036, AC003049, AC004149, Z67744, AC001224, AA215514, AA262849, AA443396, H22815, AA171842, W04162, AA682330, C18753, W01583, AA837306, AA348779, AA492008, AA639340, AA194216, AA371937, AA449692, H09426, AA782728, AA991707, AA085238, AA194029,
- 30 T03226, AA867674, AA009101, AA726511, W90906, AA028401, W54470, AA266581, AA033314, W10534, AA475518, AA606629, AA616625, AA212796, AA184252, W53289, AA240033, AA238131, W98696, AA038374, AA286525, AA265063, AA212145, AA165741, AA146458, AA021970, AA870293, AA790962, AA770919, AA175098, AA080286, W87105, AA125485, AA870257, AA793909, AA673390, AA032500, AA059905, W84293, AA511672,
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- 40 C71711, AA824977, D69290, AA264695, D68955, C74586, C72683, AA750613, C83111, AA568036, C82978.

SEQ ID NO: 181

- 45 U52191, D87072, AL022162, AL008710, Z83850, AF055066, AC004254, L25270, AC003013, U53141, AL021728, AC004997, M38703, AC004020, U91321, AP000041, Z69921, AC002551, D87016, X54171, AF055481, X83213, L05489, AC003018, AB009056, AC000069, L81890, AD000685, AC003031, AC003030, Z99715, AF043301, AE000664, AF007544, X15547,

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25 SEQ ID NO: 319

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35 SEQ ID NO: 320

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35 SEQ ID NO: 471

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25 SEQ ID NO: 498

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20 SEQ ID NO: 507

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35 SEQ ID NO: 508

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5 SEQ ID NO: 519

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 AA393069, AA393069 zi69e09.r1 Soares testis NHT Homo sapiens ... 40 0.86
 AA371600, AA371600 EST83650 Pituitary gland, subtracted (prol... 40 0.86
 AA977820, AA977820 oq78a09.s1 NCI_CGAP_Kid6 Homo sapiens cDNA... 38 3.4
 AA584760, AA584760 no04c06.s1 NCI_CGAP_Phe1 Homo sapiens cDNA... 38 3.4
 AA584615, AA584615 no08g12.s1 NCI_CGAP_Phe1 Homo sapiens cDNA... 38 3.4
 AA229827, AA229827 nc48c04.r1 NCI_CGAP_Pr3 Homo sapiens cDNA ... 38 3.4
 W21398, W21398 zb50a11.r1 Soares fetal lung NbHL19W Homo sapi... 38 3.4

AA869501, AA869501	vq08g11.r1	Barstead stromal cell line MPLR...	833	0.0
AA221749, AA221749	my28g01.r1	Barstead mouse pooled organs MP...	789	0.0
AA271363, AA271363	va71d08.r1	Soares mouse 3NME12 5 Mus muscu...	781	0.0
AA544727, AA544727	vk35d01.r1	Soares mouse mammary gland NbMM...	773	0.0
W84968, W84968	mf42e02.r1	Soares mouse embryo NbME13.5 14.5 M...	640	0.0
AA153324, AA153324	ms61e11.r1	Stratagene mouse embryonic carc...	617	e-175
AA673899, AA673899	vo86g07.r1	Barstead mouse irradiated colon...	583	e-164
AA797488, AA797488	vw28a05.r1	Soares mouse mammary gland NbMM...	519	e-145
W71831, W71831	me45b06.r1	Soares mouse embryo NbME13.5 14.5 M...	472	e-131
AA213358, AA213358	mu74e04.r1	Stratagene mouse embryonic carc...	444	e-123
W75918, W75918	me82f05.r1	Soares mouse embryo NbME13.5 14.5 M...	444	e-123
AA038141, AA038141	mi81e05.r1	Soares mouse p3NMF19.5 Mus musc...	359	3e-97
AA038288, AA038288	mi83b04.r1	Soares mouse p3NMF19.5 Mus musc...	323	1e-86
AA017742, AA017742	mh40c03.r1	Soares mouse placenta 4NbMP13.5...	297	8e-79
AA771297, AA771297	vt17g04.r1	Barstead mouse myotubes MPLRB5 ...	297	8e-79
AA105228, AA105228	mp45b11.r1	Barstead MPLRB1 Mus musculus cD...	295	3e-78
AA068340, AA068340	mm53f01.r1	Stratagene mouse embryonic carc...	293	1e-77
AA612347, AA612347	vo05c08.r1	Stratagene mouse skin (#937313)...	281	5e-74
AA038300, AA038300	mi83d04.r1	Soares mouse p3NMF19.5 Mus musc...	270	2e-70
AA500952, AA500952	vg01h04.r1	Soares mouse NbMH Mus musculus ...	252	4e-65
W08368, W08368	mb41f07.r1	Soares mouse p3NMF19.5 Mus musculus...	212	4e-53
AA052280, AA052280	ma82e12.r1	Soares mouse p3NMF19.5 Mus musc...	123	3e-26
AA064466, AA064466	ml49c05.r1	Stratagene mouse testis (#93730...	107	2e-21
AA271566, AA271566	vb74b09.r1	Soares mouse 3NME12 5 Mus muscu...	60	3e-07
C86222, C86222		Mus musculus fertilized egg cDNA 3'-end seque...	42	0.078
W83632, W83632	mf31a04.r1	Soares mouse embryo NbME13.5 14.5 M...	42	0.078
AA423627, AA423627	ve80f01.r1	Soares mouse mammary gland NbMM...	42	0.078
AA036586, AA036586	mi41h08.r1	Soares mouse embryo NbME13.5 14...	42	0.078
AA207496, AA207496	mv78g02.r1	GuayWoodford Beier mouse kidney...	42	0.078
AA120433, AA120433	mp82h11.r1	Soares 2NbMT Mus musculus cDNA ...	42	0.078
W08185, W08185	mb42h02.r1	Soares mouse p3NMF19.5 Mus musculus...	38	1.2
AA065563, AA065563	ml71b06.r1	Stratagene mouse kidney (#93731...	38	1.2
AA288756, AA288756	mr46h07.r1	Life Tech mouse embryo 15 5dpc ...	38	1.2
AA119334, AA119334	mp80e10.r1	Soares 2NbMT Mus musculus cDNA ...	38	1.2
AA163051, AA163051	ms24a10.r1	Stratagene mouse skin (#937313)...	38	1.2
N28074, N28074		MDB1392R Mouse brain, Stratagene Mus musculus ...	38	1.2
AA288757, AA288757	mr46h08.r1	Life Tech mouse embryo 15 5dpc ...	38	1.2
AA122857, AA122857	mq06a02.r1	Soares 2NbMT Mus musculus cDNA ...	38	1.2
AA617519, AA617519	vj77d05.r1	Knowles Solter mouse blastocyst...	38	1.2

W89420, W89420	mf80b03.r1	Soares mouse embryo NbME13.5 14.5 M...	38	1.2
AI047837, AI047837	ud64c11.x1	Sugano mouse liver mlia Mus mus...	38	1.2
AA840310, AA840310	vw91a10.r1	Stratagene mouse skin (#937313)...	36	4.8
AA986428, AA986428	ue13b04.x1	Sugano mouse embryo mewa Mus mu...	36	4.8
W47677, W47677	mc89g07.r1	Soares mouse embryo NbME13.5 14.5 M...	36	4.8
AA057996, AA057996	mj56c10.r1	Soares mouse embryo NbME13.5 14...	36	4.8
AA183858, AA183858	mo95h01.r1	Stratagene mouse testis (#93730...	36	4.8
AA212232, AA212232	mu43e08.r1	Soares 2NbMT Mus musculus cDNA ...	36	4.8
W41067, W41067	mc39a06.r1	Soares mouse p3NMF19.5 Mus musculus...	36	4.8
AA967594, AA967594	uh01d06.r1	Soares mouse hypothalamus NMHy ...	36	4.8
AA414093, AA414093	vc64c07.s1	Knowles Solter mouse 2 cell Mus...	36	4.8
AA123833, AA123833	mp93c03.r1	Soares 2NbMT Mus musculus cDNA ...	36	4.8
AA432920, AA432920	vd91b11.r1	Soares mouse NbMH Mus musculus ...	36	4.8
AA874496, AA874496	vx03a08.r1	Soares 2NbMT Mus musculus cDNA ...	36	4.8
AA000433, AA000433	me76e09.r1	Soares mouse embryo NbME13.5 14...	36	4.8
AA023983, AA023983	mh94a07.r1	Soares mouse placenta 4NbMP13.5...	36	4.8
AA013726, AA013726	mh12e09.r1	Soares mouse placenta 4NbMP13.5...	36	4.8
AA274648, AA274648	vb08c01.r1	Soares mouse NML Mus musculus c...	36	4.8
AA140347, AA140347	mq89g06.r1	Stratagene mouse heart (#937316...	36	4.8
AA499377, AA499377	vi89c07.r1	Stratagene mouse heart (#937316...	36	4.8
C88747, C88747		Mus musculus early blastocyst cDNA, clone 01B...	36	4.8
AA726125, AA726125	vu88c06.r1	Stratagene mouse skin (#937313)...	36	4.8
AA760311, AA760311	vv71c12.r1	Stratagene mouse skin (#937313)...	36	4.8
AA763007, AA763007	vw60b05.r1	Soares mouse mammary gland NMLM...	36	4.8
AA929878, AA929878	vz44d03.r1	Soares 2NbMT Mus musculus cDNA ...	36	4.8
W59064, W59064	md67e10.r1	Soares mouse embryo NbME13.5 14.5 M...	36	4.8
AA103519, AA103519	mo24b12.r1	Life Tech mouse embryo 13 5dpc ...	36	4.8
AA222310, AA222310	my14d08.r1	Barstead mouse heart MPLRB3 Mus...	36	4.8
W83557, W83557	mf32d02.r1	Soares mouse embryo NbME13.5 14.5 M...	36	4.8
AA168631, AA168631	ms33c05.r1	Stratagene mouse skin (#937313)...	36	4.8
AA960143, AA960143	vw60b05.s1	Soares mouse mammary gland NMLM...	36	4.8
W34557, W34557	mc58a05.r1	Soares mouse embryo NbME13.5 14.5 M...	36	4.8
W98818, W98818	mf94e06.r1	Soares mouse embryo NbME13.5 14.5 M...	36	4.8
AA008527, AA008527	mg85h01.r1	Soares mouse embryo NbME13.5 14...	36	4.8
AA008734, AA008734	mg86h03.r1	Soares mouse embryo NbME13.5 14...	36	4.8
AA510568, AA510568	vg33a10.r1	Soares mouse mammary gland NbMM...	36	4.8
AA672524, AA672524	vo59e11.r1	Soares mouse mammary gland NbMM...	36	4.8
AA052773, AA052773	mf24h01.r1	Soares mouse embryo NbME13.5 14...	36	4.8
AA096626, AA096626	mo09h06.r1	Life Tech mouse embryo 10 5dpc ...	36	4.8
AA124880, AA124880	mp73e06.r1	Soares 2NbMT Mus musculus cDNA ...	36	4.8
AA198005, AA198005	mv12b09.r1	GuayWoodford Beier mouse kidney...	36	4.8
AA624213, AA624213	vm98h06.r1	Knowles Solter mouse blastocyst...	36	4.8
AA521863, AA521863	vi08b01.r1	Barstead mouse myotubes MPLRB5 ...	36	4.8
AA692113, AA692113	vt19d03.r1	Barstead mouse myotubes MPLRB5 ...	36	4.8
W71551, W71551	me39e11.r1	Soares mouse embryo NbME13.5 14.5 M...	36	4.8

AA646501, AA646501 vn12g12.r1 Stratagene mouse heart (#937316... 36 4.8
 AA607056, AA607056 vm95e05.r1 Knowles Solter mouse blastocyst... 36 4.8
 AA163340, AA163340 ms65b10.r1 Stratagene mouse embryonic carc... 36 4.8
 AA110893, AA110893 mm02b04.r1 Stratagene mouse kidney (#93731... 36 4.8

AI030290, AI030290 UI-R-C0-jb-d-01-0-UI.s1 UI-R-C0 Rattus nor... 293 1e-77
 C71833, C71833 Rice cDNA, partial sequence (E0428_1A) 44 0.017
 AA926551, AA926551 TENS1173 T. cruzi epimastigote normalized ... 42 0.069
 AA875699, AA875699 TENU0170 T.cruzi epimastigote normalized c... 42 0.069
 AA567661, AA567661 HL01595.5prime HL Drosophila melanogaster ... 40 0.27
 C74504, C74504 Rice cDNA, partial sequence (E31753_1A) 40 0.27
 AA698333, AA698333 HL04291.5prime HL Drosophila melanogaster ... 38 1.1
 AA441429, AA441429 LD16359.5prime LD Drosophila melanogaster ... 38 1.1
 N68770, N68770 TgESTzy35b12.r1 TgRH Tachyzoite cDNA Toxoplasma... 38 1.1
 AA246440, AA246440 LD05311.5prime LD Drosophila melanogaster ... 38 1.1
 AA801776, AA801776 GM12975.5prime GM Drosophila melanogaster ... 38 1.1
 N69148, N69148 TgESTzy33d10.r1 TgRH Tachyzoite cDNA Toxoplasma... 38 1.1
 AA536484, AA536484 LD17114.5prime LD Drosophila melanogaster ... 38 1.1
 AA392544, AA392544 LD11451.5prime LD Drosophila melanogaster ... 38 1.1
 AA202696, AA202696 LD03182.5prime LD Drosophila melanogaster ... 38 1.1
 AA392367, AA392367 LD11287.5prime LD Drosophila melanogaster ... 38 1.1
 AA264629, AA264629 LD08245.5prime LD Drosophila melanogaster ... 38 1.1
 AA735318, AA735318 LD21104.5prime LD Drosophila melanogaster ... 38 1.1
 AA264558, AA264558 LD08333.5prime LD Drosophila melanogaster ... 38 1.1
 AA536476, AA536476 LD17106.5prime LD Drosophila Embryo Drosop... 38 1.1
 AA957774, AA957774 UI-R-E1-fv-f-04-0-UI.s1 UI-R-E1 Rattus nor... 38 1.1
 AA567991, AA567991 HL02092.5prime HL Drosophila melanogaster ... 38 1.1
 AA957876, AA957876 UI-R-E1-fv-f-04-0-UI.s2 UI-R-E1 Rattus nor... 38 1.1
 AA892488, AA892488 EST196291 Normalized rat kidney, Bento Soa... 38 1.1
 AA699001, AA699001 HL06668.5prime HL Drosophila melanogaster ... 36 4.3
 C19706, C19706 Rice cDNA, partial sequence (E10809_1A) 36 4.3
 D41773, RICS4574A Rice cDNA, partial sequence (S4574_2A). 36 4.3
 C40680, C40680 C.elegans cDNA clone yk247c4 : 5' end, single... 36 4.3
 AA698625, AA698625 HL05354.5prime HL Drosophila melanogaster ... 36 4.3
 C82819, C82819 Oryctolagus cuniculus corneal endothelial cDN... 36 4.3
 D46016, RICS10393A Rice cDNA, partial sequence (S10393_3A). 36 4.3
 AA536314, AA536314 LD16858.5prime LD Drosophila melanogaster ... 36 4.3
 AA801012, AA801012 EST190509 Normalized rat muscle, Bento Soa... 36 4.3
 D46541, RICS11289A Rice cDNA, partial sequence (S11289_1A). 36 4.3
 D47315, RICS12612A Rice cDNA, partial sequence (S12612_1A). 36 4.3
 AA735857, AA735857 GM09977.5prime GM Drosophila melanogaster ... 36 4.3
 AA753921, AA753921 97BS0370 Rice Immature Seed Lambda ZAPII c... 36 4.3
 D47243, RICS12505A Rice cDNA, partial sequence (S12505_1A). 36 4.3
 AA978395, AA978395 LD28411.5prime LD Drosophila melanogaster ... 36 4.3

D15134, RICC0136A Rice cDNA, partial sequence (C0136A). 36 4.3
 D46483, RICS11185A Rice cDNA, partial sequence (S11185_1A). 36 4.3
 D46618, RICS11395A Rice cDNA, partial sequence (S11395_1A). 36 4.3
 D46659, RICS11457A Rice cDNA, partial sequence (S11457_1A). 36 4.3
 D46719, RICS11572A Rice cDNA, partial sequence (S11572_1A). 36 4.3
 D48579, RICS14880A Rice cDNA, partial sequence (S14880_2A). 36 4.3
 AA802334, AA802334 GM04219.5prime GM Drosophila melanogaster ... 36 4.3
 D46066, RICS10470A Rice cDNA, partial sequence (S10470_1A). 36 4.3
 D47037, RICS12104A Rice cDNA, partial sequence (S12104_1A). 36 4.3
 D46874, RICS11807A Rice cDNA, partial sequence (S11807_2A). 36 4.3
 D47174, RICS12340A Rice cDNA, partial sequence (S12340_2A). 36 4.3
 T04578, T04578 625 Lambda-PRL2 Arabidopsis thaliana cDNA clon... 36 4.3
 C83675, C83675 Oryctolagus cuniculus corneal endothelial cDN... 36 4.3
 D47950, RICS13762A Rice cDNA, partial sequence (S13762_1A). 36 4.3
 R90044, R90044 16399 Lambda-PRL2 Arabidopsis thaliana cDNA cl... 36 4.3
 D46994, RICS12013A Rice cDNA, partial sequence (S12013_2A). 36 4.3
 AA440820, AA440820 LD15713.5prime LD Drosophila melanogaster ... 36 4.3
 C72089, C72089 Rice cDNA, partial sequence (E0963_1A) 36 4.3
 Z84004, SSZ84004 S.scrofa mRNA; expressed sequence tag (5'; ... 36 4.3
 D47519, RICS13070A Rice cDNA, partial sequence (S13070_1A). 36 4.3
 C19735, C19735 Rice cDNA, partial sequence (E10858_1A) 36 4.3
 D47231, RICS12462A Rice cDNA, partial sequence (S12462_1A). 36 4.3
 D47147, RICS12293A Rice cDNA, partial sequence (S12293_1A). 36 4.3
 AA950198, AA950198 LD30147.5prime LD Drosophila melanogaster ... 36 4.3
 Z47624, ATTS4480 A. thaliana transcribed sequence; clone TAI... 36 4.3
 D45955, RICS10259A Rice cDNA, partial sequence (S10259_1A). 36 4.3
 D47137, RICS12280A Rice cDNA, partial sequence (S12280_1A). 36 4.3
 D69927, CELK093H2F C.elegans cDNA clone yk93h2 : 5' end, sin... 36 4.3
 AA392275, AA392275 LD11117.5prime LD Drosophila melanogaster ... 36 4.3

SEQ ID NO:546

D87455, D87455 Human mRNA for KIAA0266 gene, complete cds 1164 0.0
 Z99129, HS425C14 Human DNA sequence from clone 425C14 on chr... 42 0.20
 D90900, D90900 Synechocystis sp. PCC6803 complete genome, 2/... 40 0.80
 Z74281, SCYDL233W S.cerevisiae chromosome IV reading frame O... 38 3.1
 AL021528, HS394P21 Homo sapiens DNA sequence from PAC 394P21... 38 3.1
 Z49155, HSL83D3 Human DNA from cosmid L83d3, Huntington's Di... 38 3.1
 U33761, HSU33761 Human cyclin A/CDK2-associated p45 (Skp2) mR... 38 3.1
 AF052832, AF052832 Trypanosoma cruzi CL Brener cosmid 1b21 ch... 38 3.1
 Z98600, SPAC20G4 S.pombe chromosome I cosmid c20G4 38 3.1

Y09438, SPHUSPLUS *S.pombe* hus1+ gene 38 3.1
 D29951, MUSKIF Mouse mRNA for kinesin family protein KIF1a, ... 38 3.1

HUMAN ESTs

AA151187, AA151187 zo03c11.r1 Stratagene colon (#937204) Homo... 694 0.0
 AA824593, AA824593 oc83d10.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 670 0.0
 AA954862, AA954862 op20c03.s1 NCI_CGAP_Co12 Homo sapiens cDNA... 581 e-164
 T16360, T16360 NIB1193 Normalized infant brain, Bento Soares ... 517 e-145
 R54592, R54592 yg81h10.s1 Homo sapiens cDNA clone 40102 3'. 511 e-143
 AA373594, AA373594 EST85631 HSC172 cells I Homo sapiens cDNA ... 507 e-142
 AA100660, AA100660 zl90a05.r1 Stratagene colon (#937204) Homo... 383 e-104
 R42009, R42009 yg05b04.s1 Homo sapiens cDNA clone 31336 3'. 379 e-103
 AA249614, AA249614 k3041.seq.F Human fetal heart, Lambda ZAP ... 252 5e-65
 AA360633, AA360633 EST69800 T-cell lymphoma Homo sapiens cDNA... 182 4e-44
 AA053498, AA053498 zl70b11.r1 Stratagene colon (#937204) Homo... 38 1.5
 AA992442, AA992442 or85h03.s1 NCI_CGAP_Lu5 Homo sapiens cDNA ... 38 1.5

AA065677, AA065677 mm43c03.r1 Stratagene mouse melanoma (#937... 297 4e-79
 AA529728, AA529728 vi38g12.r1 Beddington mouse embryonic regi... 42 0.035
 W91608, W91608 MTA.D10.092.A MTA adult mouse thymus library M... 42 0.035
 AA177186, AA177186 mt51a11.r1 Stratagene mouse embryonic carc... 42 0.035
 AA048008, AA048008 mj26h10.r1 Soares mouse embryo NbME13.5 14... 36 2.2
 AA637535, AA637535 vu10c02.r1 Barstead mouse myotubes MPLRB5 ... 36 2.2
 AA726355, AA726355 vu90c09.r1 Stratagene mouse skin (#937313)... 36 2.2
 AA404025, AA404025 va31c11.r1 GuayWoodford Beier mouse kidney... 36 2.2
 AA060014, AA060014 ml34d07.r1 Stratagene mouse testis (#93730... 36 2.2
 AA870617, AA870617 vq23h10.r1 Barstead stromal cell line MPLR... 36 2.2
 AA414112, AA414112 vc64f08.s1 Knowles Solter mouse 2 cell Mus... 36 2.2
 AA764250, AA764250 vv49e09.r1 Soares 2NbMT Mus musculus cDNA ... 36 2.2

H34350, H34350 EST111226 Rat PC-12 cells, NGF-treated (9 days... 36 1.9
 C40718, C40718 *C.elegans* cDNA clone yk247f9 : 5' end, single... 36 1.9
 AA817925, AA817925 UI-R-A0-af-g-04-0-UI.s1 UI-R-A0 Rattus nor... 36 1.9
 AA955650, AA955650 UI-R-E1-fc-e-10-0-UI.s1 UI-R-E1 Rattus nor... 36 1.9

SEQ ID NO:547

U66201, MMU66201 Mus musculus fibroblast growth factor homolo... 42 0.35
 U66197, HSU66197 Human fibroblast growth factor homologous fa... 42 0.35
 AF020738, AF020738 Mus musculus fibroblast growth factor-rela... 42 0.35
 U85773, HSU85773 Human phosphomannomutase (PMM2) mRNA, comple... 40 1.4
 Z46966, MMIMOGN44 M.musculus mRNA for imogen 44. 40 1.4
 AC004301, AC004301 Drosophila melanogaster DNA sequence (P1 D... 40 1.4
 U86662, LEU86662 Lycopersicon esculentum VPS41 (tVPS41) mRNA,... 40 1.4

HUMAN ESTs

W22160, W22160 63A6 Human retina cDNA Tsp509I-cleaved sublibr... 791 0.0
 AA860926, AA860926 ak22d06.s1 Soares testis NHT Homo sapiens ... 650 0.0
 AA348243, AA348243 EST54707 Hippocampus I Homo sapiens cDNA 5... 513 e-143
 AA551799, AA551799 nk04a11.s1 NCI_CGAP_Co2 Homo sapiens cDNA ... 363 4e-98
 AA327309, AA327309 EST30621 Colon I Homo sapiens cDNA 5' end 353 3e-95
 AA344913, AA344913 EST50856 Gall bladder II Homo sapiens cDNA... 337 2e-90
 AA121174, AA121174 zl88g08.s1 Stratagene colon (#937204) Homo... 317 2e-84
 AA121198, AA121198 zl88g08.r1 Stratagene colon (#937204) Homo... 317 2e-84
 AA001561, AA001561 ze46e07.s1 Soares retina N2b4HR Homo sapie... 42 0.17
 AA888147, AA888147 04h11.s1 NCI_CGAP_Co10 Homo sapiens cDNA... 40 0.67
 AA946650, AA946650 oq38h09.s1 NCI_CGAP_Kid5 Homo sapiens cDNA... 40 0.67
 AA435587, AA435587 zi85d07.s1 Soares testis NHT Homo sapiens ... 40 0.67
 AA806381, AA806381 oc22g05.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 40 0.67
 AA577174, AA577174 nm86e11.s1 NCI_CGAP_Co9 Homo sapiens cDNA ... 40 0.67
 AA215903, AA215903 hp0042.seq.F Fetal heart, Lambda ZAP Expre... 40 0.67
 AA262229, AA262229 zs25b12.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 40 0.67
 AA969632, AA969632 op38h05.s1 Soares_NFL_T_GBC_S1 Homo sapien... 40 0.67
 N35888, N35888 yy28b05.s1 Homo sapiens cDNA clone 272529 3'. 40 0.67
 AI005324, AI005324 ou13h07.x1 Soares_NFL_T_GBC_S1 Homo sapien... 40 0.67
 AA172158, AA172158 zp29a01.s1 Stratagene neuroepithelium (#93... 40 0.67
 AA860208, AA860208 ak48c10.s1 Soares testis NHT Homo sapiens ... 40 0.67
 AA814296, AA814296 nz07d08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 40 0.67
 AA873216, AA873216 oh70f04.s1 NCI_CGAP_Kid5 Homo sapiens cDNA... 40 0.67
 AA403143, AA403143 zv66d01.r1 Soares total fetus Nb2HF8 9w Ho... 40 0.67
 W45005, W45005 zc05c12.r1 Soares parathyroid tumor NbHPA Homo... 40 0.67
 W32428, W32428 zc05c12.s1 Soares parathyroid tumor NbHPA Homo... 40 0.67
 AA974988, AA974988 on59b06.s1 Soares_NFL_T_GBC_S1 Homo sapien... 40 0.67
 AA725024, AA725024 ah97h10.s1 Soares NFL T GBC S1 Homo sapien... 40 0.67
 AA757360, AA757360 ah98a01.s1 Soares NFL T GBC S1 Homo sapien... 40 0.67
 N72025, N72025 yz96g02.s1 Homo sapiens cDNA clone 290930 3'. 40 0.67
 R02514, R02514 ye70b08.r1 Homo sapiens cDNA clone 123063 5'. 40 0.67
 AA039536, AA039536 zk39h10.s1 Soares pregnant uterus NbHPU Ho... 40 0.67
 AA877455, AA877455 ob33g01.s1 NCI_CGAP_Kid5 Homo sapiens cDNA... 40 0.67
 AA041240, AA041240 zf07g05.r1 Soares fetal heart NbHH19W Homo... 40 0.67

AA903406, AA903406 ok62c11.s1 NCI_CGAP_GC4 Homo sapiens cDNA ... 40 0.67
 AA461270, AA461270 zx63b07.r1 Soares total fetus Nb2HF8 9w Ho... 40 0.67
 AA927863, AA927863 om18a08.s1 Soares_NFL_T_GBC_S1 Homo sapien... 40 0.67
 AA587486, AA587486 nm84e09.s1 NCI_CGAP_Br2 Homo sapiens cDNA ... 40 0.67
 W47466, W47466 zc34h02.r1 Soares senescent fibroblasts NbHSF ... 40 0.67
 AA022495, AA022495 ze70e04.s1 Soares fetal heart NbHH19W Homo... 40 0.67
 AA460961, AA460961 zx63b07.s1 Soares total fetus Nb2HF8 9w Ho... 40 0.67
 AA393904, AA393904 zt85e06.r1 Soares testis NHT Homo sapiens ... 40 0.67
 AA872272, AA872272 oh72a11.s1 NCI_CGAP_Kid5 Homo sapiens cDNA... 40 0.67
 W47341, W47341 zc34h02.s1 Soares senescent fibroblasts NbHSF ... 40 0.67
 N72024, N72024 yz96g01.s1 Homo sapiens cDNA clone 290928 3'. 40 0.67
 N35076, N35076 yy19b08.s1 Homo sapiens cDNA clone 271671 3'. 40 0.67
 AA813115, AA813115 aj44d06.s1 Soares testis NHT Homo sapiens ... 40 0.67
 AA826741, AA826741 85f12.s1 NCI_CGAP_Pr24 Homo sapiens cDNA... 40 0.67
 AA160827, AA160827 zo62e01.s1 Stratagene pancreas (#937208) H... 40 0.67
 AI040354, AI040354 oy33d12.x1 Soares_parathyroid_tumor_NbHPA ... 40 0.67
 AA573297, AA573297 nk98d09.s1 NCI_CGAP_Co3 Homo sapiens cDNA ... 40 0.67
 AA416559, AA416559 zu18c03.r1 Soares NhHMPu S1 Homo sapiens c... 40 0.67
 AA401079, AA401079 zv66d01.s1 Soares total fetus Nb2HF8 9w Ho... 40 0.67
 AI005204, AI005204 ou60c12.x1 NCI_CGAP_Br2 Homo sapiens cDNA ... 40 0.67
 N21678, N21678 yx63g01.s1 Soares melanocyte 2NbHM Homo sapien... 40 0.67
 AA824270, AA824270 aj29f01.s1 Soares testis NHT Homo sapiens ... 40 0.67
 AA804907, AA804907 oa89a01.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 40 0.67
 AA759038, AA759038 ah75h11.s1 Soares testis NHT Homo sapiens ... 40 0.67
 AA417295, AA417295 zu18c03.s1 Soares NhHMPu S1 Homo sapiens c... 40 0.67
 AA628544, AA628544 af27h12.s1 Soares total fetus Nb2HF8 9w Ho... 40 0.67
 AA618498, AA618498 np30a11.s1 NCI_CGAP_Pr22 Homo sapiens cDNA... 40 0.67
 AA503727, AA503727 ne49g02.s1 NCI_CGAP_Co3 Homo sapiens cDNA ... 40 0.67
 AA514777, AA514777 ni24b01.s1 NCI_CGAP_Co4 Homo sapiens cDNA ... 40 0.67
 AA040802, AA040802 zf07g05.s1 Soares fetal heart NbHH19W Homo... 40 0.67
 AA770473, AA770473 ah89h06.s1 Soares NFL T GBC S1 Homo sapien... 40 0.67
 AA759377, AA759377 ah54a10.s1 Soares testis NHT Homo sapiens ... 40 0.67
 AA629243, AA629243 zu77e03.s1 Soares testis NHT Homo sapiens ... 40 0.67
 AA262162, AA262162 zs25b12.r1 NCI_CGAP_GCB1 Homo sapiens cDNA... 40 0.67
 AA161105, AA161105 zo58c05.s1 Stratagene pancreas (#937208) H... 38 2.6
 AA852281, AA852281 NHTBCae11g05r1 Normal Human Trabecular Bon... 38 2.6
 AA948291, AA948291 oq34d02.s1 NCI_CGAP_GC4 Homo sapiens cDNA ... 38 2.6
 AA416734, AA416734 zu08c01.s1 Soares testis NHT Homo sapiens ... 38 2.6
 N98472, N98472 yy65a04.r1 Homo sapiens cDNA clone 278382 5'. 38 2.6
 AA416815, AA416815 zu08c01.r1 Soares testis NHT Homo sapiens ... 38 2.6
 AA431486, AA431486 zw72g01.s1 Soares testis NHT Homo sapiens ... 38 2.6
 H30248, H30248 yp42a01.s1 Homo sapiens cDNA clone 190056 3'. 38 2.6
 R82551, R82551 yj19d06.r1 Homo sapiens cDNA clone 149195 5'. 38 2.6

AA616807, AA616807 vn68c05.r1 Barstead mouse irradiated colon... 180 1e-43
 AA014223, AA014223 mh20a03.r1 Soares mouse placenta 4NbMP13.5... 40 0.24
 AA014768, AA014768 mi66h04.r1 Soares mouse embryo NbME13.5 14... 40 0.24
 AA185487, AA185487 mt62c07.r1 Soares 2NbMT Mus musculus cDNA ... 40 0.24
 AA103139, AA103139 mo17f05.r1 Life Tech mouse embryo 13 5dpc ... 40 0.24
 AI048515, AI048515 uh61e08.r1 Soares mouse embryonic stem cel... 40 0.24
 AA711859, AA711859 vu59c10.r1 Soares mouse mammary gland NbMM... 40 0.24
 AA009071, AA009071 mg87b11.r1 Soares mouse embryo NbME13.5 14... 40 0.24
 AA276740, AA276740 vc42a12.r1 Soares mouse 3NbMS Mus musculus... 40 0.24
 AA497479, AA497479 vh29b12.r1 Soares mouse mammary gland NbMM... 40 0.24
 AA038869, AA038869 mi95b10.r1 Soares mouse p3NMF19.5 Mus musc... 40 0.24
 AA790448, AA790448 vw04f09.r1 Soares mouse mammary gland NbMM... 40 0.24
 AA881111, AA881111 vz06e09.r1 Soares mouse mammary gland NbMM... 40 0.24
 AA007762, AA007762 mg76b03.r1 Soares mouse embryo NbME13.5 14... 40 0.24
 W83172, W83172 mf09a06.r1 Soares mouse p3NMF19.5 Mus musculus... 40 0.24
 AA106439, AA106439 ml59a08.r1 Stratagene mouse testis (#93730... 40 0.24
 AA000268, AA000268 mg32e09.r1 Soares mouse embryo NbME13.5 14... 40 0.24
 AI047077, AI047077 uh61g06.r1 Soares mouse embryonic stem cel... 40 0.24
 AA543280, AA543280 vj80h05.r1 Soares mouse mammary gland NbMM... 40 0.24
 AA106301, AA106301 ml81a09.r1 Stratagene mouse kidney (#93731... 40 0.24
 AA467482, AA467482 ve01a10.r1 Soares mouse NbMH Mus musculus ... 40 0.24
 AA797372, AA797372 vw27b08.r1 Soares mouse mammary gland NbMM... 40 0.24
 W77724, W77724 me84h06.r1 Soares mouse embryo NbME13.5 14.5 M... 40 0.24
 AA049011, AA049011 mj48c09.r1 Soares mouse embryo NbME13.5 14... 40 0.24
 AA763419, AA763419 vw54a12.r1 Soares mouse mammary gland NMLM... 40 0.24
 AA138067, AA138067 mq37c11.r1 Barstead MPLRB1 Mus musculus cD... 40 0.24
 AA475425, AA475425 vh20g09.r1 Soares mouse mammary gland NbMM... 40 0.24
 AA469884, AA469884 vf71g10.r1 Barstead mouse pooled organs MP... 40 0.24
 AA016868, AA016868 mh36e12.r1 Soares mouse placenta 4NbMP13.5... 40 0.24
 AA230758, AA230758 my32g10.r1 Barstead mouse pooled organs MP... 40 0.24
 AA833479, AA833479 uc91c03.r1 Soares mouse uterus NMPu Mus mu... 40 0.24
 W61547, W61547 md57a02.r1 Soares mouse embryo NbME13.5 14.5 M... 40 0.24
 AA033481, AA033481 mi42b07.r1 Soares mouse embryo NbME13.5 14... 40 0.24
 AA068686, AA068686 mm59a03.r1 Stratagene mouse embryonic carc... 38 0.94
 AA796056, AA796056 vo65d01.r1 Soares mouse mammary gland NbMM... 36 3.7
 C87249, C87249 Mus musculus fertilized egg cDNA 3'-end seque... 36 3.7
 AA921560, AA921560 vy52c06.r1 Stratagene mouse lung 937302 Mu... 36 3.7
 W87202, W87202 mf55g08.r1 Soares mouse embryo NbME13.5 14.5 M... 36 3.7
 AA542324, AA542324 vk53e07.r1 Stratagene mouse Tcell 937311 M... 36 3.7
 AA967316, AA967316 vj47a03.r1 Stratagene mouse skin (#937313)... 36 3.7
 W62989, W62989 md88h12.r1 Soares mouse embryo NbME13.5 14.5 M... 36 3.7
 AA530735, AA530735 vj32g11.r1 Stratagene mouse diaphragm (#93... 36 3.7
 AA218431, AA218431 my07e05.r1 Barstead mouse lung MPLRB2 Mus ... 36 3.7
 AA591243, AA591243 vm18c04.r1 Knowles Solter mouse blastocyst... 36 3.7

AI047609, AI047609 uh63g07.r1 Soares mouse embryonic stem cel... 36 3.7
 AA692425, AA692425 vt59b05.r1 Barstead mouse irradiated colon... 36 3.7
 AA966976, AA966976 ua38f11.r1 Soares mouse mammary gland NbMM... 36 3.7
 AA856298, AA856298 vw99b01.r1 Soares 2NbMT Mus musculus cDNA ... 36 3.7
 W20935, W20935 mb96c07.r1 Soares mouse p3NMF19.5 Mus musculus... 36 3.7
 AA230661, AA230661 mw15f08.r1 Soares mouse 3NME12 5 Mus muscu... 36 3.7
 AA111190, AA111190 mp66b11.r1 Soares 2NbMT Mus musculus cDNA ... 36 3.7
 AA840087, AA840087 uc99h12.r1 Soares mouse uterus NMPu Mus mu... 36 3.7
 AA089210, AA089210 mo05d10.r1 Stratagene mouse lung 937302 Mu... 36 3.7
 AI035925, AI035925 ub49e05.r1 Soares mouse mammary gland NbMM... 36 3.7
 AA824205, AA824205 vy20g08.r1 Stratagene mouse macrophage (#9... 36 3.7
 AA793845, AA793845 vr35e12.r1 Barstead mouse myotubes MPLRB5 ... 36 3.7
 AA239210, AA239210 mx89e02.r1 Soares mouse NML Mus musculus c... 36 3.7
 AA711873, AA711873 vu28e06.r1 Barstead mouse myotubes MPLRB5 ... 36 3.7
 AA645119, AA645119 vs72d03.r1 Stratagene mouse skin (#937313)... 36 3.7

AA957268, AA957268 UI-R-E1-fq-e-06-0-UI.s1 UI-R-E1 Rattus nor... 42 0.053
 C83463, C83463 Oryctolagus cuniculus corneal endothelial cDN... 38 0.84
 AA859448, AA859448 UI-R-A0-bf-b-01-0-UI.s1 UI-R-A0 Rattus nor... 38 0.84
 AA874930, AA874930 UI-R-E0-ci-b-05-0-UI.s1 UI-R-E0 Rattus nor... 38 0.84
 C82607, C82607 Oryctolagus cuniculus corneal endothelial cDN... 38 0.84
 AI009631, AI009631 EST204082 Normalized rat lung, Bento Soare... 38 0.84
 AA801145, AA801145 EST190642 Normalized rat ovary, Bento Soar... 38 0.84
 AI012760, AI012760 EST207211 Normalized rat placenta, Bento S... 38 0.84
 AA956139, AA956139 UI-R-E1-fi-h-08-0-UI.s1 UI-R-E1 Rattus nor... 38 0.84
 AA801144, AA801144 EST190641 Normalized rat ovary, Bento Soar... 38 0.84
 AA660819, AA660819 00713 MtrHE Medicago truncatula cDNA 5' ... 38 0.84
 AA859865, AA859865 UI-R-E0-cc-b-04-0-UI.s1 UI-R-E0 Rattus nor... 38 0.84
 AI009035, AI009035 EST203486 Normalized rat embryo, Bento Soa... 38 0.84
 AA859542, AA859542 UI-R-E0-br-d-03-0-UI.s1 UI-R-E0 Rattus nor... 38 0.84
 T00613, T00613 wEST01334 Caenorhabditis elegans cDNA clone CE... 38 0.84
 H32878, H32878 EST108396 Rat PC-12 cells, untreated Rattus sp... 36 3.3
 AA125602, AA125602 JM00M011.QM3 Miracidia Sjc 3/96 Schistosom... 36 3.3
 D45997, RICS10346A Rice cDNA, partial sequence (S10346_1A). 36 3.3
 AA943364, AA943364 EST198863 Normalized rat brain, Bento Soar... 36 3.3
 C68472, C68472 C.elegans cDNA clone yk305a12 : 5' end, singl... 36 3.3
 AA785775, AA785775 h4b05a1.f1 Aspergillus nidulans 24hr asexu... 36 3.3
 D46069, RICS10475A Rice cDNA, partial sequence (S10475_1A). 36 3.3
 AA660859, AA660859 00754 MtrHE Medicago truncatula cDNA 5' si... 36 3.3
 Z33974, ATTS3035 A. thaliana transcribed sequence; clone PAP... 36 3.3
 Z32603, ATTS2731 A. thaliana transcribed sequence; clone PAP... 36 3.3
 AA955567, AA955567 UI-R-E1-fa-a-08-0-UI.s1 UI-R-E1 Rattus nor... 36 3.3
 AA842765, AA842765 M-EST080 Sugarcane mature stalk Saccharum ... 36 3.3
 Z32602, ATTS2730 A. thaliana transcribed sequence; clone PAP... 36 3.3

SEQ ID NO:548

U66197, HSU66197 Human fibroblast growth factor homologous fa... 42 0.34
 AF020738, AF020738 Mus musculus fibroblast growth factor-rela... 42 0.34
 U66201, MMU66201 Mus musculus fibroblast growth factor homolo... 42 0.34
 Z46966, MMIMOGN44 M.musculus mRNA for imogen 44. 40 1.3
 AC004301, AC004301 Drosophila melanogaster DNA sequence (P1 D... 40 1.3
 U86662, LEU86662 Lycopersicon esculentum VPS41 (tVPS41) mRNA,... 40 1.3
 U85773, HSU85773 Human phosphomannomutase (PMM2) mRNA, comple... 40 1.3

HUMAN ESTs

W22160, W22160 63A6 Human retina cDNA Tsp509I-cleaved sublibr... 791 0.0
 AA860926, AA860926 ak22d06.s1 Soares testis NHT Homo sapiens ... 650 0.0
 AA348243, AA348243 EST54707 Hippocampus I Homo sapiens cDNA 5... 513 e-143
 AA551799, AA551799 nk04a11.s1 NCI_CGAP_Co2 Homo sapiens cDNA ... 363 3e-98
 AA327309, AA327309 EST30621 Colon I Homo sapiens cDNA 5' end 353 3e-95
 AA344913, AA344913 EST50856 Gall bladder II Homo sapiens cDNA... 337 2e-90
 AA121198, AA121198 zl88g08.r1 Stratagene colon (#937204) Homo... 317 2e-84
 AA121174, AA121174 zl88g08.s1 Stratagene colon (#937204) Homo... 317 2e-84
 AA001561, AA001561 ze46e07.s1 Soares retina N2b4HR Homo sapie... 42 0.16
 AA041240, AA041240 zf07g05.r1 Soares fetal heart NbHH19W Homo... 40 0.64
 AA039536, AA039536 zk39h10.s1 Soares pregnant uterus NbHPU Ho... 40 0.64
 AA040802, AA040802 zf07g05.s1 Soares fetal heart NbHH19W Homo... 40 0.64
 AA573297, AA573297 nk98d09.s1 NCI_CGAP_Co3 Homo sapiens cDNA ... 40 0.64
 N35888, N35888 yy28b05.s1 Homo sapiens cDNA clone 272529 3'. 40 0.64
 AA888147, AA888147 04h11.s1 NCI_CGAP_Co10 Homo sapiens cDNA... 40 0.64
 AA172158, AA172158 zp29a01.s1 Stratagene neuroepithelium (#93... 40 0.64
 AA877455, AA877455 ob33g01.s1 NCI_CGAP_Kid5 Homo sapiens cDNA... 40 0.64
 R02514, R02514 ye70b08.r1 Homo sapiens cDNA clone 123063 5'. 40 0.64
 AA514777, AA514777 ni24b01.s1 NCI_CGAP_Co4 Homo sapiens cDNA ... 40 0.64
 AA416734, AA416734 zu08c01.s1 Soares testis NHT Homo sapiens ... 38 2.5
 N98472, N98472 yy65a04.r1 Homo sapiens cDNA clone 278382 5'. 38 2.5
 AA416815, AA416815 zu08c01.r1 Soares testis NHT Homo sapiens ... 38 2.5
 AA431486, AA431486 zw72g01.s1 Soares testis NHT Homo sapiens ... 38 2.5
 AA948291, AA948291 oq34d02.s1 NCI_CGAP_GC4 Homo sapiens cDNA ... 38 2.5
 AA852281, AA852281 NHTBCae11g05r1 Normal Human Trabecular Bon... 38 2.5

002090-62629460

AA616807, AA616807 vn68c05.r1 Barstead mouse irradiated colon... 180 1e-43
 AA469884, AA469884 vf71g10.r1 Barstead mouse pooled organs MP... 40 0.23
 AA230758, AA230758 my32g10.r1 Barstead mouse pooled organs MP... 40 0.23
 AA038869, AA038869 mi95b10.r1 Soares mouse p3NMF19.5 Mus musc... 40 0.23
 AA763419, AA763419 vw54a12.r1 Soares mouse mammary gland NMLM... 40 0.23
 AA185487, AA185487 mt62c07.r1 Soares 2NbMT Mus musculus cDNA ... 40 0.23
 AA106439, AA106439 ml59a08.r1 Stratagene mouse testis (#93730... 40 0.23
 AA276740, AA276740 vc42a12.r1 Soares mouse 3NbMS Mus musculus... 40 0.23
 AA068686, AA068686 mm59a03.r1 Stratagene mouse embryonic carc... 38 0.91
 AA711873, AA711873 vu28e06.r1 Barstead mouse myotubes MPLRB5 ... 36 3.6
 AA856298, AA856298 vw99b01.r1 Soares 2NbMT Mus musculus cDNA ... 36 3.6
 W20935, W20935 mb96c07.r1 Soares mouse p3NMF19.5 Mus musculus... 36 3.6
 AA966976, AA966976 ua38f11.r1 Soares mouse mammary gland NbMM... 36 3.6
 AA921560, AA921560 vy52c06.r1 Stratagene mouse lung 937302 Mu... 36 3.6
 AA692425, AA692425 vt59b05.r1 Barstead mouse irradiated colon... 36 3.6
 W87202, W87202 mf55g08.r1 Soares mouse embryo NbME13.5 14.5 M... 36 3.6
 AA840087, AA840087 uc99h12.r1 Soares mouse uterus NMPu Mus mu... 36 3.6
 AA111190, AA111190 mp66b11.r1 Soares 2NbMT Mus musculus cDNA ... 36 3.6
 AA239210, AA239210 mx89e02.r1 Soares mouse NML Mus musculus c... 36 3.6
 AA793845, AA793845 vr35e12.r1 Barstead mouse myotubes MPLRB5 ... 36 3.6
 AA645119, AA645119 vs72d03.r1 Stratagene mouse skin (#937313)... 36 3.6
 AA230661, AA230661 mw15f08.r1 Soares mouse 3NME12 5 Mus muscu... 36 3.6
 AA824205, AA824205 vy20g08.r1 Stratagene mouse macrophage (#9... 36 3.6
 C87249, C87249 Mus musculus fertilized egg cDNA 3'-end seque... 36 3.6
 AA967316, AA967316 vj47a03.r1 Stratagene mouse skin (#937313)... 36 3.6
 AA591243, AA591243 vm18c04.r1 Knowles Solter mouse blastocyst... 36 3.6
 AI035925, AI035925 ub49e05.r1 Soares mouse mammary gland NbMM... 36 3.6
 AA530735, AA530735 vj32g11.r1 Stratagene mouse diaphragm (#93... 36 3.6
 AA218431, AA218431 my07e05.r1 Barstead mouse lung MPLRB2 Mus ... 36 3.6
 W62989, W62989 md88h12.r1 Soares mouse embryo NbME13.5 14.5 M... 36 3.6
 AA089210, AA089210 mo05d10.r1 Stratagene mouse lung 937302 Mu... 36 3.6
 AA796056, AA796056 vo65d01.r1 Soares mouse mammary gland NbMM... 36 3.6
 AA542324, AA542324 vk53e07.r1 Stratagene mouse Tcell 937311 M... 36 3.6

AA957268, AA957268 UI-R-E1-fq-e-06-0-UI.s1 UI-R-E1 Rattus nor... 42 0.052
 T00613, T00613 wEST01334 Caenorhabditis elegans cDNA clone CE... 38 0.81
 AA660819, AA660819 00713 MtRHE Medicago truncatula cDNA 5' ... 38 0.81
 AA956139, AA956139 UI-R-E1-fi-h-08-0-UI.s1 UI-R-E1 Rattus nor... 38 0.81
 D46069, RICS10475A Rice cDNA, partial sequence (S10475_1A). 36 3.2
 AA842765, AA842765 M-EST080 Sugarcane mature stalk Saccharum ... 36 3.2
 AA955567, AA955567 UI-R-E1-fa-a-08-0-UI.s1 UI-R-E1 Rattus nor... 36 3.2
 Z33974, ATTS3035 A. thaliana transcribed sequence; clone PAP... 36 3.2
 H32878, H32878 EST108396 Rat PC-12 cells, untreated Rattus sp... 36 3.2
 AA660859, AA660859 00754 MtRHE Medicago truncatula cDNA 5' si... 36 3.2

SEQ ID NO:549

U79271, HSU79271	Human clones 23920 and 23921 mRNA sequence	650	0.0
AC000395, AC000395	Genomic sequence from Human 9q34, complete...	42	0.28
AC004636, AC004636	Homo sapiens chromosome 5, P1 clone 1268h6...	42	0.28
M94579, HUMCEL	Human carboxyl ester lipase (CEL) gene, comple...	42	0.28
AC002097, AC002097	Homo sapiens chromosome 9q34, clone 246H5,...	42	0.28
AB006709, AB006709	Vibrio alginolyticus rpoN gene for RNA po...	42	0.28
Z47074, CEK07C10	Caenorhabditis elegans cosmid K07C10, compl...	40	1.1
AC004755, AC004755	Homo sapiens chromosome 19, fosmid 37502, ...	40	1.1
Z28051, SCYKL051W	S.cerevisiae chromosome XI reading frame O...	40	1.1
AF022655, AF022655	Homo sapiens cep250 centrosome associated ...	40	1.1
AB006708, AB006708	Arabidopsis thaliana genomic DNA, chromos...	40	1.1
AF049105, AF049105	Homo sapiens centrosomal Nek2-associated p...	40	1.1
Z28050, SCYKL050C	S.cerevisiae chromosome XI reading frame O...	40	1.1
X75781, SCXI286K	S.cerevisiae chromosome XI (28.6 kb) DNA fo...	40	1.1
Y16899, DMY16899	Drosophila melanogaster mRNA for optomotor-...	38	4.3
M87854, RATBARK1	Rattus norvegicus beta-adrenergic receptor k...	38	4.3
M74822, RATMHTLL	Rat MHC class I TL-like protein gene, comple...	38	4.3
M80776, HUMBARK1A	Human beta-adrenergic receptor kinase 1 mRN...	38	4.3
D84549, YSACA	Candida tropicalis DNA for carnitine acetyltra...	38	4.3
L23127, RATRMCI	Rattus norvegicus germline MHC class I gene, ...	38	4.3
AC004257, AC004257	Homo sapiens chromosome 19, cosmid R33209,...	38	4.3
U70850, CELF28F9	Caenorhabditis elegans cosmid F28F9	38	4.3
U88309, CELT23B3	Caenorhabditis elegans cosmid T23B3	38	4.3
X53421, DVCHOS18	D. virilis s18, s15, s19, s16 chorion prote...	38	4.3
D89245, D89245	Schizosaccharomyces pombe mRNA, partial cds, ...	38	4.3
AF009623, AF009623	Parascaris univalens PUMA1 (puma1) mRNA, c...	38	4.3
S48813, S48813	beta-adrenergic receptor kinase [rats, brain, ...	38	4.3
Z67883, CEK02A4	Caenorhabditis elegans cosmid K02A4, complet...	38	4.3
U90567, GGU90567	Gallus gallus glutamine rich protein mRNA, p...	38	4.3
M98498, BOVEZRINA	Bos taurus ezrin mRNA, complete cds.	38	4.3
M34073, MUSMHT10C	Mus musculus (clone T10-c) MHC class I cell...	38	4.3

S81843, S81843 beta-adrenergic receptor kinase 1 [Syrian hams... 38 4.3
 X61157, HSBARK H.sapiens mRNA for beta-adrenergic receptor k... 38 4.3
 U08438, HSNBARKS4 Human beta-adrenergic receptor kinase (ADRB... 38 4.3
 U39674, CELC06E2 Caenorhabditis elegans cosmid C06E2. 38 4.3

HUMAN ESTs

W29097, W29097 56d11 Human retina cDNA randomly primed sublib... 1045 0.0
 AA886109, AA886109 ny44f05.s1 NCI_CGAP_Pr12 Homo sapiens cDNA... 656 0.0
 AA829894, AA829894 oe51e12.s1 NCI_CGAP_Lu5 Homo sapiens cDNA ... 650 0.0
 AA879456, AA879456 oj91g03.s1 Soares_NFL_T_GBC_S1 Homo sapien... 650 0.0
 AA029201, AA029201 zk12f08.s1 Soares pregnant uterus NbHPU Ho... 650 0.0
 AA102109, AA102109 zk87g11.s1 Soares pregnant uterus NbHPU Ho... 650 0.0
 AA843811, AA843811 ak09c08.s1 Soares parathyroid tumor NbHPA ... 650 0.0
 W72147, W72147 zd70f08.s1 Soares fetal heart NbHH19W Homo sap... 650 0.0
 N51485, N51485 yz04e06.s1 Homo sapiens cDNA clone 282082 3'. 650 0.0
 AI033069, AI033069 ow93f02.s1 Soares_fetal_liver_spleen_1NFLS... 642 0.0
 AA161465, AA161465 zo73a06.s1 Stratagene pancreas (#937208) H... 638 0.0
 N51277, N51277 yz14d07.s1 Homo sapiens cDNA clone 283021 3'. 636 e-180
 N64528, N64528 yz91e06.s1 Homo sapiens cDNA clone 290434 3'. 636 e-180
 H99906, H99906 yx32h10.s1 Homo sapiens cDNA clone 263491 3'. 636 e-180
 AA812519, AA812519 ai79b03.s1 Soares testis NHT Homo sapiens ... 636 e-180
 R71679, R71679 yj85e08.s1 Homo sapiens cDNA clone 155558 3'. 628 e-178
 AA744290, AA744290 ny51d02.s1 NCI_CGAP_Pr18 Homo sapiens cDNA... 626 e-177
 AI038590, AI038590 ox34e03.s1 Soares_total_fetus_Nb2HF8_9w Ho... 624 e-177
 AA099913, AA099913 zk87g11.r1 Soares pregnant uterus NbHPU Ho... 624 e-177
 AA083859, AA083859 zn16d06.s1 Stratagene neuroepithelium NT2R... 622 e-176
 AA883684, AA883684 al58a05.s1 Soares NFL T GBC S1 Homo sapien... 613 e-173
 R39448, R39448 yc95d03.s1 Homo sapiens cDNA clone 23921 3'. 593 e-167
 R36854, R36854 yf52c07.s1 Homo sapiens cDNA clone 25899 3'. 591 e-167
 H98684, H98684 yx17g01.s1 Homo sapiens cDNA clone 262032 3'. 585 e-165
 R07471, R07471 ye97a06.s1 Homo sapiens cDNA clone 125650 3'. 581 e-164
 AA910762, AA910762 ol25h06.s1 Soares_NFL_T_GBC_S1 Homo sapien... 559 e-157
 AA083954, AA083954 zn17d06.s1 Stratagene neuroepithelium NT2R... 555 e-156
 AA346369, AA346369 EST52776 Fetal heart II Homo sapiens cDNA ... 545 e-153
 R54092, R54092 yg98d07.s1 Homo sapiens cDNA clone 41818 3'. 539 e-151
 H09074, H09074 yl97a06.s1 Homo sapiens cDNA clone 46164 3'. 535 e-150
 N21975, N21975 yw30c10.s1 Homo sapiens cDNA clone 253746 3'. 533 e-149
 D59844, HUM070E11A Human fetal brain cDNA 3'-end GEN-070E11. 466 e-129
 H11525, H11525 ym15h07.s1 Homo sapiens cDNA clone 48232 3'. 442 e-122
 AA971254, AA971254 op73c08.s1 Soares_NFL_T_GBC_S1 Homo sapien... 442 e-122
 W77907, W77907 zd70f08.r1 Soares fetal heart NbHH19W Homo sap... 428 e-118
 AA878973, AA878973 oj26d11.s1 NCI_CGAP_Kid3 Homo sapiens cDNA... 389 e-106
 AA715235, AA715235 nv10g01.s1 NCI_CGAP_Pr22 Homo sapiens cDNA... 357 2e-96

AA328928, AA328928 EST32475 Embryo, 12 week I Homo sapiens cD... 355 7e-96
 AA860455, AA860455 aj80f02.s1 Soares parathyroid tumor NbHPA ... 283 2e-74
 AA026096, AA026096 ze97a04.r1 Soares fetal heart NbHH19W Homo... 268 1e-69
 AA026516, AA026516 ze97a04.s1 Soares fetal heart NbHH19W Homo... 172 6e-41
 T26899, T26899 ESTDIR509 Homo sapiens cDNA clone CDDIR509 3'. 170 2e-40
 N71178, N71178 yw30c10.r1 Homo sapiens cDNA clone 253746 5'. 165 1e-38
 AA372290, AA372290 EST84170 Raji cells, cyclohexamide treated... 98 3e-18
 AI038890, AI038890 ox84g12.x1 Soares_senescent_fibroblasts_Nb... 40 0.53
 D81647, HUM180D08B Human fetal brain cDNA 5'-end GEN-180D08. 38 2.1
 AA452630, AA452630 zx33f08.r1 Soares total fetus Nb2HF8 9w Ho... 38 2.1
 AA682624, AA682624 zi19g01.s1 Soares fetal liver spleen 1NFLS... 38 2.1
 AA742364, AA742364 ny89c12.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 38 2.1
 AA907234, AA907234 ol03h08.s1 NCI_CGAP_Lu5 Homo sapiens cDNA ... 38 2.1
 T09391, T09391 EST07284 Homo sapiens cDNA clone HIBBT71 5' en... 38 2.1
 AA161236, AA161236 zo59h07.s1 Stratagene pancreas (#937208) H... 38 2.1
 AA252941, AA252941 zr50g09.r1 Soares NhHMPu S1 Homo sapiens c... 38 2.1
 AA252245, AA252245 zr64g07.s1 Soares NhHMPu S1 Homo sapiens c... 38 2.1
 AA780678, AA780678 ac70h01.s1 Stratagene fetal retina 937202 ... 38 2.1
 W05501, W05501 za84a12.r1 Soares fetal lung NbHL19W Homo sapi... 38 2.1
 AI039908, AI039908 ox25f07.x1 Soares_total_fetus_Nb2HF8_9w Ho... 38 2.1
 AA280664, AA280664 zs99f09.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 38 2.1
 AA973566, AA973566 oo46f09.s1 NCI_CGAP_Lu5 Homo sapiens cDNA ... 38 2.1
 N27253, N27253 yx17g01.r1 Homo sapiens cDNA clone 262032 5'. 38 2.1
 AA995707, AA995707 os29c09.s1 NCI_CGAP_Kid5 Homo sapiens cDNA... 38 2.1
 AI016407, AI016407 ot72e09.s1 Soares_total_fetus_Nb2HF8_9w Ho... 38 2.1
 N70619, N70619 za84a12.s1 Homo sapiens cDNA clone 299230 3'. 38 2.1
 AA242923, AA242923 zr64g07.r1 Soares NhHMPu S1 Homo sapiens c... 38 2.1
 AA938631, AA938631 oo96f07.s1 NCI_CGAP_Kid5 Homo sapiens cDNA... 38 2.1
 AA985290, AA985290 am74g03.s1 Stratagene schizo brain S11 Hom... 38 2.1

AA690806, AA690806 vt25h10.r1 Barstead mouse myotubes MPLRB5 ... 377 e-103
 AA155014, AA155014 mr99h05.r1 Stratagene mouse embryonic carc... 180 8e-44
 AA269966, AA269966 va57d06.r1 Soares mouse 3NME12 5 Mus muscu... 172 2e-41
 AA089195, AA089195 mo05h11.r1 Stratagene mouse lung 937302 Mu... 163 2e-38
 AA466212, AA466212 vg86g02.r1 Barstead mouse pooled organs MP... 68 8e-10
 AA423476, AA423476 ve76d07.r1 Soares mouse mammary gland NbMM... 60 2e-07
 AA597213, AA597213 vo28a05.r1 Barstead mouse irradiated colon... 40 0.19
 AA396266, AA396266 vb45c01.r1 Soares mouse lymph node NbMLN M... 40 0.19
 AA967806, AA967806 uh05d06.r1 Soares mouse hypothalamus NMHy ... 38 0.75
 AA591111, AA591111 vm12c06.r1 Knowles Solter mouse blastocyst... 38 0.75
 W65797, W65797 me14g02.r1 Soares mouse embryo NbME13.5 14.5 M... 38 0.75
 AA153891, AA153891 mq56e05.r1 Soares 2NbMT Mus musculus cDNA ... 38 0.75

AA784124, AA784124	d2b06a1.f1 Aspergillus nidulans 24hr asexu...	38	0.67
AI044911, AI044911	UI-R-C1-kk-e-05-0-UI.s1 UI-R-C1 Rattus nor...	36	2.6
AA550452, AA550452	1605m3 gmbPfHB3.1, G. Roman Reddy Plasmodi...	36	2.6
F20017, ATTS6056	A. thaliana transcribed sequence; clone TAP...	36	2.6
AA786697, AA786697	k5d01a1.f1 Aspergillus nidulans 24hr asexu...	36	2.6
AA433457, AA433457	SW3ICA2345SK Brugia malayi infective larva...	36	2.6

U66201, MMU66201	Mus musculus fibroblast growth factor homolo...	42	0.20
AF020738, AF020738	Mus musculus fibroblast growth factor-rela...	42	0.20
U66197, HSU66197	Human fibroblast growth factor homologous fa...	42	0.20
Z46966, MMIMOGN44	M.musculus mRNA for imogen 44.	40	0.80

AC004301, AC004301 *Drosophila melanogaster* DNA sequence (P1 D... 40 0.80
 U86662, LEU86662 *Lycopersicon esculentum* VPS41 (tVPS41) mRNA,... 40 0.80
 Y14330, HSY14330 *Homo sapiens* partial mRNA for jagged2 protein 38 3.2
 AF003521, AF003521 *Homo sapiens* Jagged 2 mRNA, complete cds 38 3.2
 AF029778, AF029778 *Homo sapiens* Jagged2 (JAG2) mRNA, complete... 38 3.2
 AF020201, AF020201 *Homo sapiens* Jagged 2 mRNA, complete cds 38 3.2
 Z71523, SCYNL247W *S.cerevisiae* chromosome XIV reading frame ... 38 3.2
 AF029779, AF029779 *Homo sapiens* hJAG2.del-E6 (JAG2) mRNA, alt... 38 3.2
 U70049, RNU70049 *Rattus norvegicus* jagged2 precursor gene, pa... 38 3.2
 X96722, SCCHXIVL *S.cerevisiae* DNA region from chromosome XIV... 38 3.2
 AF005938, AF005938 *Cavia porcellus* L-type voltage-dependent c... 38 3.2
 X78972, SBSTRBF *S.bluensis* ISP 5564 genes strB and strF 38 3.2
 X94912, HSPR22 *H.sapiens* Pr22 gene 38 3.2

HUMAN ESTs

AA860926, AA860926 ak22d06.s1 Soares testis NHT *Homo sapiens* ... 650 0.0
 AA348243, AA348243 EST54707 Hippocampus I *Homo sapiens* cDNA 5... 513 e-144
 AA551799, AA551799 nk04a11.s1 NCI_CGAP_Co2 *Homo sapiens* cDNA ... 363 2e-98
 AA327309, AA327309 EST30621 Colon I *Homo sapiens* cDNA 5' end 353 2e-95
 AA344913, AA344913 EST50856 Gall bladder II *Homo sapiens* cDNA... 337 1e-90
 AA121174, AA121174 zl88g08.s1 Stratagene colon (#937204) *Homo*... 317 1e-84
 AA121198, AA121198 zl88g08.r1 Stratagene colon (#937204) *Homo*... 317 1e-84
 AA001561, AA001561 ze46e07.s1 Soares retina N2b4HR *Homo sapie*... 42 0.098
 AI005204, AI005204 ou60c12.x1 NCI_CGAP_Br2 *Homo sapiens* cDNA ... 40 0.39
 AA757360, AA757360 ah98a01.s1 Soares NFL T GBC S1 *Homo sapien*... 40 0.39
 AI005324, AI005324 ou13h07.x1 Soares_NFL_T_GBC_S1 *Homo sapien*... 40 0.39
 AA416559, AA416559 zu18c03.r1 Soares NhHMPu S1 *Homo sapiens* c... 40 0.39
 AA262162, AA262162 zs25b12.r1 NCI_CGAP_GCB1 *Homo sapiens* cDNA... 40 0.39
 AA824270, AA824270 aj29f01.s1 Soares testis NHT *Homo sapiens* ... 40 0.39
 AA826741, AA826741 85f12.s1 NCI_CGAP_Pr24 *Homo sapiens* cDNA... 40 0.39
 AA813115, AA813115 aj44d06.s1 Soares testis NHT *Homo sapiens* ... 40 0.39
 AA403143, AA403143 zv66d01.r1 Soares total fetus Nb2HF8 9w Ho... 40 0.39
 AA725024, AA725024 ah97h10.s1 Soares NFL T GBC S1 *Homo sapien*... 40 0.39
 AA804907, AA804907 oa89a01.s1 NCI_CGAP_GCB1 *Homo sapiens* cDNA... 40 0.39
 AA628544, AA628544 af27h12.s1 Soares total fetus Nb2HF8 9w Ho... 40 0.39
 AA618498, AA618498 np30a11.s1 NCI_CGAP_Pr22 *Homo sapiens* cDNA... 40 0.39
 AA503727, AA503727 ne49g02.s1 NCI_CGAP_Co3 *Homo sapiens* cDNA ... 40 0.39
 AA460961, AA460961 zx63b07.s1 Soares total fetus Nb2HF8 9w Ho... 40 0.39
 AA770473, AA770473 ah89h06.s1 Soares NFL T GBC S1 *Homo sapien*... 40 0.39
 AA759377, AA759377 ah54a10.s1 Soares testis NHT *Homo sapiens* ... 40 0.39
 AA629243, AA629243 zu77e03.s1 Soares testis NHT *Homo sapiens* ... 40 0.39
 AA903406, AA903406 ok62c11.s1 NCI_CGAP_GC4 *Homo sapiens* cDNA ... 40 0.39
 AA215903, AA215903 hp0042.seq.F Fetal heart, Lambda ZAP Expre... 40 0.39

AA160827, AA160827 zo62e01.s1 Stratagene pancreas (#937208) H... 40 0.39
 AA577174, AA577174 nm86e11.s1 NCI_CGAP_Co9 Homo sapiens cDNA ... 40 0.39
 AA969632, AA969632 op38h05.s1 Soares_NFL_T_GBC_S1 Homo sapien... 40 0.39
 N72025, N72025 yz96g02.s1 Homo sapiens cDNA clone 290930 3'. 40 0.39
 AA974988, AA974988 on59b06.s1 Soares_NFL_T_GBC_S1 Homo sapien... 40 0.39
 W32428, W32428 zc05c12.s1 Soares parathyroid tumor NbHPA Homo... 40 0.39
 N21678, N21678 yx63g01.s1 Soares melanocyte 2NbHM Homo sapien... 40 0.39
 AA860208, AA860208 ak48c10.s1 Soares testis NHT Homo sapiens ... 40 0.39
 AA814296, AA814296 nz07d08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 40 0.39
 AA806381, AA806381 oc22g05.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 40 0.39
 AA435587, AA435587 zt85d07.s1 Soares testis NHT Homo sapiens ... 40 0.39
 W45005, W45005 zc05c12.r1 Soares parathyroid tumor NbHPA Homo... 40 0.39
 AA393904, AA393904 zt85e06.r1 Soares testis NHT Homo sapiens ... 40 0.39
 AA759038, AA759038 ah75h11.s1 Soares testis NHT Homo sapiens ... 40 0.39
 AA927863, AA927863 om18a08.s1 Soares_NFL_T_GBC_S1 Homo sapien... 40 0.39
 AA461270, AA461270 zx63b07.r1 Soares total fetus Nb2HF8 9w Ho... 40 0.39
 AA417295, AA417295 zul8c03.s1 Soares NhHMPu S1 Homo sapiens c... 40 0.39
 W47466, W47466 zc34h02.r1 Soares senescent fibroblasts NbHSF ... 40 0.39
 AA262229, AA262229 zs25b12.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 40 0.39
 AA587486, AA587486 nn84e09.s1 NCI_CGAP_Br2 Homo sapiens cDNA ... 40 0.39
 AA401079, AA401079 zv66d01.s1 Soares total fetus Nb2HF8 9w Ho... 40 0.39
 AA872272, AA872272 oh72a11.s1 NCI_CGAP_Kid5 Homo sapiens cDNA... 40 0.39
 W47341, W47341 zc34h02.s1 Soares senescent fibroblasts NbHSF ... 40 0.39
 N72024, N72024 yz96g01.s1 Homo sapiens cDNA clone 290928 3'. 40 0.39
 N35076, N35076 yy19b08.s1 Homo sapiens cDNA clone 271671 3'. 40 0.39
 AI040354, AI040354 oy33d12.x1 Soares_parathyroid_tumor_NbHPA ... 40 0.39
 AA946650, AA946650 oq38h09.s1 NCI_CGAP_Kid5 Homo sapiens cDNA... 40 0.39
 AA022495, AA022495 ze70e04.s1 Soares fetal heart NbHH19W Homo... 40 0.39
 AA873216, AA873216 oh70f04.s1 NCI_CGAP_Kid5 Homo sapiens cDNA... 40 0.39
 R82551, R82551 yj19d06.r1 Homo sapiens cDNA clone 149195 5'. 38 1.5
 H30248, H30248 yp42a01.s1 Homo sapiens cDNA clone 190056 3'. 38 1.5
 AA161105, AA161105 zo58c05.s1 Stratagene pancreas (#937208) H... 38 1.5
 AA948291, AA948291 oq34d02.s1 NCI_CGAP_GC4 Homo sapiens cDNA ... 38 1.5
 AA416734, AA416734 zu08c01.s1 Soares testis NHT Homo sapiens ... 38 1.5
 AA431486, AA431486 zw72g01.s1 Soares testis NHT Homo sapiens ... 38 1.5
 AA416815, AA416815 zu08c01.r1 Soares testis NHT Homo sapiens ... 38 1.5

AA616807, AA616807 vn68c05.r1 Barstead mouse irradiated colon... 180 6e-44
 AA467482, AA467482 ve01a10.r1 Soares mouse NbMH Mus musculus ... 40 0.14
 AA543280, AA543280 vj80h05.r1 Soares mouse mammary gland NbMM... 40 0.14
 AA009071, AA009071 mg87b11.r1 Soares mouse embryo NbME13.5 14... 40 0.14
 AA106439, AA106439 ml59a08.r1 Stratagene mouse testis (#93730... 40 0.14

AA014768, AA014768	mi66h04.r1	Soares mouse embryo NbME13.5 14...	40	0.14
AA881111, AA881111	vz06e09.r1	Soares mouse mammary gland NbMM...	40	0.14
AA049011, AA049011	mj48c09.r1	Soares mouse embryo NbME13.5 14...	40	0.14
AA185487, AA185487	mt62c07.r1	Soares 2NbMT Mus musculus cDNA ...	40	0.14
AA763419, AA763419	vw54a12.r1	Soares mouse mammary gland NMLM...	40	0.14
AA016868, AA016868	mh36e12.r1	Soares mouse placenta 4NbMP13.5...	40	0.14
AA833479, AA833479	uc91c03.r1	Soares mouse uterus NMPu Mus mu...	40	0.14
AA790448, AA790448	vw04f09.r1	Soares mouse mammary gland NbMM...	40	0.14
AA711859, AA711859	vu59c10.r1	Soares mouse mammary gland NbMM...	40	0.14
AA469884, AA469884	vf71g10.r1	Barstead mouse pooled organs MP...	40	0.14
AA230758, AA230758	my32g10.r1	Barstead mouse pooled organs MP...	40	0.14
AA497479, AA497479	vh29b12.r1	Soares mouse mammary gland NbMM...	40	0.14
AA138067, AA138067	mq37c11.r1	Barstead MPLRB1 Mus musculus cD...	40	0.14
AA103139, AA103139	mo17f05.r1	Life Tech mouse embryo 13 5dpc ...	40	0.14
AI047077, AI047077	uh61g06.r1	Soares mouse embryonic stem cel...	40	0.14
AI048515, AI048515	uh61e08.r1	Soares mouse embryonic stem cel...	40	0.14
W61547, W61547	md57a02.r1	Soares mouse embryo NbME13.5 14.5 M...	40	0.14
AA007762, AA007762	mg76b03.r1	Soares mouse embryo NbME13.5 14...	40	0.14
AA000268, AA000268	mg32e09.r1	Soares mouse embryo NbME13.5 14...	40	0.14
AA475425, AA475425	vh20g09.r1	Soares mouse mammary gland NbMM...	40	0.14
AA014223, AA014223	mh20a03.r1	Soares mouse placenta 4NbMP13.5...	40	0.14
AA797372, AA797372	vw27b08.r1	Soares mouse mammary gland NbMM...	40	0.14
AA106301, AA106301	ml81a09.r1	Stratagene mouse kidney (#93731...	40	0.14
AA033481, AA033481	mi42b07.r1	Soares mouse embryo NbME13.5 14...	40	0.14
W77724, W77724	me84h06.r1	Soares mouse embryo NbME13.5 14.5 M...	40	0.14
W83172, W83172	mf09a06.r1	Soares mouse p3NMF19.5 Mus musculus...	40	0.14
AA038869, AA038869	mi95b10.r1	Soares mouse p3NMF19.5 Mus musc...	40	0.14
AA068686, AA068686	mm59a03.r1	Stratagene mouse embryonic carc...	38	0.55
AA111190, AA111190	mp66b11.r1	Soares 2NbMT Mus musculus cDNA ...	36	2.2
AA840087, AA840087	uc99h12.r1	Soares mouse uterus NMPu Mus mu...	36	2.2
AA239210, AA239210	mx89e02.r1	Soares mouse NML Mus musculus c...	36	2.2
AA824205, AA824205	vy20g08.r1	Stratagene mouse macrophage (#9...	36	2.2
C87249, C87249		Mus musculus fertilized egg cDNA 3'-end seque...	36	2.2
AA089210, AA089210	mo05d10.r1	Stratagene mouse lung 937302 Mu...	36	2.2
AA711873, AA711873	vu28e06.r1	Barstead mouse myotubes MPLRB5 ...	36	2.2
AA793845, AA793845	vr35e12.r1	Barstead mouse myotubes MPLRB5 ...	36	2.2
AA645119, AA645119	vs72d03.r1	Stratagene mouse skin (#937313)...	36	2.2
AA967316, AA967316	vj47a03.r1	Stratagene mouse skin (#937313)...	36	2.2
W87202, W87202	mf55g08.r1	Soares mouse embryo NbME13.5 14.5 M...	36	2.2
AA218431, AA218431	my07e05.r1	Barstead mouse lung MPLRB2 Mus ...	36	2.2
AA796056, AA796056	vo65d01.r1	Soares mouse mammary gland NbMM...	36	2.2
AA542324, AA542324	vk53e07.r1	Stratagene mouse Tcell 937311 M...	36	2.2
AA530735, AA530735	vj32g11.r1	Stratagene mouse diaphragm (#93...	36	2.2
AI047609, AI047609	uh63g07.r1	Soares mouse embryonic stem cel...	36	2.2
AA591243, AA591243	vm18c04.r1	Knowles Solter mouse blastocyst...	36	2.2

AA856298, AA856298 vw99b01.r1 Soares 2NbMT Mus musculus cDNA ... 36 2.2
 AA966976, AA966976 ua38f11.r1 Soares mouse mammary gland NbMM... 36 2.2

AA957268, AA957268 UI-R-E1-fq-e-06-0-UI.s1 UI-R-E1 Rattus nor... 42 0.031
 AA801145, AA801145 EST190642 Normalized rat ovary, Bento Soar... 38 0.48
 AI012760, AI012760 EST207211 Normalized rat placenta, Bento S... 38 0.48
 AA874930, AA874930 UI-R-E0-ci-b-05-0-UI.s1 UI-R-E0 Rattus nor... 38 0.48
 C82607, C82607 Oryctolagus cuniculus corneal endothelial cDN... 38 0.48
 AA859865, AA859865 UI-R-E0-cc-b-04-0-UI.s1 UI-R-E0 Rattus nor... 38 0.48
 C83463, C83463 Oryctolagus cuniculus corneal endothelial cDN... 38 0.48
 AA801144, AA801144 EST190641 Normalized rat ovary, Bento Soar... 38 0.48
 AA859448, AA859448 UI-R-A0-bf-b-01-0-UI.s1 UI-R-A0 Rattus nor... 38 0.48
 AI009631, AI009631 EST204082 Normalized rat lung, Bento Soare... 38 0.48
 AI009035, AI009035 EST203486 Normalized rat embryo, Bento Soa... 38 0.48
 AA859542, AA859542 UI-R-E0-br-d-03-0-UI.s1 UI-R-E0 Rattus nor... 38 0.48
 H32878, H32878 EST108396 Rat PC-12 cells, untreated Rattus sp... 36 1.9
 AA943364, AA943364 EST198863 Normalized rat brain, Bento Soar... 36 1.9
 Z32602, ATTS2730 A. thaliana transcribed sequence; clone PAP... 36 1.9
 Z33974, ATTS3035 A. thaliana transcribed sequence; clone PAP... 36 1.9
 Z32603, ATTS2731 A. thaliana transcribed sequence; clone PAP... 36 1.9
 AA660859, AA660859 00754 MtrHE Medicago truncatula cDNA 5' si... 36 1.9
 AA842765, AA842765 M-EST080 Sugarcane mature stalk Saccharum ... 36 1.9
 AA125602, AA125602 JM00M011.QM3 Miracidia Sjc 3/96 Schistosom... 36 1.9
 AA785775, AA785775 h4b05a1.fl Aspergillus nidulans 24hr asexu... 36 1.9

SEQ ID NO:551

U66201, MMU66201 Mus musculus fibroblast growth factor homolo... 42 0.36
 AF020738, AF020738 Mus musculus fibroblast growth factor-rela... 42 0.36
 U66197, HSU66197 Human fibroblast growth factor homologous fa... 42 0.36
 U86662, LEU86662 Lycopersicon esculentum VPS41 (tVPS41) mRNA,... 40 1.4
 U85773, HSU85773 Human phosphomannomutase (PMM2) mRNA, comple... 40 1.4
 Z46966, MMIMOGN44 M.musculus mRNA for imogen 44. 40 1.4
 AC004301, AC004301 Drosophila melanogaster DNA sequence (P1 D... 40 1.4

HUMAN ESTs

W22160, W22160 63A6 Human retina cDNA Tsp509I-cleaved sublibr... 791 0.0
 AA860926, AA860926 ak22d06.s1 Soares testis NHT Homo sapiens ... 650 0.0

AA348243, AA348243 EST54707 Hippocampus I Homo sapiens cDNA 5... 513 e-143
 AA551799, AA551799 nk04a11.s1 NCI_CGAP_Co2 Homo sapiens cDNA ... 363 4e-98
 AA327309, AA327309 EST30621 Colon I Homo sapiens cDNA 5' end 353 4e-95
 AA344913, AA344913 EST50856 Gall bladder II Homo sapiens cDNA... 337 2e-90
 AA121174, AA121174 zl88g08.s1 Stratagene colon (#937204) Homo... 317 2e-84
 AA121198, AA121198 zl88g08.r1 Stratagene colon (#937204) Homo... 317 2e-84
 AA001561, AA001561 ze46e07.s1 Soares retina N2b4HR Homo sapie... 42 0.17
 AA877455, AA877455 ob33g01.s1 NCI_CGAP_Kid5 Homo sapiens cDNA... 40 0.68
 N35888, N35888 yy28b05.s1 Homo sapiens cDNA clone 272529 3'. 40 0.68
 AA040802, AA040802 zf07g05.s1 Soares fetal heart NbHH19W Homo... 40 0.68
 AA573297, AA573297 nk98d09.s1 NCI_CGAP_Co3 Homo sapiens cDNA ... 40 0.68
 AA041240, AA041240 zf07g05.r1 Soares fetal heart NbHH19W Homo... 40 0.68
 AA514777, AA514777 ni24b01.s1 NCI_CGAP_Co4 Homo sapiens cDNA ... 40 0.68
 R02514, R02514 ye70b08.r1 Homo sapiens cDNA clone 123063 5'. 40 0.68
 AA039536, AA039536 zk39h10.s1 Soares pregnant uterus NbHPU Ho... 40 0.68
 AA888147, AA888147 04h11.s1 NCI_CGAP_Co10 Homo sapiens cDNA... 40 0.68
 AA172158, AA172158 zp29a01.s1 Stratagene neuroepithelium (#93... 40 0.68
 AA416734, AA416734 zu08c01.s1 Soares testis NHT Homo sapiens ... 38 2.7
 N98472, N98472 yy65a04.r1 Homo sapiens cDNA clone 278382 5'. 38 2.7
 AA416815, AA416815 zu08c01.r1 Soares testis NHT Homo sapiens ... 38 2.7
 AA852281, AA852281 NHTBCae11g05r1 Normal Human Trabecular Bon... 38 2.7
 AA948291, AA948291 oq34d02.s1 NCI_CGAP_GC4 Homo sapiens cDNA ... 38 2.7
 R14449, R14449 yf81h09.r1 Homo sapiens cDNA clone 29034 5'. 38 2.7
 AA431486, AA431486 zw72g01.s1 Soares testis NHT Homo sapiens ... 38 2.7

AA616807, AA616807 vn68c05.r1 Barstead mouse irradiated colon... 180 1e-43
 AA469884, AA469884 vf71g10.r1 Barstead mouse pooled organs MP... 40 0.24
 AA038869, AA038869 mi95b10.r1 Soares mouse p3NMF19.5 Mus musc... 40 0.24
 AA185487, AA185487 mt62c07.r1 Soares 2NbMT Mus musculus cDNA ... 40 0.24
 AA230758, AA230758 my32g10.r1 Barstead mouse pooled organs MP... 40 0.24
 AA276740, AA276740 vc42a12.r1 Soares mouse 3NbMS Mus musculus... 40 0.24
 AA763419, AA763419 vw54a12.r1 Soares mouse mammary gland NMLM... 40 0.24
 AA106439, AA106439 ml59a08.r1 Stratagene mouse testis (#93730... 40 0.24
 AA250010, AA250010 mz59b12.r1 Soares mouse lymph node NbMLN M... 38 0.97
 AA068686, AA068686 mm59a03.r1 Stratagene mouse embryonic carc... 38 0.97
 AA139459, AA139459 mq86a03.r1 Stratagene mouse melanoma (#937... 38 0.97
 AA881111, AA881111 vz06e09.r1 Soares mouse mammary gland NbMM... 36 3.8
 AA692425, AA692425 vt59b05.r1 Barstead mouse irradiated colon... 36 3.8
 AA049011, AA049011 mj48c09.r1 Soares mouse embryo NbME13.5 14... 36 3.8
 AA966976, AA966976 ua38f11.r1 Soares mouse mammary gland NbMM... 36 3.8
 AI047077, AI047077 uh61g06.r1 Soares mouse embryonic stem cel... 36 3.8
 AA103139, AA103139 mo17f05.r1 Life Tech mouse embryo 13 5dpc ... 36 3.8

AA840087, AA840087 uc99h12.r1 Soares mouse uterus NMPu Mus mu... 36 3.8
 AA543280, AA543280 vj80h05.r1 Soares mouse mammary gland NbMM... 36 3.8
 AA007762, AA007762 mg76b03.r1 Soares mouse embryo NbME13.5 14... 36 3.8
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 AA591243, AA591243 vm18c04.r1 Knowles Solter mouse blastocyst... 36 3.8
 AA921560, AA921560 vy52c06.r1 Stratagene mouse lung 937302 Mu... 36 3.8
 W20935, W20935 mb96c07.r1 Soares mouse p3NMF19.5 Mus musculus... 36 3.8
 AA793845, AA793845 vr35e12.r1 Barstead mouse myotubes MPLRB5 ... 36 3.8
 AA856298, AA856298 vw99b01.r1 Soares 2NbMT Mus musculus cDNA ... 36 3.8
 AA833479, AA833479 uc91c03.r1 Soares mouse uterus NMPu Mus mu... 36 3.8
 AA218431, AA218431 my07e05.r1 Barstead mouse lung MPLRB2 Mus ... 36 3.8
 AA089210, AA089210 mo05d10.r1 Stratagene mouse lung 937302 Mu... 36 3.8
 AI047609, AI047609 uh63g07.r1 Soares mouse embryonic stem cel... 36 3.8
 AA797372, AA797372 vw27b08.r1 Soares mouse mammary gland NbMM... 36 3.8
 AA138067, AA138067 mq37c11.r1 Barstead MPLRB1 Mus musculus cD... 36 3.8
 W83172, W83172 mf09a06.r1 Soares mouse p3NMF19.5 Mus musculus... 36 3.8
 AA542324, AA542324 vk53e07.r1 Stratagene mouse Tcell 937311 M... 36 3.8
 AA967316, AA967316 vj47a03.r1 Stratagene mouse skin (#937313)... 36 3.8
 AI035925, AI035925 ub49e05.r1 Soares mouse mammary gland NbMM... 36 3.8
 AA497479, AA497479 vh29b12.r1 Soares mouse mammary gland NbMM... 36 3.8
 W87202, W87202 mf55g08.r1 Soares mouse embryo NbME13.5 14.5 M... 36 3.8
 AA016868, AA016868 mh36e12.r1 Soares mouse placenta 4NbMP13.5... 36 3.8
 AA467482, AA467482 ve01a10.r1 Soares mouse NbMH Mus musculus ... 36 3.8
 AA014768, AA014768 mi66h04.r1 Soares mouse embryo NbME13.5 14... 36 3.8
 AA711859, AA711859 vu59c10.r1 Soares mouse mammary gland NbMM... 36 3.8
 AA530735, AA530735 vj32g11.r1 Stratagene mouse diaphragm (#93... 36 3.8
 AA009071, AA009071 mg87b11.r1 Soares mouse embryo NbME13.5 14... 36 3.8
 AA711873, AA711873 vu28e06.r1 Barstead mouse myotubes MPLRB5 ... 36 3.8
 AA645119, AA645119 vs72d03.r1 Stratagene mouse skin (#937313)... 36 3.8
 AA106301, AA106301 ml81a09.r1 Stratagene mouse kidney (#93731... 36 3.8
 AA111190, AA111190 mp66b11.r1 Soares 2NbMT Mus musculus cDNA ... 36 3.8
 C87249, C87249 Mus musculus fertilized egg cDNA 3'-end seque... 36 3.8
 AA796056, AA796056 vo65d01.r1 Soares mouse mammary gland NbMM... 36 3.8
 AA230661, AA230661 mw15f08.r1 Soares mouse 3NME12 5 Mus muscu... 36 3.8
 AA033481, AA033481 mi42b07.r1 Soares mouse embryo NbME13.5 14... 36 3.8
 AA000268, AA000268 mg32e09.r1 Soares mouse embryo NbME13.5 14... 36 3.8
 AI048515, AI048515 uh61e08.r1 Soares mouse embryonic stem cel... 36 3.8
 W61547, W61547 md57a02.r1 Soares mouse embryo NbME13.5 14.5 M... 36 3.8
 AA790448, AA790448 vw04f09.r1 Soares mouse mammary gland NbMM... 36 3.8
 AA824205, AA824205 vy20g08.r1 Stratagene mouse macrophage (#9... 36 3.8
 AA475425, AA475425 vh20g09.r1 Soares mouse mammary gland NbMM... 36 3.8
 W62989, W62989 md88h12.r1 Soares mouse embryo NbME13.5 14.5 M... 36 3.8
 W77724, W77724 me84h06.r1 Soares mouse embryo NbME13.5 14.5 M... 36 3.8
 AA239210, AA239210 mx89e02.r1 Soares mouse NML Mus musculus c... 36 3.8

276X

AA957268, AA957268 UI-R-E1-fq-e-06-0-UI.s1 UI-R-E1 Rattus nor... 42 0.055
 AA891284, AA891284 EST195087 Normalized rat heart, Bento Soar... 40 0.22
 Z83055, RNZ83055 R.norvegicus mRNA; expressed sequence tag; ... 40 0.22
 AI010967, AI010967 EST205418 Normalized rat muscle, Bento Soa... 40 0.22
 AA852049, AA852049 EST194818 Normalized rat spleen, Bento Soa... 40 0.22
 H33489, H33489 EST109542 Rat PC-12 cells, NGF-treated (9 days... 40 0.22
 AA799616, AA799616 EST189113 Normalized rat heart, Bento Soar... 40 0.22
 Z83044, RNZ83044 R.norvegicus mRNA; expressed sequence tag; ... 40 0.22
 AA660819, AA660819 00713 MtRHE Medicago truncatula cDNA 5' 38 0.86
 AA956139, AA956139 UI-R-E1-fi-h-08-0-UI.s1 UI-R-E1 Rattus nor... 38 0.86
 T00613, T00613 wEST01334 Caenorhabditis elegans cDNA clone CE... 38 0.86
 AA785775, AA785775 h4b05a1.f1 Aspergillus nidulans 24hr asexu... 36 3.4
 AA660859, AA660859 00754 MtRHE Medicago truncatula cDNA 5' si... 36 3.4
 AA943364, AA943364 EST198863 Normalized rat brain, Bento Soar... 36 3.4
 C68472, C68472 C.elegans cDNA clone yk305a12 : 5' end, singl... 36 3.4
 AA800635, AA800635 EST190132 Normalized rat lung, Bento Soare... 36 3.4
 Z32602, ATTS2730 A. thaliana transcribed sequence; clone PAP... 36 3.4
 Z32603, ATTS2731 A. thaliana transcribed sequence; clone PAP... 36 3.4
 AA842765, AA842765 M-EST080 Sugarcane mature stalk Saccharum ... 36 3.4
 AA955567, AA955567 UI-R-E1-fa-a-08-0-UI.s1 UI-R-E1 Rattus nor... 36 3.4
 H32878, H32878 EST108396 Rat PC-12 cells, untreated Rattus sp... 36 3.4
 Z33974, ATTS3035 A. thaliana transcribed sequence; clone PAP... 36 3.4
 D45997, RICS10346A Rice cDNA, partial sequence (S10346_1A). 36 3.4
 AA125602, AA125602 JM00M011.QM3 Miracidia Sjc 3/96 Schistosom... 36 3.4
 AA800634, AA800634 EST190131 Normalized rat lung, Bento Soare... 36 3.4
 D46069, RICS10475A Rice cDNA, partial sequence (S10475_1A). 36 3.4

SEQ ID NO:552

U66201, MMU66201 Mus musculus fibroblast growth factor homolo... 42 0.38
 AF020738, AF020738 Mus musculus fibroblast growth factor-rela... 42 0.38
 U66197, HSU66197 Human fibroblast growth factor homologous fa... 42 0.38
 Z46966, MMIMOGN44 M.musculus mRNA for imogen 44. 40 1.5
 U86662, LEU86662 Lycopersicon esculentum VPS41 (tVPS41) mRNA,... 40 1.5
 U85773, HSU85773 Human phosphomannomutase (PMM2) mRNA, comple... 40 1.5

HUMAN ESTs

W22160, W22160 63A6 Human retina cDNA Tsp509I-cleaved sublibr... 791 0.0
 AA860926, AA860926 ak22d06.s1 Soares testis NHT Homo sapiens ... 650 0.0

002030-66629460

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 AA551799, AA551799 nk04a11.s1 NCI_CGAP_Co2 Homo sapiens cDNA ... 363 4e-98
 AA327309, AA327309 EST30621 Colon I Homo sapiens cDNA 5' end 353 4e-95
 AA344913, AA344913 EST50856 Gall bladder II Homo sapiens cDNA... 337 2e-90
 AA121198, AA121198 zl88g08.r1 Stratagene colon (#937204) Homo... 317 2e-84
 AA121174, AA121174 zl88g08.s1 Stratagene colon (#937204) Homo... 317 2e-84
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 AA172158, AA172158 zp29a01.s1 Stratagene neuroepithelium (#93... 40 0.72
 N35888, N35888 yy28b05.s1 Homo sapiens cDNA clone 272529 3'. 40 0.72
 AA877455, AA877455 ob33g01.s1 NCI_CGAP_Kid5 Homo sapiens cDNA... 40 0.72
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 AA040802, AA040802 zf07g05.s1 Soares fetal heart NbHH19W Homo... 40 0.72
 R02514, R02514 ye70b08.r1 Homo sapiens cDNA clone 123063 5'. 40 0.72
 AA514777, AA514777 ni24b01.s1 NCI_CGAP_Co4 Homo sapiens cDNA ... 40 0.72
 AA041240, AA041240 zf07g05.r1 Soares fetal heart NbHH19W Homo... 40 0.72
 AA888147, AA888147 04h11.s1 NCI_CGAP_Co10 Homo sapiens cDNA... 40 0.72
 AA039536, AA039536 zk39h10.s1 Soares pregnant uterus NbHPU Ho... 40 0.72
 AA416734, AA416734 zu08c01.s1 Soares testis NHT Homo sapiens ... 38 2.8
 N25839, N25839 yx22e05.r1 Homo sapiens cDNA clone 262496 5'. 38 2.8
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 N98472, N98472 yy65a04.r1 Homo sapiens cDNA clone 278382 5'. 38 2.8
 AA416815, AA416815 zu08c01.r1 Soares testis NHT Homo sapiens ... 38 2.8
 AA852281, AA852281 NHTBCae11g05r1 Normal Human Trabecular Bon... 38 2.8
 AA948291, AA948291 oq34d02.s1 NCI_CGAP_GC4 Homo sapiens cDNA ... 38 2.8

AA616807, AA616807 vn68c05.r1 Barstead mouse irradiated colon... 180 1e-43
 AA185487, AA185487 mt62c07.r1 Soares 2NbMT Mus musculus cDNA ... 40 0.26
 AA276740, AA276740 vc42a12.r1 Soares mouse 3NbMS Mus musculus... 40 0.26
 AA469884, AA469884 vf71g10.r1 Barstead mouse pooled organs MP... 40 0.26
 AA230758, AA230758 my32g10.r1 Barstead mouse pooled organs MP... 40 0.26
 AA038869, AA038869 mi95b10.r1 Soares mouse p3NMF19.5 Mus musc... 40 0.26
 AA106439, AA106439 ml59a08.r1 Stratagene mouse testis (#93730... 40 0.26
 AA763419, AA763419 vw54a12.r1 Soares mouse mammary gland NMLM... 40 0.26
 AA139459, AA139459 mq86a03.r1 Stratagene mouse melanoma (#937... 38 1.0
 AA068686, AA068686 mm59a03.r1 Stratagene mouse embryonic carc... 38 1.0
 AA218431, AA218431 my07e05.r1 Barstead mouse lung MPLRB2 Mus ... 36 4.0
 AI047077, AI047077 uh61g06.r1 Soares mouse embryonic stem cel... 36 4.0
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 AA645119, AA645119 vs72d03.r1 Stratagene mouse skin (#937313)... 36 4.0
 AA530735, AA530735 vj32g11.r1 Stratagene mouse diaphragm (#93... 36 4.0

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AA793845, AA793845	vr35e12.r1	Barstead mouse myotubes MPLRB5 ...	36	4.0
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AA106301, AA106301	ml81a09.r1	Stratagene mouse kidney (#93731...	36	4.0
AA543280, AA543280	vj80h05.r1	Soares mouse mammary gland NbMM...	36	4.0
AA007762, AA007762	mg76b03.r1	Soares mouse embryo NbME13.5 14...	36	4.0
AA921560, AA921560	vy52c06.r1	Stratagene mouse lung 937302 Mu...	36	4.0
AA692425, AA692425	vt59b05.r1	Barstead mouse irradiated colon...	36	4.0
AA833479, AA833479	uc91c03.r1	Soares mouse uterus NMPu Mus mu...	36	4.0
AA824205, AA824205	vy20g08.r1	Stratagene mouse macrophage (#9...	36	4.0
AA033481, AA033481	mi42b07.r1	Soares mouse embryo NbME13.5 14...	36	4.0
W61547, W61547	md57a02.r1	Soares mouse embryo NbME13.5 14.5 M...	36	4.0
AA796056, AA796056	vo65d01.r1	Soares mouse mammary gland NbMM...	36	4.0
AA467482, AA467482	ve01a10.r1	Soares mouse NbMH Mus musculus ...	36	4.0
AA239210, AA239210	mx89e02.r1	Soares mouse NML Mus musculus c...	36	4.0
AA881111, AA881111	vz06e09.r1	Soares mouse mammary gland NbMM...	36	4.0
AA542324, AA542324	vk53e07.r1	Stratagene mouse Tcell 937311 M...	36	4.0
AA089210, AA089210	mo05d10.r1	Stratagene mouse lung 937302 Mu...	36	4.0
W77724, W77724	me84h06.r1	Soares mouse embryo NbME13.5 14.5 M...	36	4.0
AI048515, AI048515	uh61e08.r1	Soares mouse embryonic stem cel...	36	4.0
AA009071, AA009071	mg87b11.r1	Soares mouse embryo NbME13.5 14...	36	4.0
AA475425, AA475425	vh20g09.r1	Soares mouse mammary gland NbMM...	36	4.0
AA230661, AA230661	mw15f08.r1	Soares mouse 3NME12 5 Mus muscu...	36	4.0
AA138067, AA138067	mq37c11.r1	Barstead MPLRB1 Mus musculus cD...	36	4.0
W83172, W83172	mf09a06.r1	Soares mouse p3NMF19.5 Mus musculus...	36	4.0
AA797372, AA797372	vw27b08.r1	Soares mouse mammary gland NbMM...	36	4.0
AA711859, AA711859	vu59c10.r1	Soares mouse mammary gland NbMM...	36	4.0
AA967316, AA967316	vj47a03.r1	Stratagene mouse skin (#937313)...	36	4.0
W87202, W87202	mf55g08.r1	Soares mouse embryo NbME13.5 14.5 M...	36	4.0
AA103139, AA103139	mo17f05.r1	Life Tech mouse embryo 13 5dpc ...	36	4.0
AA014223, AA014223	mh20a03.r1	Soares mouse placenta 4NbMP13.5...	36	4.0
W62989, W62989	md88h12.r1	Soares mouse embryo NbME13.5 14.5 M...	36	4.0
W20935, W20935	mb96c07.r1	Soares mouse p3NMF19.5 Mus musculus...	36	4.0
AA966976, AA966976	ua38f11.r1	Soares mouse mammary gland NbMM...	36	4.0
AA856298, AA856298	vw99b01.r1	Soares 2NbMT Mus musculus cDNA ...	36	4.0
AA014768, AA014768	mi66h04.r1	Soares mouse embryo NbME13.5 14...	36	4.0
AA497479, AA497479	vh29b12.r1	Soares mouse mammary gland NbMM...	36	4.0
AA049011, AA049011	mj48c09.r1	Soares mouse embryo NbME13.5 14...	36	4.0
AA016868, AA016868	mh36e12.r1	Soares mouse placenta 4NbMP13.5...	36	4.0
AI047609, AI047609	uh63g07.r1	Soares mouse embryonic stem cel...	36	4.0
AA591243, AA591243	vm18c04.r1	Knowles Solter mouse blastocyst...	36	4.0

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T00613, T00613 wEST01334 Caenorhabditis elegans cDNA clone CE... 38 0.90
AA956139, AA956139 UI-R-E1-fi-h-08-0-UI.s1 UI-R-E1 Rattus nor... 38 0.90
AA660819, AA660819 00713 MtrHE Medicago truncatula cDNA 5' 38 0.90
AA125602, AA125602 JM00M011.QM3 Miracidia Sjc 3/96 Schistosom... 36 3.6
Z33974, ATTS3035 A. thaliana transcribed sequence; clone PAP... 36 3.6
C68472, C68472 C.elegans cDNA clone yk305a12 : 5' end, singl... 36 3.6
AA785775, AA785775 h4b05a1.fl Aspergillus nidulans 24hr asexu... 36 3.6
Z32602, ATTS2730 A. thaliana transcribed sequence; clone PAP... 36 3.6
AA943364, AA943364 EST198863 Normalized rat brain, Bento Soar... 36 3.6
Z32603, ATTS2731 A. thaliana transcribed sequence; clone PAP... 36 3.6
AA842765, AA842765 M-EST080 Sugarcane mature stalk Saccharum ... 36 3.6
D45997, RICS10346A Rice cDNA, partial sequence (S10346_1A). 36 3.6
AA955567, AA955567 UI-R-E1-fa-a-08-0-UI.s1 UI-R-E1 Rattus nor... 36 3.6
AA800634, AA800634 EST190131 Normalized rat lung, Bento Soare... 36 3.6
AA660859, AA660859 00754 MtrHE Medicago truncatula cDNA 5' si... 36 3.6
AA800635, AA800635 EST190132 Normalized rat lung, Bento Soare... 36 3.6
D46069, RICS10475A Rice cDNA, partial sequence (S10475_1A). 36 3.6
H32878, H32878 EST108396 Rat PC-12 cells, untreated Rattus sp... 36 3.6

SEQ ID NO:553

Z99297, HS262D12 Homo sapiens DNA sequence from PAC 262D12 o... 1963 0.0
Z81540, CEF46B3 Caenorhabditis elegans cosmid F46B3, complet... 40 0.89
U67488, U67488 Methanococcus jannaschii section 30 of 150 of ... 38 3.5
AE000786, AE000786 Borrelia burgdorferi plasmid lp28-2, compl... 38 3.5
L02053, OMMGSHTR1 Ommastrephes sloani glutathione transferase... 38 3.5
AC004521, ATAC004521 Arabidopsis thaliana chromosome II BAC F... 38 3.5
L41250, DROGPDHN Drosophila nebulosa glycerol-3-phosphate deh... 38 3.5
AE000619, HPAE000619 Helicobacter pylori section 97 of 134 of... 38 3.5
U39720, Mycoplasma genitalium ackA, licA, mucB, rpL10, rpL32... 38 3.5
AC004533, HUAC004533 Homo sapiens Chromosome 16 BAC clone CIT... 38 3.5
U62292, HSU62292 Human elastin (ELN) gene, partial cds 38 3.5

HUMAN ESTs

W02630, W02630 za52c02.r1 Soares fetal liver spleen 1NFLS Hom... 1009 0.0
AA557183, AA557183 nl74f12.s1 NCI_CGAP_Br2 Homo sapiens cDNA ... 874 0.0
AA761171, AA761171 nz09e11.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 866 0.0
AA976975, AA976975 oq26g11.s1 NCI_CGAP_GC4 Homo sapiens cDNA ... 854 0.0
AA449515, AA449515 zx06b11.r1 Soares total fetus Nb2HF8 9w Ho... 848 0.0

AA678392, AA678392 zi26h10.s1 Soares fetal liver spleen 1NFLS... 848 0.0
AA909198, AA909198 ol12d06.s1 Soares_NFL_T_GBC_S1 Homo sapien... 831 0.0
W79208, W79208 zd79g05.r1 Soares fetal heart NbHH19W Homo sap... 813 0.0
W03125, W03125 za53c02.r1 Soares fetal liver spleen 1NFLS Hom... 807 0.0
W94750, W94750 ze13h08.r1 Soares fetal heart NbHH19W Homo sap... 785 0.0
AA354894, AA354894 EST63217 Jurkat T-cells V Homo sapiens cDN... 771 0.0
H70075, H70075 yr92b03.r1 Homo sapiens cDNA clone 212717 5'. 745 0.0
W77859, W77859 zd70b08.r1 Soares fetal heart NbHH19W Homo sap... 728 0.0
AA425424, AA425424 zw48f03.s1 Soares total fetus Nb2HF8 9w Ho... 718 0.0
AA476893, AA476893 zu29f09.r1 Soares ovary tumor NbHOT Homo s... 688 0.0
AA456676, AA456676 aa01h02.s1 Soares NhHMPu S1 Homo sapiens c... 688 0.0
AA662309, AA662309 nu97c11.s1 NCI_CGAP_Pr22 Homo sapiens cDNA... 668 0.0
W72135, W72135 zd70b08.s1 Soares fetal heart NbHH19W Homo sap... 650 0.0
N74362, N74362 za52c02.s1 Homo sapiens cDNA clone 296162 3'. 622 e-176
N66917, N66917 za47d09.s1 Homo sapiens cDNA clone 295697 3'. 585 e-165
AA251287, AA251287 zs04c06.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 583 e-164
AA971082, AA971082 op70h01.s1 Soares_NFL_T_GBC_S1 Homo sapien... 567 e-160
W78165, W78165 zd79g05.s1 Soares fetal heart NbHH19W Homo sap... 565 e-159
AA253290, AA253290 zr71g03.r1 Soares NhHMPu S1 Homo sapiens c... 559 e-157
AA729063, AA729063 nw22f08.s1 NCI_CGAP_GCB0 Homo sapiens cDNA... 557 e-157
AA987313, AA987313 or81h06.s1 NCI_CGAP_Lu5 Homo sapiens cDNA ... 553 e-155
AA300954, AA300954 EST13832 Testis tumor Homo sapiens cDNA 5'... 541 e-152
AA425594, AA425594 zw48f03.r1 Soares total fetus Nb2HF8 9w Ho... 529 e-148
N24014, N24014 yx87g10.s1 Homo sapiens cDNA clone 268770 3'. 523 e-146
AA947355, AA947355 od86e12.s1 NCI_CGAP_Ov2 Homo sapiens cDNA ... 504 e-140
AA121074, AA121074 zl88b06.s1 Stratagene colon (#937204) Homo... 460 e-127
AA742964, AA742964 ny15d01.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 454 e-126
AA306814, AA306814 EST177885 Colon carcinoma (HCC) cell line ... 452 e-125
W87699, W87699 zh65b11.r1 Soares fetal liver spleen 1NFLS S1 ... 446 e-123
W87700, W87700 zh65b11.s1 Soares fetal liver spleen 1NFLS S1 ... 438 e-121
AA449084, AA449084 zx06b11.s1 Soares total fetus Nb2HF8 9w Ho... 398 e-109
N99231, N99231 zb76f11.s1 Soares senescent fibroblasts NbHSF ... 391 e-106
N49900, N49900 yv24d04.s1 Homo sapiens cDNA clone 243655 3'. 383 e-104
AA782911, AA782911 ai62a10.s1 Soares testis NHT Homo sapiens ... 365 6e-99
AA936553, AA936553 on23g11.s1 NCI_CGAP_Lu5 Homo sapiens cDNA ... 361 9e-98
N74414, N74414 za53c02.s1 Homo sapiens cDNA clone 296258 3'. 353 2e-95
AA834628, AA834628 od98a10.s1 NCI_CGAP_Ov2 Homo sapiens cDNA ... 341 8e-92
AA693756, AA693756 zi55f11.s1 Soares fetal liver spleen 1NFLS... 341 8e-92
AA909616, AA909616 ol09d06.s1 Soares_NFL_T_GBC_S1 Homo sapien... 341 8e-92
H69662, H69662 yr92b03.s1 Homo sapiens cDNA clone 212717 3'. 321 8e-86
AA249558, AA249558 jj7521.seq.F Human fetal heart, Lambda ZAP... 317 1e-84
AA911960, AA911960 oh88g08.s1 NCI_CGAP_Co8 Homo sapiens cDNA ... 317 1e-84
AA969099, AA969099 op55e06.s1 Soares_NFL_T_GBC_S1 Homo sapien... 303 2e-80
AA766191, AA766191 oa12g08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 212 5e-53
AA689312, AA689312 nx05e10.s1 NCI CGAP GC3 Homo sapiens cDNA ... 200 2e-49

AA418586, AA418586 zv93e05.r1 Soares NhHMPu S1 Homo sapiens c... 182 5e-44
 AA418570, AA418570 zv93e05.s1 Soares NhHMPu S1 Homo sapiens c... 182 5e-44
 AA534939, AA534939 nf82f03.s1 NCI_CGAP_Co3 Homo sapiens cDNA ... 167 3e-39
 AA888430, AA888430 nw74e05.s1 NCI_CGAP_Pr12 Homo sapiens cDNA... 167 3e-39
 N50003, N50003 yv24d04.r1 Homo sapiens cDNA clone 243655 5' s... 149 6e-34
 AA535102, AA535102 nf84f06.s1 NCI_CGAP_Co3 Homo sapiens cDNA ... 135 1e-29
 AA262335, AA262335 zr71g03.s1 Soares NhHMPu S1 Homo sapiens c... 129 6e-28
 AA766681, AA766681 oa34c05.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 105 9e-21
 AA761492, AA761492 nz27a05.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 101 1e-19
 AA688350, AA688350 nv15a05.s1 NCI_CGAP_Pr22 Homo sapiens cDNA... 90 5e-16
 AA347041, AA347041 EST53285 Fetal heart II Homo sapiens cDNA ... 76 8e-12
 T94395, T94395 ye35e02.s1 Homo sapiens cDNA clone 119738 3'. 46 0.007
 AA833565, AA833565 aj46a02.s1 Soares testis NHT Homo sapiens ... 46 0.007
 AA095460, AA095460 l4630.seq.F Fetal heart, Lambda ZAP Expres... 40 0.43
 AA904415, AA904415 ok07e06.s1 Soares_NFL_T_GBC_S1 Homo sapien... 40 0.43
 AI018800, AI018800 ov32h04.x1 Soares_testis_NHT Homo sapiens ... 38 1.7
 AA631083, AA631083 nq77e07.s1 NCI_CGAP_Pr22 Homo sapiens cDNA... 38 1.7

AA399772, AA399772 vd70g05.r1 Beddington mouse embryonic regi... 347 5e-94
 AA467106, AA467106 vd98b04.r1 Soares mouse NbMH Mus musculus ... 309 1e-82
 AI046844, AI046844 uh55c11.r1 Soares mouse embryonic stem cel... 208 3e-52
 AA475075, AA475075 vh11g05.r1 Soares mouse mammary gland NbMM... 194 4e-48
 AA646094, AA646094 vs31e06.r1 Stratagene mouse Tcell 937311 M... 186 1e-45
 AA390020, AA390020 vb30e07.r1 Soares mouse lymph node NbMLN M... 170 6e-41
 AA245553, AA245553 my52g04.r1 Barstead mouse pooled organs MP... 170 6e-41
 AA930741, AA930741 vs57b02.r1 Stratagene mouse skin (#937313)... 155 4e-36
 W62610, W62610 md58c06.r1 Soares mouse embryo NbME13.5 14.5 M... 117 8e-25
 AA239270, AA239270 my40e01.r1 Barstead mouse pooled organs MP... 109 2e-22
 AA015148, AA015148 mh16e01.r1 Soares mouse placenta 4NbMP13.5... 54 1e-05
 AA764095, AA764095 vw09h02.r1 Soares 2NbMT Mus musculus cDNA ... 38 0.61
 AA238570, AA238570 my35h02.r1 Barstead mouse pooled organs MP... 38 0.61
 AA600576, AA600576 vm75f08.r1 Knowles Solter mouse blastocyst... 38 0.61
 AA636273, AA636273 vq76a10.s1 Knowles Solter mouse 2 cell Mus... 36 2.4
 AA051407, AA051407 mj41f08.r1 Soares mouse embryo NbME13.5 14... 36 2.4
 AA823136, AA823136 vw41b03.r1 Soares mouse mammary gland NbMM... 36 2.4
 W83831, W83831 mf26a06.r1 Soares mouse embryo NbME13.5 14.5 M... 36 2.4
 D77944, MUSC0D06 Mouse embryonal carcinoma F9 cell cDNA, C0D06 36 2.4
 AA915408, AA915408 vz29h04.r1 Soares 2NbMT Mus musculus cDNA ... 36 2.4
 AI047229, AI047229 uh63a09.r1 Soares mouse embryonic stem cel... 36 2.4
 AA271880, AA271880 va73d01.r1 Soares mouse 3NME12 5 Mus muscu... 36 2.4
 AA475165, AA475165 vg95f01.r1 Barstead mouse pooled organs MP... 36 2.4
 AA619774, AA619774 vl58a05.s1 Knowles Solter mouse 2 cell Mus... 36 2.4

AA673116, AA673116 vn49g11.r1 Barstead mouse myotubes MPLRB5 ... 36 2.4
 AA870623, AA870623 vq24a07.r1 Barstead stromal cell line MPLR... 36 2.4
 W58907, W58907 md52f12.r1 Soares mouse embryo NbME13.5 14.5 M... 36 2.4
 AA690593, AA690593 vu53d05.r1 Soares mouse mammary gland NbMM... 36 2.4
 AA754801, AA754801 vu21f03.r1 Barstead mouse myotubes MPLRB5 ... 36 2.4
 AA271607, AA271607 va72a12.r1 Soares mouse 3NME12 5 Mus muscu... 36 2.4
 AA064256, AA064256 mj66a03.r1 Soares mouse p3NMF19.5 Mus musc... 36 2.4
 AA475144, AA475144 vg95d01.r1 Barstead mouse pooled organs MP... 36 2.4
 AA197736, AA197736 mv02g08.r1 GuayWoodford Beier mouse kidney... 36 2.4

AA817944, AA817944 UI-R-A0-ag-e-01-0-UI.s1 UI-R-A0 Rattus nor... 40 0.14
 F14714, SSC8B01 S.scrofa mRNA; expressed sequence tag (5'; c... 38 0.54
 H91505, H91505 SWMFCFA089SK Brugia malayi microfilaria cDNA (S... 36 2.1
 AA998610, AA998610 UI-R-C0-if-c-04-0-UI.s1 UI-R-C0 Rattus nor... 36 2.1
 AA893562, AA893562 EST197365 Normalized rat liver, Bento Soar... 36 2.1
 AI008397, AI008397 EST202848 Normalized rat embryo, Bento Soa... 36 2.1

SEQ ID NO:554

Z92544, HS313D11 Human DNA sequence from cosmid 313D11 from ... 700 0.0
 Z46940, HSPRMTNP2 H.sapiens PRM1 gene, PRM2 gene and TNP2 gene 44 0.048
 U85039, TMU85039 Theileria mutans 32 kDa immunodominant pirop... 42 0.19
 U85251, TMU85251 Theileria mutans 32 kDa immunodominant pirop... 42 0.19
 AF003630, AF003630 Theileria mutans clone 15, 32 kDa immunodo... 42 0.19
 AF003629, AF003629 Theileria mutans clone 9, 32 kDa immunodom... 42 0.19
 AB007884, AB007884 Homo sapiens KIAA0424 mRNA, partial cds 42 0.19
 U85040, TMU85040 Theileria mutans 32 kDa immunodominant pirop... 42 0.19
 Z97343, ATFCA8 Arabidopsis thaliana DNA chromosome 4, ESSA I... 40 0.75
 L19655, TOSRNA1X Tomato ringspot virus polyprotein (RNA-1) ge... 40 0.75
 M73822, TOSRNA1A Tomato ringspot virus RNA1 gene, 5' end. 40 0.75
 L02543, BOVMTNNT Bos taurus nicotinamide nucleotide transhydr... 40 0.75
 J03534, BOVNAD Bovine mitochondrial nicotinamide nucleotide t... 40 0.75
 M62862, TRBRTE Trypanosoma cruzi retrotransposon encoding gag... 40 0.75
 X72711, MMREPCFC M.musculus mRNA for replication factor C, l... 38 3.0
 M88489, MUSNBP Mus musculus nonamer binding protein mRNA, com... 38 3.0
 U36441, MMU36441 Mus musculus differentiation specific elemen... 38 3.0
 AB002354, AB002354 Human mRNA for KIAA0356 gene, complete cds 38 3.0
 J03149, CATFMSC Cat (F.domesticus) c-fms proto-oncogene mRNA ... 38 3.0
 J05475, CHKVICOLL Chicken type VI collagen alpha 2 (VI) subun... 38 3.0

AF038163, AF038163 Homo sapiens interleukin-15 (IL-15) gene, ... 38 3.0
 X75917, HSFBMBF H.sapiens mRNA for fetal beta-MHC binding fa... 38 3.0
 X06542, DMHSPG3 Drosophila heat shock gene 3 from 67B locus 38 3.0
 D17315, DRODAGK Fruit fly mRNA for diacylglycerol kinase, co... 38 3.0
 Z58600, HS45E3F H.sapiens CpG DNA, clone 45e3, forward read ... 38 3.0
 D78638, D78638 Xenopus laevis mRNA for DNA (cytosine-5-)-met... 38 3.0
 Z49204, MMNADPTRH M.musculus mRNA for NADP transhydrogenase. 38 3.0
 L10425, BPEMETC Bordetella avium beta-cystathionase-lyase (me... 38 3.0
 U01222, U01222 Mus musculus activator 1 large subunit (A1-p14... 38 3.0
 U15037, MMU15037 Mus musculus replication factor C large subu... 38 3.0
 K01643, FCSSMONC Feline sarcoma virus (McDonough strain) tran... 38 3.0
 Z57538, HS183C6F H.sapiens CpG DNA, clone 183c6, forward rea... 38 3.0
 U07157, MMU07157 Mus musculus ISRE-binding protein (IBF-1) mR... 38 3.0
 Z64961, HS183F7R H.sapiens CpG DNA, clone 183f7, reverse rea... 38 3.0

HUMAN ESTs

SEQ ID NO:555

AF039693, AF039693 Homo sapiens unknown protein mRNA, complet... 916 0.0
 S51239, S51239 calreticulin [Aplysia californica=marine snail... 48 0.005
 Z74035, CEF47G9 Caenorhabditis elegans cosmid F47G9, complet... 46 0.019
 AF022814, AF022814 Fugu rubripes transcription factor (SLP-1)... 44 0.073
 X82638, CSCYTOX C.sordelii cytotoxin gene 42 0.29
 U63063, SCU63063 Saccharomyces cerevisiae something about sil... 42 0.29
 X63501, SCRPC53 S.cerevisiae RPC53 gene for RNA polymerase C... 42 0.29
 U67572, U67572 Methanococcus jannaschii section 114 of 150 of... 42 0.29
 Z74201, SCYDL153C S.cerevisiae chromosome IV reading frame O... 42 0.29
 U66032, MTU66032 Methanosarcina thermophila CO dehydrogenase/... 42 0.29
 Z95620, SPBC3D6 S.pombe chromosome II cosmid c3D6 42 0.29
 X97751, SCIV23 S.cerevisiae chrIV genes STE7, CLB3, MSH5, RP... 42 0.29
 X65541, ATCAN A.thaliana mRNA for carbonic anhydrase 42 0.29
 L14750, ATHCARANHY Arabidopsis thaliana carbonic anhydrase ge... 42 0.29
 U00995, U00995 Rattus norvegicus TA1 mRNA, complete cds. 40 1.1
 S73876, S73876 FPR3=FKBP-70 [Saccharomyces cerevisiae, Genomi... 40 1.1
 U12825, SCU12825 Saccharomyces cerevisiae transcription facto... 40 1.1
 Z74237, SCYDL189W S.cerevisiae chromosome IV reading frame O... 40 1.1
 U76906, REU76906 Rhizobium etli FixK (fixK), FixN (fixN), mon... 40 1.1

AF050157, MMHC135G15 *Mus musculus* major histocompatibility lo... 40 1.1
 X58857, SCPH22 *S.cerevisiae* PPH22 gene for protein phosphat... 40 1.1
 X79379, SCPROIS *S.cerevisiae* gene for proline isomerase 40 1.1
 Z68341, CEF01G4 *Caenorhabditis elegans* cosmid F01G4, complet... 40 1.1
 M17192, MUSHOX1 Mouse homeodomain protein (Hox1.1) mRNA, comp... 40 1.1
 U50307, CELF43H9 *Caenorhabditis elegans* cosmid F43H9. 40 1.1
 S73144, S73144 bone sialoprotein [cattle, fetal bone cells, m... 40 1.1
 L34569, YSCFPR3A *Saccharomyces cerevisiae* (clone pBYNG1) prol... 40 1.1
 D78303, D78303 *Rattus norvegicus* YT521 mRNA for RNA splicing... 40 1.1
 X83276, SCDNAIV *S.cerevisiae* DNA for ORFs from chromosome IV 40 1.1
 U54558, HSU54558 Human translation initiation factor eIF3 p66... 40 1.1
 Z50109, CEC09H10 *Caenorhabditis elegans* cosmid C09H10, compl... 40 1.1
 X56983, EAVATP1 *E.arvense* gene for catalytic 70kDa V-ATPase ... 40 1.1
 AB011125, AB011125 *Homo sapiens* mRNA for KIAA0553 protein, p... 40 1.1
 Z46373, SC8248 *S.cerevisiae* chromosome XIII cosmid 8248 40 1.1
 AF039042, CELZK697 *Caenorhabditis elegans* cosmid ZK697 40 1.1
 Z28028, SCYKL028W *S.cerevisiae* chromosome XI reading frame O... 40 1.1
 AC005266, AC005266 *Homo sapiens* chromosome 19, cosmid F23465,... 38 4.5
 U60822, HSU60822 Human dystrophin (DMD) gene, exons 7, 8 and ... 38 4.5
 AJ003141, HVAJ3141 *Hordeum vulgare* mRNA for stress-related p... 38 4.5
 M26250, CRAGAP43 Goldfish (*C.auratus*) growth-associated prote... 38 4.5
 X95267, GGRYR3 *G.gallus* mRNA for ryanodine receptor type 3 38 4.5
 L37092, MUSCDPK *Mus musculus* cyclin-dependent kinase homologu... 38 4.5
 Z72507, CEF17C11 *Caenorhabditis elegans* cosmid F17C11, compl... 38 4.5
 U29608, DMU29608 *Drosophila melanogaster* large tumor suppress... 38 4.5
 Z49072, CET24A11 *Caenorhabditis elegans* cosmid T24A11, compl... 38 4.5
 M83142, RATBGASTR *Rattus norvegicus* beta-galactoside-alpha 2,... 38 4.5
 Z20656, HSCAMHCA *Homo sapiens* of cardiac alpha-myosin heavy ... 38 4.5
 M82937, YSACS2A *Candida albicans* chitin synthase 2 (CHS2) gen... 38 4.5
 U28888, MMU28888 *Mus musculus* neurogenic differentiation fact... 38 4.5
 S66408, S66408 c-erbB=proto-oncogene {exon 1, promoter} [chic... 38 4.5
 AC002396, AC002396 *Arabidopsis thaliana* chromosome I BAC F3I6... 38 4.5
 AE000665, MMAE000665 *Mus musculus* TCR beta locus from bases 5... 38 4.5
 L39837, DROWARTS *Drosophila melanogaster* tumor supressor (war... 38 4.5
 AG000377, AG000377 *Homo sapiens* genomic DNA, 21q region, clo... 38 4.5
 X05632, HSMHCAG1 Human alpha-MHC gene for myosin heavy chain... 38 4.5
 AC002108, AC002108 Genomic sequence from Mouse 4, complete se... 38 4.5
 U37219, HSU37219 Human cyclophilin-like protein CyP-60 mRNA, ... 38 4.5
 M58633, MUSP58GTA Mouse p58/GTA protein kinase mRNA, complete... 38 4.5
 M25162, HUMMYHC08 Human cardiac alpha-myosin heavy chain (MYH... 38 4.5
 Z46259, SCRPD3COS *S.cerevisiae* FY1676 RPD3 gene. 38 4.5
 U09558, LJU09558 *Lactobacillus johnsonii* ATCC 11506 insertion... 38 4.5
 U66160, MMUSC104 *Mus musculus* extracellular matrix associated... 38 4.5
 Z73126, SCYLL021W *S.cerevisiae* chromosome XII reading frame ... 38 4.5
 U83981, HSU83981 *Homo sapiens* apoptosis associated protein (G... 38 4.5

U59897, MRU59897 *Macropus robustus* hypoxanthine phosphoribosy... 38 4.5
 D38256, YSCSCT1 Yeast gene for suppressor of ctr mutation 38 4.5
 X69838, HSG9A *H.sapiens* mRNA for G9a 38 4.5
 X52952, RNCMOSO Rat mRNA for c-mos 38 4.5
 U37221, HSU37221 Human cyclophilin-like protein mRNA, partial... 38 4.5
 X65880, DPRH4OP1 *D.pseudoobscura* rh4 opsin gene, exon 1 38 4.5
 U58971, NTU58971 *Nicotiana tabacum* calmodulin-binding protein... 38 4.5
 Z35773, SCYBL012C *S.cerevisiae* chromosome II reading frame O... 38 4.5
 X67668, MMHMG2 *M.musculus* mRNA for high mobility group 2 pro... 38 4.5
 L81727, HSL81727 *Homo sapiens* (subclone 1_d5 from P1 H69) DNA... 38 4.5
 AL023800, HS833B2 Human DNA sequence *** SEQUENCING IN PROGR... 38 4.5
 X62438, HVPERO *H.vulgare* mRNA for peroxidase 38 4.5
 AC004096, AC004096 Mouse Cosmid ma66a100 from 14D1-D2, comple... 38 4.5
 AL008980, PFSC03050 *Plasmodium falciparum* DNA *** SEQUENCING... 38 4.5
 U64827, MMU64827 *Mus musculus* extracellular matrix associated... 38 4.5
 AC003010, HUAC003010 *Homo sapiens* Chromosome 16 BAC clone CIT... 38 4.5
 AE001002, AE001002 *Archaeoglobus fulgidus* section 105 of 172 ... 38 4.5
 U86662, LEU86662 *Lycopersicon esculentum* VPS41 (tVPS41) mRNA,... 38 4.5
 M20386, CHKEGFR Chicken epidermal growth factor receptor (CER... 38 4.5
 M77637, CHKEGF *Gallus gallus* EGF/TGF-alpha receptor (c-erbB) ... 38 4.5
 U08185, MMU08185 *Mus musculus* BALB/c zinc-finger protein Blim... 38 4.5
 AC004231, AC004231 *Homo sapiens* chromosome 17, clone hRPC.111... 38 4.5
 Z50100, HVC39SAT *H.vulgare* GAA-satellite DNA 38 4.5
 X53731, SCSA2G *S. cerevisiae* SPA2 gene 38 4.5
 U37220, HSU37220 Human cyclophilin-like protein mRNA, partial... 38 4.5
 X97560, SC32KBF *S.cerevisiae* 32kb DNA fragment of chromosome... 38 4.5
 AB011479, AB011479 *Arabidopsis thaliana* genomic DNA, chromos... 38 4.5
 U89340, LVU89340 *Lytechinus variegatus* Endo16 homolog (LvEndo1... 38 4.5
 U73850, TCU73850 *Trypanosoma cruzi* 29 kDa proteasome subunit ... 38 4.5
 AB006698, AB006698 *Arabidopsis thaliana* genomic DNA, chromos... 38 4.5
 D37888, CYIMYC2 *Cyprinus carpio* c-myc gene for c-Myc, comple... 38 4.5
 AF017349, MMDSGIII 7 *Mus musculus* desmoglein 3 (Dsg3) gene, i... 38 4.5
 X91807, OSTA136 *O.sativa* mRNA for alpha-tubulin (clone OSTA-... 38 4.5
 Z71587, SCYNL311C *S.cerevisiae* chromosome XIV reading frame ... 38 4.5
 AE000742, AE000742 *Aquifex aeolicus* section 74 of 109 of the ... 38 4.5

HUMAN ESTs

AA324311, AA324311 EST27136 Cerebellum II *Homo sapiens* cDNA 5... 593 e-167
 AA639190, AA639190 ns04a01.r1 NCI_CGAP_Ew1 *Homo sapiens* cDNA ... 513 e-143
 AA172199, AA172199 zo96a06.r1 Stratagene ovarian cancer (#937... 505 e-141
 AA588066, AA588066 nk10d08.s1 NCI_CGAP_Co2 *Homo sapiens* cDNA ... 502 e-140
 AA412036, AA412036 zt68d09.s1 Soares testis NHT *Homo sapiens* ... 502 e-140
 AA508745, AA508745 ni23a03.s1 NCI_CGAP_Co4 *Homo sapiens* cDNA ... 502 e-140

AA480337, AA480337 ne33a03.s1 NCI_CGAP_Co3 Homo sapiens cDNA ... 502 e-140
 AA902270, AA902270 ok69e04.s1 NCI_CGAP_GC4 Homo sapiens cDNA ... 502 e-140
 AA947303, AA947303 ok20d04.s1 Soares_NSF_F8_9W_OT_PA_P_S1 Hom... 502 e-140
 R23642, R23642 yh35e03.r1 Homo sapiens cDNA clone 131740 5'. 490 e-136
 AA811913, AA811913 ob51d06.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 464 e-128
 AA172083, AA172083 zo96a06.s1 Stratagene ovarian cancer (#937... 464 e-128
 AA725458, AA725458 ail6g01.s1 Soares parathyroid tumor NbHPA ... 400 e-109
 R26558, R26558 yh35e02.s1 Homo sapiens cDNA clone 131738 3'. 359 5e-97
 AA402403, AA402403 zt68d09.r1 Soares testis NHT Homo sapiens ... 315 6e-84
 R58372, R58372 G3243 Fetal heart Homo sapiens cDNA clone G324... 262 8e-68
 AA389703, AA389703 M421 Fetal heart, Lambda ZAP Express Homo ... 202 6e-50
 W25749, W25749 11b4 Human retina cDNA randomly primed sublibr... 103 4e-20
 W27158, W27158 22h9 Human retina cDNA randomly primed sublibr... 66 1e-08
 T65784, T65784 yc11f10.s1 Homo sapiens cDNA clone 80395 3' si... 42 0.14
 AA179601, AA179601 zp49f10.r1 Stratagene HeLa cell s3 937216 ... 42 0.14
 AA928679, AA928679 on48e08.s1 NCI_CGAP_Co8 Homo sapiens cDNA ... 40 0.55
 AA887972, AA887972 nq95g11.s1 NCI_CGAP_Co10 Homo sapiens cDNA... 40 0.55
 W46946, W46946 zc40c05.s1 Soares senescent fibroblasts NbHSF ... 40 0.55
 AA887862, AA887862 nq99b08.s1 NCI_CGAP_Co10 Homo sapiens cDNA... 40 0.55
 AA554819, AA554819 ni34d08.s1 NCI_CGAP_Lu1 Homo sapiens cDNA ... 40 0.55
 AA557362, AA557362 nl81d12.s1 NCI_CGAP_Br2 Homo sapiens cDNA ... 40 0.55
 AA252258, AA252258 zr29e04.s1 Stratagene NT2 neuronal precurs... 40 0.55
 N34310, N34310 yy52b10.s1 Homo sapiens cDNA clone 277147 3' s... 40 0.55
 AA552228, AA552228 nk06b04.s1 NCI_CGAP_Co2 Homo sapiens cDNA ... 40 0.55
 AI017648, AI017648 ou99b02.x1 NCI_CGAP_Kid3 Homo sapiens cDNA... 40 0.55
 T17395, T17395 NIB846 Normalized infant brain, Bento Soares H... 40 0.55
 AA219659, AA219659 zr05e10.s1 Stratagene NT2 neuronal precurs... 40 0.55
 AA463841, AA463841 zx67f06.r1 Soares total fetus Nb2HF8 9w Ho... 40 0.55
 N66817, N66817 za09b11.s1 Homo sapiens cDNA clone 292029 3' s... 40 0.55
 AA167358, AA167358 zp06f12.s1 Stratagene ovarian cancer (#937... 40 0.55
 AA063505, AA063505 zf70d02.r1 Soares pineal gland N3HPG Homo ... 40 0.55
 AA731625, AA731625 nw64a04.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 40 0.55
 AA100119, AA100119 zl80g04.s1 Stratagene colon (#937204) Homo... 40 0.55
 AA181572, AA181572 zp51d04.s1 Stratagene HeLa cell s3 937216 ... 40 0.55
 AA327182, AA327182 EST30459 Colon I Homo sapiens cDNA 5' end ... 40 0.55
 R48608, R48608 yj65f07.s1 Homo sapiens cDNA clone 153637 3' s... 40 0.55
 AA678485, AA678485 ah06e04.s1 Gessler Wilms tumor Homo sapien... 40 0.55
 AA082353, AA082353 zn38c11.r1 Stratagene endothelial cell 937... 40 0.55
 AA633213, AA633213 nq57c06.s1 NCI_CGAP_Co9 Homo sapiens cDNA ... 40 0.55
 W38410, W38410 zc77g09.s1 Pancreatic Islet Homo sapiens cDNA ... 40 0.55
 AA345893, AA345893 EST51967 Gall bladder I Homo sapiens cDNA ... 40 0.55
 N26876, N26876 yx97f06.s1 Homo sapiens cDNA clone 269699 3' s... 40 0.55
 N95279, N95279 zb60c09.s1 Soares fetal lung NbHL19W Homo sapi... 40 0.55
 AI041637, AI041637 ox92h08.x1 Soares_senescent_fibroblasts_Nb... 40 0.55
 N67830, N67830 za05d12.s1 Homo sapiens cDNA clone 291671 3' s... 40 0.55

AA535094, AA535094 nf84e06.s1 NCI_CGAP_Co3 Homo sapiens cDNA ... 40 0.55
 AA514414, AA514414 nf57d11.s1 NCI_CGAP_Co3 Homo sapiens cDNA ... 40 0.55
 T56802, T56802 ya71h07.s2 Homo sapiens cDNA clone 67165 3' co... 40 0.55
 N68147, N68147 yz55f12.s1 Homo sapiens cDNA clone 286991 3' s... 40 0.55
 AA535811, AA535811 nf93g10.s1 NCI_CGAP_Co3 Homo sapiens cDNA ... 40 0.55
 AA115591, AA115591 zl05g09.s1 Soares pregnant uterus NbHPU Ho... 40 0.55
 N75851, N75851 za96g11.s1 Homo sapiens cDNA clone 300452 3'. 40 0.55
 AA534433, AA534433 nf80a08.s1 NCI_CGAP_Co3 Homo sapiens cDNA ... 40 0.55
 H99778, H99778 yx36g01.s1 Homo sapiens cDNA clone 263856 3' s... 40 0.55
 AA970859, AA970859 oo81h03.s1 NCI_CGAP_Kid5 Homo sapiens cDNA... 40 0.55
 F02131, HSC0PF092 H. sapiens partial cDNA sequence; clone c-... 40 0.55
 AA810279, AA810279 od14g11.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 40 0.55
 AA595146, AA595146 nl84b01.s1 NCI_CGAP_Br2 Homo sapiens cDNA ... 40 0.55
 AA632386, AA632386 np67e06.s1 NCI_CGAP_Br2 Homo sapiens cDNA ... 40 0.55
 AA135124, AA135124 zo24c04.s1 Stratagene colon (#937204) Homo... 40 0.55
 AA143500, AA143500 zo31b10.s1 Stratagene colon (#937204) Homo... 40 0.55
 AA854992, AA854992 aj53g12.s1 Soares testis NHT Homo sapiens ... 40 0.55
 AA156872, AA156872 zl20h07.s1 Soares pregnant uterus NbHPU Ho... 40 0.55
 AA160994, AA160994 zq41c12.s1 Stratagene hNT neuron (#937233)... 40 0.55
 AA961724, AA961724 or60a10.s1 NCI_CGAP_GC3 Homo sapiens cDNA ... 40 0.55
 AA551210, AA551210 nj27e09.s1 NCI_CGAP_AA1 Homo sapiens cDNA ... 40 0.55
 R44103, R44103 yg27c10.s1 Homo sapiens cDNA clone 33636 3'. 40 0.55
 AA938086, AA938086 oj08h08.s1 NCI_CGAP_Mel3 Homo sapiens cDNA... 40 0.55
 AA576021, AA576021 nm57d11.s1 NCI_CGAP_Br3 Homo sapiens cDNA ... 40 0.55
 AA722725, AA722725 zg86b09.s1 Soares fetal heart NbHH19W Homo... 40 0.55
 AA678948, AA678948 ah08h11.s1 Gessler Wilms tumor Homo sapien... 40 0.55
 W07435, W07435 za96g11.r1 Soares fetal lung NbHL19W Homo sapi... 40 0.55
 T34639, T34639 EST72167 Homo sapiens cDNA 5' end similar to s... 40 0.55
 AA632245, AA632245 np67b09.s1 NCI_CGAP_Br2 Homo sapiens cDNA ... 40 0.55
 R98701, R98701 yr31f08.s1 Homo sapiens cDNA clone 206919 3'. 40 0.55
 R76418, R76418 yi58a10.s1 Homo sapiens cDNA clone 143418 3'. 40 0.55
 AI028447, AI028447 ow08b09.x1 Soares parathyroid tumor NbHPA ... 40 0.55
 AI002929, AI002929 an15e12.s1 Gessler Wilms tumor Homo sapien... 40 0.55
 AA779388, AA779388 ae26a03.s1 Soares NbHFB Homo sapiens cDNA ... 40 0.55
 AA776220, AA776220 ah10f02.s1 Gessler Wilms tumor Homo sapien... 40 0.55
 AA815223, AA815223 oc05c04.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 40 0.55
 W60807, W60807 zd27b08.s1 Soares fetal heart NbHH19W Homo sap... 40 0.55
 AA666007, AA666007 ag71g01.s1 Gessler Wilms tumor Homo sapien... 40 0.55
 AA643849, AA643849 np26f07.s1 NCI_CGAP_Pr22 Homo sapiens cDNA... 40 0.55
 AA846740, AA846740 aj99b12.s1 Soares parathyroid tumor NbHPA ... 40 0.55
 AA598498, AA598498 ae38h01.s1 Gessler Wilms tumor Homo sapien... 40 0.55
 AA535972, AA535972 nf95a01.s1 NCI_CGAP_Co3 Homo sapiens cDNA ... 40 0.55
 AA488544, AA488544 ab37g06.r1 Stratagene HeLa cell s3 937216 ... 40 0.55
 AA866044, AA866044 oh52g07.s1 NCI_CGAP_GC4 Homo sapiens cDNA ... 40 0.55
 C14370, C14370 Human fetal brain cDNA 5'-end GEN-050F01 40 0.55

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AA237204, AA237204	mx18d02.r1	Soares mouse NML Mus musculus c...	167	1e-39
AA563402, AA563402	vl75d08.r1	Knowles Solter mouse blastocyst...	38	0.78
AA413261, AA413261	ve52f04.r1	Beddington mouse embryonic regi...	38	0.78
AA097645, AA097645	mm36f09.r1	Stratagene mouse skin (#937313)...	38	0.78
AA122578, AA122578	mn25b08.r1	Beddington mouse embryonic regi...	38	0.78
AA122581, AA122581	mn25c08.r1	Beddington mouse embryonic regi...	38	0.78
AA646168, AA646168	vn11e06.r1	Stratagene mouse Tcell 937311 M...	36	3.1
AA200881, AA200881	mu03c09.r1	Soares mouse 3NbMS Mus musculus...	36	3.1
AI048938, AI048938	uc84h06.y1	Sugano mouse kidney mkia Mus mu...	36	3.1
AA217675, AA217675	mv01b09.r1	Soares mouse lymph node NbMLN M...	36	3.1
AI006387, AI006387	ua71d09.r1	Soares 2NbMT Mus musculus cDNA ...	36	3.1
AA162722, AA162722	mn42b07.r1	Beddington mouse embryonic regi...	36	3.1
AA207387, AA207387	mv89a11.r1	GuayWoodford Beier mouse kidney...	36	3.1
AA511382, AA511382	vg14b04.r1	Soares mouse NbMH Mus musculus ...	36	3.1
AA123112, AA123112	mn30g01.r1	Beddington mouse embryonic regi...	36	3.1
AA106683, AA106683	ml83h06.r1	Stratagene mouse kidney (#93731...	36	3.1
AA105882, AA105882	ml84h07.r1	Stratagene mouse kidney (#93731...	36	3.1
W12171, W12171	ma59a10.r1	Soares mouse p3NMF19.5 Mus musculus...	36	3.1
AA208446, AA208446	mv85e01.r1	GuayWoodford Beier mouse kidney...	36	3.1
AA451370, AA451370	vf84h02.r1	Soares mouse mammary gland NbMM...	36	3.1
AA244639, AA244639	mx02g12.r1	Soares mouse NML Mus musculus c...	36	3.1
AA267119, AA267119	mz74d07.r1	Soares mouse lymph node NbMLN M...	36	3.1
AA561847, AA561847	vl27a12.r1	Stratagene mouse Tcell 937311 M...	36	3.1
AA237313, AA237313	mx17b11.r1	Soares mouse NML Mus musculus c...	36	3.1
AA145817, AA145817	mq68a12.r1	Soares 2NbMT Mus musculus cDNA ...	36	3.1
AA052080, AA052080	mf69f12.r1	Soares mouse embryo NbME13.5 14...	36	3.1
AA000646, AA000646	mg23f09.r1	Soares mouse embryo NbME13.5 14...	36	3.1
AA510521, AA510521	vh59a05.r1	Soares mouse mammary gland NbMM...	36	3.1
AI006122, AI006122	ua86h01.r1	Soares mouse mammary gland NbMM...	36	3.1
AA987039, AA987039	uc74e05.x1	Sugano mouse liver mlia Mus mus...	36	3.1
W77413, W77413	me64d06.r1	Soares mouse embryo NbME13.5 14.5 M...	36	3.1
AA114809, AA114809	mn17e09.r1	Beddington mouse embryonic regi...	36	3.1
AA793564, AA793564	vn54c05.r1	Barstead mouse myotubes MPLRB5 ...	36	3.1
AA174537, AA174537	mt10f09.r1	Soares mouse 3NbMS Mus musculus...	36	3.1
W62181, W62181	md87d08.r1	Soares mouse embryo NbME13.5 14.5 M...	36	3.1
AA272905, AA272905	va39d01.r1	Soares mouse 3NME12 5 Mus muscu...	36	3.1
AA286005, AA286005	va30e05.r1	GuayWoodford Beier mouse kidney...	36	3.1
AA212823, AA212823	mw81c07.r1	Soares mouse NML Mus musculus c...	36	3.1
AA125061, AA125061	mq83d10.r1	Stratagene mouse melanoma (#937...	36	3.1

AA519228, AA519228 TgESTzz39h02.s1 TgME49 invivo Bradyzoite c... 44 0.011

AA520185, AA520185 TgESTzz39d03.s1 TgME49 invivo Bradyzoite c... 44 0.011
 AA531917, AA531917 TgESTzz48f01.r1 TgME49 invivo Bradyzoite c... 44 0.011
 AA519997, AA519997 TgESTzz36h03.r1 TgME49 invivo Bradyzoite c... 44 0.011
 AA520811, AA520811 TgESTzz64d05.r1 TgME49 invivo Bradyzoite c... 44 0.011
 AA520866, AA520866 TgESTzz68e05.r1 TgME49 invivo Bradyzoite c... 44 0.011
 AA519844, AA519844 TgESTzz36c03.r1 TgME49 invivo Bradyzoite c... 44 0.011
 AA274295, AA274295 TgESTzz24c11.s1 TgME49 invivo Bradyzoite c... 44 0.011
 AA520901, AA520901 TgESTzz65a05.r1 TgME49 invivo Bradyzoite c... 44 0.011
 AA519829, AA519829 TgESTzz36a02.r1 TgME49 invivo Bradyzoite c... 44 0.011
 AA531839, AA531839 TgESTzz47h05.r1 TgME49 invivo Bradyzoite c... 44 0.011
 C70525, C70525 C.elegans cDNA clone yk409g6 : 5' end, single... 44 0.011
 AA520235, AA520235 TgESTzz53c06.r1 TgME49 invivo Bradyzoite c... 42 0.044
 T42800, T42800 6063 Lambda-PRL2 Arabidopsis thaliana cDNA clo... 42 0.044
 R29976, R29976 12581 Lambda-PRL2 Arabidopsis thaliana cDNA cl... 42 0.044
 H32045, H32045 EST106774 Rat PC-12 cells, untreated Rattus sp... 40 0.18
 AA819924, AA819924 MF5MA171.AE3 S. mansoni female adult Lambd... 40 0.18
 H37128, H37128 15257 Lambda-PRL2 Arabidopsis thaliana cDNA cl... 40 0.18
 T04367, T04367 414 Lambda-PRL2 Arabidopsis thaliana cDNA clon... 40 0.18
 R90528, R90528 16883 Lambda-PRL2 Arabidopsis thaliana cDNA cl... 40 0.18
 AA660422, AA660422 00298 MtrHE Medicago truncatula cDNA 5' 40 0.18
 U94861, RRU94861 Rattus norvegicus clone HCY3 mRNA sequence 40 0.18
 F14275, ATTS5197 A. thaliana transcribed sequence; clone YBY... 38 0.69
 W43730, W43730 23107 CD4-16 Arabidopsis thaliana cDNA clone H... 38 0.69
 N65025, N65025 20065 Lambda-PRL2 Arabidopsis thaliana cDNA cl... 38 0.69
 AI001628, AI001628 EST0210 Tilapia brain cDNA library in pUC1... 38 0.69
 H74687, H74687 383 Brassica napus cDNA clone R25R. 38 0.69
 AA395597, AA395597 27394 Lambda-PRL2 Arabidopsis thaliana cDN... 38 0.69
 AA753070, AA753070 97AS2091 Rice Immature Seed Lambda ZAPII c... 38 0.69
 D41274, RICS3647A Rice cDNA, partial sequence (S3647_1A). 38 0.69
 Z25731, ATTS1208 A. thaliana transcribed sequence; clone VCV... 38 0.69
 N82780, N82780 TgESTzy34e03.r1 TgRH Tachyzoite cDNA Toxoplas... 38 0.69
 AA597822, AA597822 29889 Lambda-PRL2 Arabidopsis thaliana cDN... 38 0.69
 AA948906, AA948906 LD27590.5prime LD Drosophila melanogaster ... 38 0.69
 AI013695, AI013695 EST208370 Normalized rat spleen, Bento Soa... 38 0.69
 AA753263, AA753263 96BS0294 Rice Immature Seed Lambda ZAPII c... 38 0.69
 F14402, ATTS5324 A. thaliana transcribed sequence; clone TAP... 36 2.7
 T46158, T46158 9421 Lambda-PRL2 Arabidopsis thaliana cDNA clo... 36 2.7
 C91400, C91400 Dictyostelium discoideum slug cDNA, clone SSK169 36 2.7
 T46009, T46009 9272 Lambda-PRL2 Arabidopsis thaliana cDNA clo... 36 2.7
 AA440655, AA440655 LD15510.5prime LD Drosophila melanogaster ... 36 2.7
 AA559374, AA559374 MU002092.NH3 York-Harrop-lung-A Schistosom... 36 2.7
 Z32623, ATTS2751 A. thaliana transcribed sequence; clone YAP... 36 2.7
 T43683, T43683 6946 Lambda-PRL2 Arabidopsis thaliana cDNA clo... 36 2.7
 AA263535, AA263535 LD06645.5prime LD Drosophila melanogaster ... 36 2.7
 C37095, C37095 C.elegans cDNA clone yk482c11 : 3' end, singl... 36 2.7

C57017, C57017 *C.elegans* cDNA clone yk308h9 : 3' end, single... 36 2.7
 C93857, C93857 *Dictyostelium discoideum* slug cDNA, clone SSL794 36 2.7
 C92242, C92242 *Dictyostelium discoideum* slug cDNA, clone SSD283 36 2.7
 Z33976, ATTS3037 *A. thaliana* transcribed sequence; clone YAP... 36 2.7
 R62091, R62091 EST351 *Strongylocentrotus purpuratus* cDNA 5' end. 36 2.7
 AA567455, AA567455 HL01288.5prime HL *Drosophila melanogaster* ... 36 2.7
 C74456, C74456 Rice cDNA, partial sequence (E31357_1A) 36 2.7
 AA753227, AA753227 97AS2316 Rice Immature Seed Lambda ZAPII c... 36 2.7
 C92456, C92456 *Dictyostelium discoideum* slug cDNA, clone SSE569 36 2.7
 T20458, T20458 2466 Lambda-PRL2 *Arabidopsis thaliana* cDNA clo... 36 2.7
 R29905, R29905 12510 Lambda-PRL2 *Arabidopsis thaliana* cDNA cl... 36 2.7
 M79841, M79841 wEST00378 *Caenorhabditis elegans* cDNA clone CE... 36 2.7
 Z17562, ATTS0136 *A. thaliana* transcribed sequence; clone TAT... 36 2.7
 D71983, CELK084H2R *C.elegans* cDNA clone yk84h2 : 3' end, sin... 36 2.7
 T20404, T20404 2412 Lambda-PRL2 *Arabidopsis thaliana* cDNA clo... 36 2.7
 AI012789, AI012789 EST207240 Normalized rat placenta, Bento S... 36 2.7
 U83048, BTU83048 *Bos taurus* clone 0429 mRNA sequence 36 2.7
 AA660182, AA660182 00022 MtRHE *Medicago truncatula* cDNA 5' si... 36 2.7
 D48514, RICS14740A Rice cDNA, partial sequence (S14740_1A). 36 2.7
 C90110, C90110 *Dictyostelium discoideum* slug cDNA, clone SSI103 36 2.7
 H36880, H36880 15009 Lambda-PRL2 *Arabidopsis thaliana* cDNA cl... 36 2.7
 AA699152, AA699152 HL07807.5prime HL *Drosophila melanogaster* ... 36 2.7
 C11922, C11922 *C.elegans* cDNA clone yk144a11 : 5' end, singl... 36 2.7
 AA816691, AA816691 LD03795.5prime LD *Drosophila melanogaster* ... 36 2.7

SEQ ID NO:556

X99668, MM22A3 *M.musculus* mRNA for exon from unknown gene 22A3 260 5e-67
 Z83760, CICOS41 *Ciona intestinalis* DNA sequence from cosmid ... 40 0.94
 Z75710, CED1081 *Caenorhabditis elegans* cosmid D1081, complet... 40 0.94
 U73628, HSU73628 Human chromosome 11 101h11 cosmid, complete ... 40 0.94
 X99757, DMDYDTRO *D.melanogaster* mRNA for dystrophin 38 3.7
 U51189, HIVU51189 HIV-1 clone 93th253 from Thailand, complete... 38 3.7
 AC004118, AC004118 *Drosophila melanogaster* (P1 DS06238 (D26))... 38 3.7
 U50313, CELF44C4 *Caenorhabditis elegans* cosmid F44C4. 38 3.7
 AC004503, AC004503 *Homo sapiens* chromosome 5, P1 clone 1354A7... 38 3.7
 M16840, WHTCPA2 Wheat Asp-tRNA gene. 38 3.7
 Y13381, RNAMPH1 *Rattus norvegicus* mRNA for amphiphysin, amph1 38 3.7
 AC002994, AC002994 *Homo sapiens* chromosome 17, clone HRPC987K... 38 3.7
 AB008271, AB008271 *Arabidopsis thaliana* genomic DNA, chromos... 38 3.7
 D49701, ASNNIAD *Aspergillus oryzae* niaD gene for nitrate red... 38 3.7

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X59422, HSPLD1 H.sapiens Pl dl1 repetitive DNA 38 3.7
 Z98555, PFSC03027 Plasmodium falciparum DNA *** SEQUENCING I... 38 3.7

HUMAN ESTs

AA315671, AA315671 EST187451 Colon carcinoma (HCC) cell line ... 932 0.0
 U56653, HSU56653 Human heat shock inducible mRNA 769 0.0
 AA487685, AA487685 ab23b09.r1 Stratagene lung (#937210) Homo ... 751 0.0
 AA044797, AA044797 zk67g12.r1 Soares pregnant uterus NbHPU Ho... 749 0.0
 AA314922, AA314922 EST186735 HCC cell line (matastasis to liv... 698 0.0
 AA082278, AA082278 zn42d12.r1 Stratagene endothelial cell 937... 668 0.0
 H22613, H22613 yn64f03.r1 Homo sapiens cDNA clone 173213 5'. 624 e-177
 AA044743, AA044743 zk67g12.s1 Soares pregnant uterus NbHPU Ho... 622 e-176
 AA487470, AA487470 ab23b09.s1 Stratagene lung (#937210) Homo ... 601 e-170
 AA121057, AA121057 zm22b03.r1 Stratagene pancreas (#937208) H... 581 e-164
 AA194396, AA194396 zq05g05.s1 Stratagene muscle 937209 Homo s... 535 e-150
 AA384283, AA384283 EST97787 Thyroid Homo sapiens cDNA 5' end 535 e-150
 AA669015, AA669015 ab88f01.s1 Stratagene lung (#937210) Homo ... 535 e-150
 AA194336, AA194336 zq05g05.r1 Stratagene muscle 937209 Homo s... 505 e-141
 R96173, R96173 yt84e09.r1 Homo sapiens cDNA clone 231016 5'. 486 e-135
 AA028934, AA028934 zk08b09.s1 Soares pregnant uterus NbHPU Ho... 484 e-134
 AA564849, AA564849 nj22c04.s1 NCI_CGAP_AA1 Homo sapiens cDNA ... 442 e-122
 AA932576, AA932576 oo57g10.s1 NCI_CGAP_Lu5 Homo sapiens cDNA ... 440 e-121
 AA876265, AA876265 oi12g09.s1 NCI_CGAP_GC4 Homo sapiens cDNA ... 434 e-120
 AA025525, AA025525 ze86a11.s1 Soares fetal heart NbHH19W Homo... 430 e-118
 U56654, HSU56654 Human heat shock inducible mRNA 426 e-117
 AA746600, AA746600 nx18c02.s1 NCI_CGAP_GC3 Homo sapiens cDNA ... 406 e-111
 AA876346, AA876346 oj24a11.s1 NCI_CGAP_Kid5 Homo sapiens cDNA... 406 e-111
 W23082, W23082 78D1 Human retina cDNA Tsp509I-cleaved sublibr... 402 e-110
 AI034059, AI034059 owl4h11.x1 Soares_parathyroid_tumor_NbHPA ... 357 2e-96
 AA662934, AA662934 nu92d09.s1 NCI_CGAP_Pr22 Homo sapiens cDNA... 323 2e-86
 AA844331, AA844331 ai95f01.s1 Soares parathyroid tumor NbHPA ... 301 8e-80
 AA249866, AA249866 y0761.seq.F Human fetal heart, Lambda ZAP ... 297 1e-78
 R19215, R19215 yg24b07.r1 Homo sapiens cDNA clone 33126 5'. 280 3e-73
 T39355, T39355 ya04g08.r1 Homo sapiens cDNA clone 60542 5'. 254 2e-65
 AA731264, AA731264 nw57c08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 220 2e-55
 AA768549, AA768549 oa67c07.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 220 2e-55
 AA668506, AA668506 ac49a11.s1 Stratagene hNT neuron (#937233)... 216 4e-54
 T55337, T55337 yb79b05.s1 Homo sapiens cDNA clone 77361 3'. 198 8e-49
 AA860575, AA860575 aj86a09.s1 Soares parathyroid tumor NbHPA ... 198 8e-49
 AA335548, AA335548 EST39962 Epididymus Homo sapiens cDNA 5' end 109 6e-22
 R13183, R13183 yf73f02.r1 Homo sapiens cDNA clone 27960 5'. 58 2e-06
 T80034, T80034 yd04c06.r1 Homo sapiens cDNA clone 24672 5'. 38 1.8
 AA595230, AA595230 nl84g02.s1 NCI_CGAP_Br2 Homo sapiens cDNA ... 38 1.8

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AA871935, AA871935 vq42h02.r1 Barstead bowel MPLRB9 Mus muscu... 664 0.0
 AA062330, AA062330 ml35e10.r1 Stratagene mouse testis (#93730... 589 e-167
 AI048164, AI048164 ud71b09.y1 Sugano mouse liver mlia Mus mus... 537 e-151
 W08037, W08037 mb37h01.r1 Soares mouse p3NMF19.5 Mus musculus... 462 e-128
 AA387311, AA387311 vc19a03.r1 Ko mouse embryo 11 5dpc Mus mus... 264 6e-69
 AA163072, AA163072 ms31a11.r1 Stratagene mouse skin (#937313)... 212 2e-53
 AA596763, AA596763 vm60a10.r1 Stratagene mouse Tcell 937311 M... 178 3e-43
 AA562549, AA562549 vl63a11.r1 Knowles Solter mouse blastocyst... 143 2e-32
 AA212378, AA212378 mu44c03.r1 Soares 2NbMT Mus musculus cDNA ... 113 1e-23
 AA450862, AA450862 vg55h12.r1 Beddington mouse embryonic regi... 111 5e-23
 AA990073, AA990073 ua59a01.r1 Soares 2NbMT Mus musculus cDNA ... 86 3e-15
 AA921175, AA921175 vy54b10.r1 Stratagene mouse lung 937302 Mu... 78 8e-13
 AA261119, AA261119 mz89e01.r1 Soares mouse NML Mus musculus c... 38 0.65
 AI005952, AI005952 ua80f06.r1 Soares 2NbMT Mus musculus cDNA ... 36 2.6
 AA123274, AA123274 mn23a08.r1 Beddington mouse embryonic regi... 36 2.6
 AI036828, AI036828 vw96c02.r1 Stratagene mouse skin (#937313)... 36 2.6

H35787, H35787 EST109178 Rat PC-12 cells, NGF-treated (9 days... 105 3e-21
 AA686082, AA686082 EST109179 Rat PC-12 cells, NGF-treated (9 ... 86 3e-15
 C23464, C23464 Jpanese flounder liver cDNA, LE5(10) 72 4e-11
 C23465, C23465 Jpanese flounder liver cDNA, LE5(10) 56 2e-06
 AA520314, AA520314 TgESTzz38h12.r1 TgME49 invivo Bradyzoite c... 38 0.57
 AA520085, AA520085 TgESTzz37g05.r1 TgME49 invivo Bradyzoite c... 38 0.57
 AA520033, AA520033 TgESTzz36f10.r1 TgME49 invivo Bradyzoite c... 38 0.57
 AA012516, AA012516 TgESTzz23f04.r1 TgME49cDNA Toxoplasma gond... 38 0.57
 AA274286, AA274286 TgESTzz24c01.s1 TgME49 invivo Bradyzoite c... 38 0.57
 AA660585, AA660585 00471 MtRHE Medicago truncatula cDNA 5' si... 38 0.57
 L35828, BNAESTBD Brassica rapa (clone F0621) expressed sequen... 38 0.57
 AA520070, AA520070 TgESTzz37e05.r1 TgME49 invivo Bradyzoite c... 38 0.57
 C30080, C30080 C.elegans cDNA clone yk236c3 : 3' end, single... 36 2.3
 C39044, C39044 C.elegans cDNA clone yk505a4 : 3' end, single... 36 2.3
 C55023, C55023 C.elegans cDNA clone yk422a3 : 3' end, single... 36 2.3
 AA542589, AA542589 fa08d06.s1 Zebrafish ICRFzfls Danio rerio ... 36 2.3
 N25370, N25370 EST000480 Schistosoma mansoni cDNA clone SMTBA... 36 2.3
 AA820625, AA820625 LD24443.5prime LD Drosophila melanogaster ... 36 2.3
 AA494922, AA494922 fa12g10.r1 Zebrafish ICRFzfls Danio rerio ... 36 2.3
 AA495181, AA495181 fa04d06.s1 Zebrafish ICRFzfls Danio rerio ... 36 2.3
 D73287, CELK116G6R C.elegans cDNA clone yk116g6 : 3' end, si... 36 2.3
 C28238, C28238 Rice cDNA, partial sequence (C60429_1A) 36 2.3

SEQ ID NO:557

AF039693, AF039693 Homo sapiens unknown protein mRNA, complet... 948 0.0
 S51239, S51239 calreticulin [*Aplysia californica*=marine snail... 56 1e-05
 Z74035, CEF47G9 *Caenorhabditis elegans* cosmid F47G9, complet... 46 0.012
 U25723, CPU25723 *Cavia porcellus* alpha-2B adrenoceptor gene, ... 44 0.047
 AL021407, HS13D10 Homo sapiens DNA sequence from PAC 13D10 o... 42 0.19
 U67572, U67572 *Methanococcus jannaschii* section 114 of 150 of... 42 0.19
 V01470, ZMZE01 *Zea mays* gene encoding a zein gene (clone lam... 42 0.19
 U06631, HSU06631 Human (H326) mRNA, complete cds. 42 0.19
 X82638, CSCYTOX *C.sordelii* cytotoxin gene 42 0.19
 AE000926, AE000926 *Methanobacterium thermoautotrophicum* from ... 42 0.19
 AC004135, AC004135 Genomic sequence for *Arabidopsis thaliana* ... 42 0.19
 AC003010, HUAC003010 Homo sapiens Chromosome 16 BAC clone CIT... 40 0.74
 AF050157, MMHC135G15 *Mus musculus* major histocompatibility lo... 40 0.74
 AC002352, AC002352 Homo sapiens 12q24 PAC P256D10 complete se... 40 0.74
 X07699, MMNUCLEO Mouse nucleolin gene 40 0.74
 X02399, MMHOM6 Mouse embryonal carcinoma DNA fragment contai... 40 0.74
 M93661, RATNOTCHX Rat notch 2 mRNA. 40 0.74
 M17440, MUSMHC4H2S Mouse MHC (H-2) S region complement compon... 40 0.74
 U15972, MMU15972 *Mus musculus* homeobox (*Hoxa7*) gene, complete... 40 0.74
 AB001601, AB001601 Homo sapiens DBP2 mRNA for ATP-dependent ... 40 0.74
 U09820, HSU09820 Human helicase II (*RAD54L*) mRNA, complete cds. 40 0.74
 AB011149, AB011149 Homo sapiens mRNA for KIAA0577 protein, c... 40 0.74
 U26259, MMU26259 *Mus musculus* C2-H2 zinc finger protein mRNA,... 40 0.74
 L48363, MUSZFPTR *Mus musculus* zinc finger protein gene, compl... 40 0.74
 AC003113, AC003113 *Arabidopsis thaliana* BAC F24O1 chromosome ... 40 0.74
 D76432, D76432 Mouse mRNA for transcriptional repressor delt... 40 0.74
 U72937, HSU72937 Human putative DNA dependent ATPase and heli... 40 0.74
 U72915, HSATRX16 Human putative DNA dependent ATPase and heli... 40 0.74
 U00995, U00995 *Rattus norvegicus* TA1 mRNA, complete cds. 40 0.74
 Z48618, SCCHVII35 *S.cerevisiae* genes for *RAD54*, *ACE1*(*CUP2*), ... 40 0.74
 U75653, HSU75653 Human zinc finger helicase (*Znf-HX*) mRNA, co... 40 0.74
 Z72672, SCYGL150C *S.cerevisiae* chromosome VII reading frame ... 40 0.74
 Z50109, CEC09H10 *Caenorhabditis elegans* cosmid C09H10, compl... 40 0.74
 AF013969, AF013969 *Mus musculus* antigen containing epitope to... 40 0.74
 M95627, HUMAAMP1X Homo sapiens angio-associated migratory cel... 40 0.74
 U72936, HSU72936 Human putative DNA dependent ATPase and heli... 40 0.74
 M88753, DROHTCHRPI Fruitfly heterochromatin protein-1 gene, c... 40 0.74
 U76906, REU76906 *Rhizobium etli* FixK (*fixK*), FixN (*fixN*), mon... 40 0.74
 U97085, HSXNP14 Homo sapiens X-linked nuclear protein (*ATRX*) ... 40 0.74
 L34363, HUMNUCPRO Human X-linked nuclear protein (*XNP*) gene, ... 40 0.74
 U72938, HSU72938 Human putative DNA dependent ATPase and heli... 40 0.74

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X56983, EAVATP1	E.arvense gene for catalytic 70kDa V-ATPase ...	40	0.74
U88539, MMU88539	Mus musculus chromatin structural protein ho...	40	0.74
U07704, HSU07704	Human protein kinase PITSLRE isoform PBETA21...	38	2.9
U07705, HSU07705	Human protein kinase PITSLRE isoform PBETA22...	38	2.9
AF019612, AF019612	Homo sapiens S2P mRNA, complete cds	38	2.9
U04818, HSU04818	Human protein kinase PITSLRE alpha 2-4 mRNA,...	38	2.9
AB002381, AB002381	Human mRNA for KIAA0383 gene, partial cds	38	2.9
AB009520, AB009520	Pyrococcus horikoshii OT3 genomic DNA, 13...	38	2.9
Z83848, HS57A13	Human DNA sequence from PAC 57A13 between ma...	38	2.9
AC004592, AC004592	Homo sapiens PAC clone DJ0244J05 from 5q31...	38	2.9
L11710, ZEFZCMYC	Brachydanio rerio c-myc oncoprotein mRNA, co...	38	2.9
D43920, CHKMETASE	Chicken mRNA for DNA (cytosine-5-)-methylt...	38	2.9
U49056, RNU49056	Rattus norvegicus CTD-binding SR-like protei...	38	2.9
U04824, HSU04824	Human protein kinase PITSLRE alpha 2-1 mRNA,...	38	2.9
U78045, HSU78045	Human collagenase and stromelysin genes, com...	38	2.9
U04816, HSU04816	Human protein kinase PITSLRE alpha 2-2 mRNA,...	38	2.9
U04817, HSU04817	Human protein kinase PITSLRE alpha 2-3 mRNA,...	38	2.9

HUMAN ESTs

AA639190, AA639190 ns04a01.r1 NCI_CGAP_Ew1 Homo sapiens cDNA ... 519 e-145
AA172199, AA172199 zo96a06.r1 Stratagene ovarian cancer (#937... 513 e-144
R23642, R23642 yh35e03.r1 Homo sapiens cDNA clone 131740 5'. 490 e-136
AA902270, AA902270 ok69e04.s1 NCI_CGAP_GC4 Homo sapiens cDNA ... 450 e-124
AA947303, AA947303 ok20d04.s1 Soares_NSF_F8_9W_OT_PA_P_S1 Hom... 402 e-110
AA588066, AA588066 nk10d08.s1 NCI_CGAP_Co2 Homo sapiens cDNA ... 347 1e-93
AA412036, AA412036 zt68d09.s1 Soares testis NHT Homo sapiens ... 347 1e-93
AA480337, AA480337 ne33a03.s1 NCI_CGAP_Co3 Homo sapiens cDNA ... 347 1e-93
AA508745, AA508745 ni23a03.s1 NCI_CGAP_Co4 Homo sapiens cDNA ... 347 1e-93
AA172083, AA172083 zo96a06.s1 Stratagene ovarian cancer (#937... 315 4e-84
AA811913, AA811913 ob51d06.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 299 2e-79
AA402403, AA402403 zt68d09.r1 Soares testis NHT Homo sapiens ... 299 2e-79
AA725458, AA725458 ai16g01.s1 Soares parathyroid tumor NbHPA ... 250 2e-64
R26558, R26558 yh35e02.s1 Homo sapiens cDNA clone 131738 3'. 250 2e-64
W25749, W25749 11b4 Human retina cDNA randomly primed sublibr... 103 3e-20
W27158, W27158 22h9 Human retina cDNA randomly primed sublibr... 66 6e-09
AA737681, AA737681 nw63c04.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 42 0.090
T65784, T65784 yc11f10.s1 Homo sapiens cDNA clone 80395 3' si... 42 0.090
R52021, R52021 yg84h09.r1 Homo sapiens cDNA clone 40181 5' si... 42 0.090
AA569993, AA569993 nm47h04.s1 NCI_CGAP_Br2 Homo sapiens cDNA ... 42 0.090
R50149, R50149 yj61c05.s1 Homo sapiens cDNA clone 153224 3' s... 42 0.090
R87930, R87930 yo47a11.s1 Homo sapiens cDNA clone 181052 3' s... 42 0.090
AA812204, AA812204 ob84f01.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 42 0.090
AA770224, AA770224 ah82e12.s1 Soares testis NHT Homo sapiens ... 42 0.090

D29591, HUMNK752 Human keratinocyte cDNA, clone 752 40 0.36
 AA324325, AA324325 EST27219 Cerebellum II Homo sapiens cDNA 5... 40 0.36
 AA053063, AA053063 zl71c03.r1 Stratagene colon (#937204) Homo... 40 0.36
 T35539, T35539 EST86964 Homo sapiens cDNA 5' end similar to N... 40 0.36
 AA974278, AA974278 oq14d03.s1 NCI_CGAP_GC4 Homo sapiens cDNA ... 40 0.36
 W26196, W26196 22b5 Human retina cDNA randomly primed sublibr... 40 0.36
 H92585, H92585 yt89c03.s1 Homo sapiens cDNA clone 231460 3'. 40 0.36
 AA232334, AA232334 zr27b04.r1 Stratagene NT2 neuronal precurs... 40 0.36
 N55775, N55775 J2481F Homo sapiens cDNA clone J2481 5'. 40 0.36
 R98701, R98701 yr31f08.s1 Homo sapiens cDNA clone 206919 3'. 40 0.36
 C14370, C14370 Human fetal brain cDNA 5'-end GEN-050F01 40 0.36
 H19156, H19156 yn50c01.r1 Homo sapiens cDNA clone 171840 5'. 40 0.36
 AA299557, AA299557 EST12080 Uterus tumor I Homo sapiens cDNA ... 40 0.36
 W84460, W84460 zd89d12.r1 Soares fetal heart NbHH19W Homo sap... 40 0.36
 T54194, T54194 ya90a02.r2 Homo sapiens cDNA clone 68906 5'. 40 0.36
 AA100203, AA100203 zm16f12.r1 Stratagene pancreas (#937208) H... 38 1.4
 AA993061, AA993061 ot92h08.s1 Soares_total_fetus_Nb2HF8_9w Ho... 38 1.4
 R53406, R53406 yj70d07.r1 Homo sapiens cDNA clone 154093 5' s... 38 1.4
 H99671, H99671 yx35b03.s1 Homo sapiens cDNA clone 263693 3'. 38 1.4
 W03410, W03410 za07c09.r1 Soares melanocyte 2NbHM Homo sapien... 38 1.4
 N35475, N35475 yy24b03.s1 Homo sapiens cDNA clone 272141 3'. 38 1.4
 AA630851, AA630851 nt57f04.s1 NCI_CGAP_Pr3 Homo sapiens cDNA ... 38 1.4
 N66458, N66458 yz41b08.s1 Homo sapiens cDNA clone 285591 3'. 38 1.4
 AA736438, AA736438 zh31b09.s1 Soares pineal gland N3HPG Homo ... 38 1.4
 AA911761, AA911761 og19b01.s1 NCI_CGAP_PNS1 Homo sapiens cDNA... 38 1.4
 AA085513, AA085513 zn43a10.r1 Stratagene HeLa cell s3 937216 ... 38 1.4
 AA678530, AA678530 ah02e05.s1 Gessler Wilms tumor Homo sapien... 38 1.4
 AA782011, AA782011 ai75b12.s1 Soares testis NHT Homo sapiens ... 38 1.4
 F12352, HSC38H091 H. sapiens partial cDNA sequence; clone c-... 38 1.4
 AA861288, AA861288 ak33g01.s1 Soares testis NHT Homo sapiens ... 38 1.4
 AA908705, AA908705 ol01b09.s1 NCI_CGAP_Lu5 Homo sapiens cDNA ... 38 1.4
 AA298850, AA298850 EST114450 Thyroid Homo sapiens cDNA 5' end 38 1.4

AA237204, AA237204 mx18d02.r1 Soares mouse NML Mus musculus c... 172 1e-41
 AI047347, AI047347 ud65c01.y1 Sugano mouse liver mlia Mus mus... 42 0.032
 AA832736, AA832736 vw45g10.r1 Soares mouse mammary gland NbMM... 42 0.032
 AA960471, AA960471 vw63a05.s1 Soares mouse mammary gland NMLM... 40 0.13
 AA880584, AA880584 vw92e01.r1 Stratagene mouse skin (#937313)... 40 0.13
 AA107508, AA107508 mp05e07.r1 Life Tech mouse embryo 8 5dpc 1... 40 0.13
 AA116682, AA116682 mn28c06.r1 Beddington mouse embryonic regi... 40 0.13
 AA522310, AA522310 vi45b02.r1 Beddington mouse embryonic regi... 40 0.13
 AA162231, AA162231 mn44h02.r1 Beddington mouse embryonic regi... 40 0.13

AA414037, AA414037 vc68g03.s1 Knowles Solter mouse 2 cell Mus... 40 0.13
AA596585, AA596585 vm58e12.r1 Stratagene mouse Tcell 937311 M... 38 0.51
AA863563, AA863563 vx05a10.r1 Soares 2NbMT Mus musculus cDNA ... 38 0.51
AA795177, AA795177 vq94g04.r1 Knowles Solter mouse blastocyst... 38 0.51
AA914764, AA914764 vy92h04.r1 Soares mouse mammary gland NbMM... 38 0.51
AA590440, AA590440 vm20c04.r1 Knowles Solter mouse blastocyst... 38 0.51
AA563402, AA563402 vl75d08.r1 Knowles Solter mouse blastocyst... 38 0.51
AA260352, AA260352 va93c10.r1 Soares mouse 3NME12 5 Mus muscu... 38 0.51
AA444734, AA444734 ve75d10.r1 Soares mouse mammary gland NbMM... 38 0.51
C85885, C85885 Mus musculus fertilized egg cDNA 3'-end seque... 38 0.51
AA794590, AA794590 vu78h12.r1 Stratagene mouse skin (#937313)... 38 0.51
AA529643, AA529643 vi38a09.r1 Beddington mouse embryonic regi... 38 0.51
AA607084, AA607084 vm84a09.r1 Knowles Solter mouse blastocyst... 38 0.51
AA636994, AA636994 vn05g06.r1 Knowles Solter mouse blastocyst... 38 0.51
AA675676, AA675676 vr73h08.s1 Knowles Solter mouse 2 cell Mus... 38 0.51
AA163890, AA163890 ms52f09.r1 Life Tech mouse embryo 13 5dpc ... 38 0.51
C80539, C80539 Mus musculus 3.5-dpc blastocyst cDNA 3'-end s... 38 0.51
AA051352, AA051352 mj53a09.r1 Soares mouse embryo NbME13.5 14... 38 0.51
W36885, W36885 mb64f09.r1 Soares mouse p3NMF19.5 Mus musculus... 38 0.51
AA930627, AA930627 vy67c05.r1 Stratagene mouse macrophage (#9... 38 0.51
AA244639, AA244639 mx02g12.r1 Soares mouse NML Mus musculus c... 36 2.0
AA967267, AA967267 vz70e08.r1 Soares mouse mammary gland NbMM... 36 2.0
AI048938, AI048938 uc84h06.y1 Sugano mouse kidney mkia Mus mu... 36 2.0
AA162722, AA162722 mn42b07.r1 Beddington mouse embryonic regi... 36 2.0
AA170036, AA170036 ms52d01.r1 Life Tech mouse embryo 13 5dpc ... 36 2.0
AA511382, AA511382 vg14b04.r1 Soares mouse NbMH Mus musculus ... 36 2.0
AA555634, AA555634 vk49f08.r1 Stratagene mouse Tcell 937311 M... 36 2.0
AA212823, AA212823 mw81c07.r1 Soares mouse NML Mus musculus c... 36 2.0
AA606813, AA606813 vm90h12.r1 Knowles Solter mouse blastocyst... 36 2.0
AA591610, AA591610 vk49d08.r1 Stratagene mouse Tcell 937311 M... 36 2.0
AA987039, AA987039 uc74e05.x1 Sugano mouse liver mlia Mus mus... 36 2.0
AA105882, AA105882 ml84h07.r1 Stratagene mouse kidney (#93731... 36 2.0
AA451370, AA451370 vf84h02.r1 Soares mouse mammary gland NbMM... 36 2.0
AA612185, AA612185 vo03d05.r1 Stratagene mouse skin (#937313)... 36 2.0
AA103424, AA103424 mo21e05.r1 Life Tech mouse embryo 13 5dpc ... 36 2.0
AA145817, AA145817 mq68a12.r1 Soares 2NbMT Mus musculus cDNA ... 36 2.0
AA272905, AA272905 va39d01.r1 Soares mouse 3NME12 5 Mus muscu... 36 2.0
AA237313, AA237313 mx17b11.r1 Soares mouse NML Mus musculus c... 36 2.0
AA267119, AA267119 mz74d07.r1 Soares mouse lymph node NbMLN M... 36 2.0
AA106683, AA106683 ml83h06.r1 Stratagene mouse kidney (#93731... 36 2.0
AA125061, AA125061 mq83d10.r1 Stratagene mouse melanoma (#937... 36 2.0
AA655241, AA655241 vq84c07.s1 Knowles Solter mouse 2 cell Mus... 36 2.0
AA512835, AA512835 vg13f11.r1 Soares mouse NbMH Mus musculus ... 36 2.0

C70525, C70525 *C.elegans* cDNA clone yk409g6 : 5' end, single... 44 0.007
 F15112, SSO4D09 *S.scrofa* mRNA; expressed sequence tag (5'; c... 42 0.029
 AA684640, AA684640 EST104989 Rat PC-12 cells, untreated Rattu... 40 0.11
 H32045, H32045 EST106774 Rat PC-12 cells, untreated Rattus sp... 40 0.11
 AA660422, AA660422 00298 MtRHE *Medicago truncatula* cDNA 5' 40 0.11
 C59696, C59696 *C.elegans* cDNA clone yk440e1 : 3' end, single... 38 0.45
 AI008699, AI008699 EST203150 Normalized rat embryo, Bento Soa... 38 0.45
 AA753263, AA753263 96BS0294 Rice Immature Seed Lambda ZAPII c... 38 0.45
 T38461, T38461 EST103957 *Saccharomyces cerevisiae* cDNA 3' end. 38 0.45
 C59257, C59257 *C.elegans* cDNA clone yk386b12 : 3' end, singl... 38 0.45
 AA948906, AA948906 LD27590.5prime LD *Drosophila melanogaster* ... 38 0.45
 AI001628, AI001628 EST0210 *Tilapia* brain cDNA library in pUC1... 38 0.45
 H31962, H31962 EST106545 Rat PC-12 cells, untreated Rattus sp... 38 0.45
 AA979509, AA979509 LD34118.5prime LD *Drosophila melanogaster* ... 38 0.45
 D41274, RICS3647A Rice cDNA, partial sequence (S3647_1A). 38 0.45
 C58362, C58362 *C.elegans* cDNA clone yk366a8 : 3' end, single... 38 0.45
 C57756, C57756 *C.elegans* cDNA clone yk298b9 : 3' end, single... 38 0.45
 AA753070, AA753070 97AS2091 Rice Immature Seed Lambda ZAPII c... 38 0.45
 H74687, H74687 383 *Brassica napus* cDNA clone R25R. 38 0.45
 C10513, C10513 *C.elegans* cDNA clone yk147e9 : 3' end, single... 38 0.45
 C55569, C55569 *C.elegans* cDNA clone yk191d1 : 3' end, single... 38 0.45
 C94819, C94819 *Sus scrofa* mRNA; expressed sequence tag (5'; ... 38 0.45
 C32982, C32982 *C.elegans* cDNA clone yk338a12 : 3' end, singl... 38 0.45
 AA816691, AA816691 LD03795.5prime LD *Drosophila melanogaster* ... 36 1.8
 AA519844, AA519844 TgESTzz36c03.r1 TgME49 invivo Bradyzoite c... 36 1.8
 AA531839, AA531839 TgESTzz47h05.r1 TgME49 invivo Bradyzoite c... 36 1.8
 AA660182, AA660182 00022 MtRHE *Medicago truncatula* cDNA 5' si... 36 1.8
 D71983, CELK084H2R *C.elegans* cDNA clone yk84h2 : 3' end, sin... 36 1.8
 R29905, R29905 12510 Lambda-PRL2 *Arabidopsis thaliana* cDNA cl... 36 1.8
 AA519997, AA519997 TgESTzz36h03.r1 TgME49 invivo Bradyzoite c... 36 1.8
 U83048, BTU83048 *Bos taurus* clone 0429 mRNA sequence 36 1.8
 AA440655, AA440655 LD15510.5prime LD *Drosophila melanogaster* ... 36 1.8
 AA559374, AA559374 MU002092.NH3 York-Harrop-lung-A *Schistosom*... 36 1.8
 C93857, C93857 *Dictyostelium discoideum* slug cDNA, clone SSL794 36 1.8
 AA520901, AA520901 TgESTzz65a05.r1 TgME49 invivo Bradyzoite c... 36 1.8
 T46158, T46158 9421 Lambda-PRL2 *Arabidopsis thaliana* cDNA clo... 36 1.8
 AA520866, AA520866 TgESTzz68e05.r1 TgME49 invivo Bradyzoite c... 36 1.8
 Z17562, ATTS0136 *A. thaliana* transcribed sequence; clone TAT... 36 1.8
 AA520811, AA520811 TgESTzz64d05.r1 TgME49 invivo Bradyzoite c... 36 1.8
 AA567455, AA567455 HL01288.5prime HL *Drosophila melanogaster* ... 36 1.8
 AA519228, AA519228 TgESTzz39h02.s1 TgME49 invivo Bradyzoite c... 36 1.8
 AA531917, AA531917 TgESTzz48f01.r1 TgME49 invivo Bradyzoite c... 36 1.8
 AA519829, AA519829 TgESTzz36a02.r1 TgME49 invivo Bradyzoite c... 36 1.8
 AA520185, AA520185 TgESTzz39d03.s1 TgME49 invivo Bradyzoite c... 36 1.8
 C37095, C37095 *C.elegans* cDNA clone yk482c11 : 3' end, singl... 36 1.8

T46009, T46009 9272 Lambda-PRL2 Arabidopsis thaliana cDNA clo... 36 1.8
 T20458, T20458 2466 Lambda-PRL2 Arabidopsis thaliana cDNA clo... 36 1.8
 F14402, ATTS5324 A. thaliana transcribed sequence; clone TAP... 36 1.8
 T20404, T20404 2412 Lambda-PRL2 Arabidopsis thaliana cDNA clo... 36 1.8
 AA274295, AA274295 TgESTzz24c11.s1 TgME49 invivo Bradyzoite c... 36 1.8
 AA699152, AA699152 HL07807.5prime HL Drosophila melanogaster ... 36 1.8
 AA902065, AA902065 NCM1A12T3 Mycelial Neurospora crassa cDNA ... 36 1.8

SEQ ID NO:558

AF016585, AF016585 Streptomyces caelestis cytochrome P-450 hy... 42 0.092
 U50719, MSU50719 Manduca sexta neuroglian mRNA, complete cds 40 0.36
 Z97208, SPAC15A10 S.pombe chromosome I cosmid c15A10 40 0.36
 AC003063, AC003063 Mus musculus Chromosome 16 BAC Clone b40-o... 40 0.36
 X66455, MMFGFR2 M.musculus promoter region of fibroblast gro... 40 0.36
 D83785, D83785 Human mRNA for KIAA0200 gene, complete cds 40 0.36
 AC000398, AC000398 Genomic sequence from Mouse 11, complete s... 38 1.4
 AF062345, AF062345 Caulobacter crescentus Sts1 (sts1), S-laye... 38 1.4
 X12359, RCNIFR12 Rhodobacter capsulatus nifR1 and nifR2 gene 38 1.4
 X72382, RCNIFR3 R.capsulatus nifR3 DNA 38 1.4

HUMAN ESTs

R36714, R36714 yh93g06.s1 Homo sapiens cDNA clone 137338 3'. 775 0.0
 D61030, HUM149A04B Human fetal brain cDNA 5'-end GEN-149A04. 666 0.0
 D60944, HUM141D02B Human fetal brain cDNA 5'-end GEN-141D02. 656 0.0
 H03308, H03308 yj47d09.s1 Homo sapiens cDNA clone 151889 3'. 609 e-172
 AA435561, AA435561 zt73d09.s1 Soares testis NHT Homo sapiens ... 587 e-166
 AA977877, AA977877 oq56d03.s1 NCI_CGAP_Kid5 Homo sapiens cDNA... 571 e-161
 AA846787, AA846787 aj41h03.s1 Soares testis NHT Homo sapiens ... 563 e-159
 AA972542, AA972542 oo82e01.s1 NCI_CGAP_Kid5 Homo sapiens cDNA... 561 e-158
 AA954270, AA954270 on72e06.s1 Soares_NFL_T_GBC_S1 Homo sapien... 557 e-157
 AA740333, AA740333 ob23c02.s1 NCI_CGAP_Kid5 Homo sapiens cDNA... 557 e-157
 AA999722, AA999722 ov04c06.s1 NCI_CGAP_Kid3 Homo sapiens cDNA... 555 e-156
 AA970621, AA970621 op40h08.s1 Soares_NFL_T_GBC_S1 Homo sapien... 551 e-155
 AA932930, AA932930 oo04g11.s1 Soares_NFL_T_GBC_S1 Homo sapien... 541 e-152
 AA725406, AA725406 ai13b11.s1 Soares parathyroid tumor NbHPA ... 539 e-152
 W74439, W74439 zd75d10.s1 Soares fetal heart NbHH19W Homo sap... 539 e-152
 AA868538, AA868538 ak43e08.s1 Soares testis NHT Homo sapiens ... 539 e-152
 R79832, R79832 yi89b08.s1 Homo sapiens cDNA clone 146391 3' s... 537 e-151

R63227, R63227 yi07e06.s1 Homo sapiens cDNA clone 138562 3'. 535 e-150
 AI027967, AI027967 ov84d04.x1 Soares_testis_NHT Homo sapiens ... 535 e-150
 AA776717, AA776717 ah49d07.s1 Soares testis NHT Homo sapiens ... 535 e-150
 AI040961, AI040961 ov53d06.x1 Soares_testis_NHT Homo sapiens ... 533 e-150
 AI024835, AI024835 ov35h09.x1 Soares_testis_NHT Homo sapiens ... 533 e-150
 AA740667, AA740667 ob01g12.s1 NCI_CGAP_Kid3 Homo sapiens cDNA... 531 e-149
 AA994527, AA994527 ou42h06.s1 Soares_NFL_T_GBC_S1 Homo sapien... 531 e-149
 AA932728, AA932728 oo31g06.s1 NCI_CGAP_Lu5 Homo sapiens cDNA ... 529 e-149
 AI001978, AI001978 ot39f03.s1 Soares_testis_NHT Homo sapiens ... 529 e-149
 N37092, N37092 yy41g08.s1 Homo sapiens cDNA clone 273854 3'. 529 e-149
 N27547, N27547 yy01e05.s1 Homo sapiens cDNA clone 269984 3'. 527 e-148
 AA883578, AA883578 al46b08.s1 Soares NFL T GBC S1 Homo sapien... 527 e-148
 AA890154, AA890154 al53f07.s1 Soares_NFL_T_GBC_S1 Homo sapien... 525 e-147
 AA757222, AA757222 ah56f11.s1 Soares testis NHT Homo sapiens ... 525 e-147
 AA456074, AA456074 aa17b07.s1 Soares NhHMPu S1 Homo sapiens c... 523 e-147
 AA884285, AA884285 am32f04.s1 Soares NFL T GBC S1 Homo sapien... 523 e-147
 AA969436, AA969436 op53e12.s1 Soares_NFL_T_GBC_S1 Homo sapien... 521 e-146
 AA952918, AA952918 on55h11.s1 Soares_NFL_T_GBC_S1 Homo sapien... 521 e-146
 AA971938, AA971938 op88b01.s1 Soares_NFL_T_GBC_S1 Homo sapien... 521 e-146
 R25112, R25112 yh36b12.s1 Homo sapiens cDNA clone 131807 3'. 519 e-146
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 AA758323, AA758323 ah65e11.s1 Soares testis NHT Homo sapiens ... 519 e-146
 AA972041, AA972041 op88e06.s1 Soares_NFL_T_GBC_S1 Homo sapien... 519 e-146
 R76443, R76443 yi58e11.s1 Homo sapiens cDNA clone 143468 3'. 519 e-146
 AA917965, AA917965 om37e04.s1 Soares_NFL_T_GBC_S1 Homo sapien... 517 e-145
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 AA906270, AA906270 oj98e12.s1 Soares_NFL_T_GBC_S1 Homo sapien... 517 e-145
 AA758549, AA758549 ah70b04.s1 Soares testis NHT Homo sapiens ... 517 e-145
 AA927156, AA927156 om20f05.s1 Soares_NFL_T_GBC_S1 Homo sapien... 515 e-144
 AA976254, AA976254 oo30f08.s1 NCI_CGAP_Lu5 Homo sapiens cDNA ... 515 e-144
 R23891, R23891 yh28a12.s1 Homo sapiens cDNA clone 131038 3'. 515 e-144
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 AA483809, AA483809 ne41c08.s1 NCI_CGAP_Co3 Homo sapiens cDNA ... 513 e-144
 AA962659, AA962659 or31f10.s1 NCI_CGAP_GC3 Homo sapiens cDNA ... 511 e-143
 AA724803, AA724803 ai05f02.s1 Soares parathyroid tumor NbHPA ... 511 e-143
 AA410432, AA410432 zv12c09.s1 Soares NhHMPu S1 Homo sapiens c... 511 e-143
 AA775373, AA775373 ad19c07.s1 Soares NbHFB Homo sapiens cDNA ... 511 e-143
 AA758038, AA758038 ah67h09.s1 Soares testis NHT Homo sapiens ... 509 e-143
 AA904368, AA904368 ol15d02.s1 Soares_NFL_T_GBC_S1 Homo sapien... 509 e-143
 AA861386, AA861386 ak37b11.s1 Soares testis NHT Homo sapiens ... 507 e-142
 R31547, R31547 yh72g03.s1 Homo sapiens cDNA clone 135316 3'. 505 e-141
 AA843421, AA843421 ak07f11.s1 Soares parathyroid tumor NbHPA ... 504 e-141
 H02479, H02479 yj35e10.s1 Homo sapiens cDNA clone 150762 3'. 504 e-141
 N29346, N29346 yw85c12.s1 Homo sapiens cDNA clone 259030 3'. 504 e-141
 AA815351, AA815351 ai63g05.s1 Soares testis NHT Homo sapiens ... 504 e-141

AA923373, AA923373 ol46e03.s1 Soares_NFL_T_GBC_S1 Homo sapien... 502 e-140
H01218, H01218 yj31c08.s1 Homo sapiens cDNA clone 150350 3'. 500 e-140
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AA628621, AA628621 af40c02.s1 Soares total fetus Nb2HF8 9w Ho... 500 e-140
AA442745, AA442745 zv60a07.s1 Soares testis NHT Homo sapiens ... 498 e-139
AA777492, AA777492 zj02e07.s1 Soares fetal liver spleen 1NFLS... 498 e-139
R73670, R73670 yi55f03.s1 Homo sapiens cDNA clone 143165 3'. 498 e-139
H12460, H12460 yj12d05.s1 Homo sapiens cDNA clone 148521 3'. 498 e-139
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R76230, R76230 yi71g11.s1 Homo sapiens cDNA clone 144740 3'. 494 e-138
AA970616, AA970616 op40h03.s1 Soares_NFL_T_GBC_S1 Homo sapien... 494 e-138
AA912408, AA912408 ol23a05.s1 Soares_NFL_T_GBC_S1 Homo sapien... 492 e-137
AA910051, AA910051 ol40e08.s1 Soares_NFL_T_GBC_S1 Homo sapien... 492 e-137
AA815444, AA815444 ai65b11.s1 Soares testis NHT Homo sapiens ... 492 e-137
R76814, R76814 yi62f06.s1 Homo sapiens cDNA clone 143843 3'. 488 e-136
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R65987, R65987 yi23e10.s1 Homo sapiens cDNA clone 140106 3'. 486 e-136
R63480, R63480 yi08e11.s1 Homo sapiens cDNA clone 138668 3'. 486 e-136
AA885425, AA885425 am12h09.s1 Soares NFL T GBC S1 Homo sapien... 486 e-136
AA884231, AA884231 am32a01.s1 Soares NFL T GBC S1 Homo sapien... 484 e-135
AA885048, AA885048 am11a12.s1 Soares NFL T GBC S1 Homo sapien... 482 e-134
AA996162, AA996162 os14f10.s1 NCI_CGAP_Lu5 Homo sapiens cDNA ... 482 e-134
AA748637, AA748637 ny10a02.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 482 e-134
AI031908, AI031908 ow47e12.x1 Soares_parathyroid_tumor_NbHPA ... 482 e-134
AA884703, AA884703 am18e02.s1 Soares NFL T GBC S1 Homo sapien... 480 e-134
AA928243, AA928243 on87c10.s1 Soares_NFL_T_GBC_S1 Homo sapien... 480 e-134
AI025986, AI025986 ow03a09.s1 Soares_parathyroid_tumor_NbHPA ... 478 e-133
AA897637, AA897637 oj72g07.s1 Soares_NFL_T_GBC_S1 Homo sapien... 472 e-131
AA877346, AA877346 01c07.s1 NCI_CGAP_Co10 Homo sapiens cDNA... 472 e-131
AA833569, AA833569 aj46b02.s1 Soares testis NHT Homo sapiens ... 472 e-131
AA832163, AA832163 oc91b02.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 470 e-131
R89052, R89052 ym99e08.s1 Homo sapiens cDNA clone 167078 3'. 470 e-131
N26589, N26589 yx91f03.s1 Homo sapiens cDNA clone 269117 3'. 460 e-128
R73883, R73883 yi56c03.s1 Homo sapiens cDNA clone 143236 3'. 454 e-126
AA579968, AA579968 ng51c03.s1 NCI_CGAP_Co3 Homo sapiens cDNA ... 444 e-123
AA843427, AA843427 ak07g06.s1 Soares parathyroid tumor NbHPA ... 438 e-121
AA705903, AA705903 ah42g12.s1 Soares testis NHT Homo sapiens ... 436 e-121
AA835882, AA835882 oc81d05.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 434 e-120
AA812583, AA812583 aj43b02.s1 Soares testis NHT Homo sapiens ... 432 e-119
AA512970, AA512970 nj16b08.s1 NCI_CGAP_Pr22 Homo sapiens cDNA... 432 e-119
R26664, R26664 yh35g10.s1 Homo sapiens cDNA clone 131778 3'. 428 e-118
AA429715, AA429715 zv60a07.r1 Soares testis NHT Homo sapiens ... 414 e-114
H17430, H17430 ym40f09.s1 Homo sapiens cDNA clone 50607 3'. 404 e-111
AA436117, AA436117 zu03d10.r1 Soares testis NHT Homo sapiens ... 402 e-110
AA099077, AA099077 zl77a09.s1 Stratagene colon (#937204) Homo... 400 e-110

R72440, R72440 yj90h02.s1 Homo sapiens cDNA clone 156051 3'. 379 e-103
 AA577436, AA577436 nm96h06.s1 NCI_CGAP_Co9 Homo sapiens cDNA ... 351 4e-95
 AA516390, AA516390 nf55e03.s1 NCI_CGAP_Co3 Homo sapiens cDNA ... 347 6e-94
 AA534533, AA534533 nf80h06.s1 NCI_CGAP_Co3 Homo sapiens cDNA ... 341 3e-92
 AA541583, AA541583 ni89f05.s1 NCI_CGAP_Pr21 Homo sapiens cDNA... 311 3e-83
 N72191, N72191 yz99f07.s1 Homo sapiens cDNA clone 291205 3'. 303 8e-81
 AA905015, AA905015 ok09b08.s1 Soares_NFL_T_GBC_S1 Homo sapien... 303 8e-81
 AA393148, AA393148 zt73d09.r1 Soares testis NHT Homo sapiens ... 287 4e-76
 AA939048, AA939048 op56h04.s1 Soares_NFL_T_GBC_S1 Homo sapien... 256 2e-66
 AA412317, AA412317 zt97c05.r1 Soares testis NHT Homo sapiens ... 246 2e-63
 R65986, R65986 yi23e10.r1 Homo sapiens cDNA clone 140106 5'. 238 4e-61
 AA400827, AA400827 zt76c07.s1 Soares testis NHT Homo sapiens ... 232 2e-59
 W00472, W00472 yz99f07.r1 Homo sapiens cDNA clone 291205 5'. 180 8e-44
 AA860558, AA860558 aj81e09.s1 Soares parathyroid tumor NbHPA ... 180 8e-44
 AA455577, AA455577 aa17b07.r1 Soares NhHMPu S1 Homo sapiens c... 176 1e-42
 AA583931, AA583931 nn64e04.s1 NCI_CGAP_Lar1 Homo sapiens cDNA... 172 2e-41
 AA907332, AA907332 ol22g11.s1 Soares_NFL_T_GBC_S1 Homo sapien... 168 3e-40
 R71169, R71169 yi53a12.r1 Homo sapiens cDNA clone 142942 5'. 159 3e-37
 W79084, W79084 zd75d10.r1 Soares fetal heart NbHH19W Homo sap... 155 4e-36
 AA295914, AA295914 EST101137 Thymus III Homo sapiens cDNA 5' end 135 4e-30
 AA860415, AA860415 aj60d10.s1 Soares testis NHT Homo sapiens ... 100 2e-19
 H01351, H01351 yi99a07.r1 Homo sapiens cDNA clone 147348 5'. 98 9e-19
 AA709286, AA709286 ai21g07.s1 Soares testis NHT Homo sapiens ... 96 3e-18
 AA931370, AA931370 oo03d01.s1 Soares_NFL_T_GBC_S1 Homo sapien... 96 3e-18
 AA501911, AA501911 ng54a08.s1 NCI_CGAP_Li2 Homo sapiens cDNA ... 94 1e-17
 AA548419, AA548419 nj14g09.s1 NCI_CGAP_Pr22 Homo sapiens cDNA... 92 5e-17
 AA588892, AA588892 no23b06.s1 NCI_CGAP_Pr22 Homo sapiens cDNA... 92 5e-17
 AI025228, AI025228 ov40h08.x1 Soares_testis_NHT Homo sapiens ... 76 3e-12
 R73757, R73757 yi55f03.r1 Homo sapiens cDNA clone 143165 5'. 74 1e-11
 R23710, R23710 yh35g10.r1 Homo sapiens cDNA clone 131778 5'. 56 3e-06
 N40362, N40362 yy01e05.r1 Homo sapiens cDNA clone 269984 5'. 50 2e-04
 H59895, H59895 yr04c12.r1 Homo sapiens cDNA clone 204310 5'. 48 7e-04
 H12509, H12509 yj12d05.r1 Homo sapiens cDNA clone 148521 5'. 44 0.011
 N20344, N20344 yx38d02.s1 Homo sapiens cDNA clone 264003 3'. 38 0.70
 AA614692, AA614692 np52b10.s1 NCI_CGAP_Br1.1 Homo sapiens cDN... 38 0.70
 H30707, H30707 yo78f07.r1 Homo sapiens cDNA clone 184069 5'. 36 2.7
 H52973, H52973 yq82e04.r1 Homo sapiens cDNA clone 202302 5'. 36 2.7
 AA218550, AA218550 zq96b02.r1 Stratagene NT2 neuronal precurs... 36 2.7
 AA312481, AA312481 EST183215 Jurkat T-cells VI Homo sapiens c... 36 2.7
 AA632009, AA632009 np74c07.s1 NCI_CGAP_Br2 Homo sapiens cDNA ... 36 2.7
 H13363, H13363 yl71b10.r1 Homo sapiens cDNA clone 43343 5'. 36 2.7
 AI022018, AI022018 ow64d01.x1 Soares_senescent_fibroblasts_Nb... 36 2.7
 AA781996, AA781996 ai75a06.s1 Soares testis NHT Homo sapiens ... 36 2.7
 N21623, N21623 yx60a09.s1 Homo sapiens cDNA clone 266104 3'. 36 2.7
 AA326194, AA326194 EST29340 Cerebellum II Homo sapiens cDNA 5... 36 2.7

C76071, C76071 Mus musculus 3.5-dpc blastocyst cDNA 3'-end s... 250 4e-65
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 AA561635, AA561635 vl01h07.r1 Knowles Solter mouse blastocyst... 234 2e-60
 AA288419, AA288419 vb14h01.r1 Soares mouse NML Mus musculus c... 220 3e-56
 AA212883, AA212883 mw78e10.r1 Soares mouse NML Mus musculus c... 220 3e-56
 AA268018, AA268018 vb08e07.r1 Soares mouse NML Mus musculus c... 212 8e-54
 AA692427, AA692427 vt59b07.r1 Barstead mouse irradiated colon... 200 3e-50
 W18566, W18566 mb98h02.r1 Soares mouse p3NMF19.5 Mus musculus... 192 7e-48
 AA543948, AA543948 vj69b08.r1 Knowles Solter mouse blastocyst... 147 4e-34
 W41070, W41070 mc39b06.r1 Soares mouse p3NMF19.5 Mus musculus... 123 5e-27
 Z31174, MMTTEST52 M.musculus expressed sequence tag MTEST52 117 3e-25
 AA530723, AA530723 vj32f07.r1 Stratagene mouse diaphragm (#93... 74 5e-12
 AA966940, AA966940 ua38c01.r1 Soares mouse mammary gland NbMM... 72 2e-11
 AA111079, AA111079 mp50e01.r1 Barstead MPLRB1 Mus musculus cD... 44 0.004
 AA049187, AA049187 mj51a02.r1 Soares mouse embryo NbME13.5 14... 36 0.99
 AA058246, AA058246 mg74e12.r1 Soares mouse embryo NbME13.5 14... 36 0.99
 AA153730, AA153730 mq60a02.r1 Soares 2NbMT Mus musculus cDNA ... 36 0.99
 AA473959, AA473959 vd02b12.s1 Knowles Solter mouse 2 cell Mus... 36 0.99
 W47887, W47887 mc83h09.r1 Soares mouse embryo NbME13.5 14.5 M... 36 0.99
 AA033312, AA033312 mi43g01.r1 Soares mouse embryo NbME13.5 14... 36 0.99
 AA980820, AA980820 ua46a04.r1 Soares mouse mammary gland NbMM... 36 0.99
 Z31139, MMTTEST427 M.musculus expressed sequence tag MTEST427 36 0.99
 C76637, C76637 Mus musculus 3.5-dpc blastocyst cDNA 3'-end s... 34 3.9
 AI049314, AI049314 uc87b10.y1 Sugano mouse kidney mkia Mus mu... 34 3.9
 AA670807, AA670807 vs70b02.r1 Stratagene mouse skin (#937313)... 34 3.9
 AA727571, AA727571 vv01h11.r1 Stratagene mouse skin (#937313)... 34 3.9
 AA571966, AA571966 vg12f07.r1 Soares mouse NbMH Mus musculus ... 34 3.9
 W37059, W37059 mb73f10.r1 Soares mouse p3NMF19.5 Mus musculus... 34 3.9
 AA760280, AA760280 vv74h11.r1 Stratagene mouse skin (#937313)... 34 3.9
 AA799036, AA799036 vn40c12.r1 Stratagene mouse skin (#937313)... 34 3.9
 AA432831, AA432831 vf28g07.r1 Knowles Solter mouse 8 cell Mus... 34 3.9
 AA562435, AA562435 vk98c01.r1 Knowles Solter mouse blastocyst... 34 3.9
 AA726680, AA726680 vu93g12.r1 Stratagene mouse skin (#937313)... 34 3.9
 AA217464, AA217464 mu87d11.r1 Soares mouse lymph node NbMLN M... 34 3.9
 AA790564, AA790564 vx71e06.r1 Stratagene mouse skin (#937313)... 34 3.9
 AA033172, AA033172 mi37f06.r1 Soares mouse embryo NbME13.5 14... 34 3.9
 AA616204, AA616204 vo96h02.r1 Soares mouse mammary gland NbMM... 34 3.9
 AA982055, AA982055 ua37h05.r1 Soares mouse mammary gland NbMM... 34 3.9
 W47850, W47850 mc82h10.r1 Soares mouse embryo NbME13.5 14.5 M... 34 3.9
 AA537538, AA537538 vk48c12.r1 Soares mouse mammary gland NbMM... 34 3.9
 AA636986, AA636986 vn05f04.r1 Knowles Solter mouse blastocyst... 34 3.9

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 AA944260, AA944260 EST199759 Normalized rat embryo, Bento Soa... 38 0.22
 AI008930, AI008930 EST203381 Normalized rat embryo, Bento Soa... 36 0.87
 D15788, RICC1258A Rice cDNA, partial sequence (C1258A). 36 0.87
 AA963741, AA963741 UI-R-C0-gt-b-09-0-UI.s1 UI-R-C0 Rattus nor... 36 0.87
 AA951235, AA951235 LD31601.3prime LD Drosophila melanogaster ... 34 3.5
 C20118, C20118 Rice cDNA, partial sequence (E11542_2A) 34 3.5
 AA820317, AA820317 LD23876.5prime LD Drosophila melanogaster ... 34 3.5
 AA950448, AA950448 LD30237.3prime LD Drosophila melanogaster ... 34 3.5

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U83883, RNU83883 Rattus norvegicus p105 coactivator mRNA, com... 42 0.11
 V00722, MMBGL1 Mouse gene for beta-1-globin. 40 0.45
 X14061, MMBGCXD M.musculus beta-globin complex DNA for y, bh... 40 0.45
 U20824, EHVU20824 Equine herpesvirus 2, complete genome 38 1.8
 U04106, PFU04106 Pleurotus fossulatus D1822, mating group VI,... 38 1.8
 U04101, POU04101 Pleurotus ostreatus D1742, Japan, mating gro... 38 1.8
 AC005174, AC005174 Homo sapiens clone UWGC:g1564a012 from 7p1... 38 1.8
 M18680, HUMRGAPS Homo sapiens 5S rRNA pseudogene. 38 1.8
 AL022121, MTV025 Mycobacterium tuberculosis H37Rv complete g... 38 1.8
 AF038379, AF038379 Leishmania amazonensis ribosomal protein S... 38 1.8
 Z11528, THIGPMR T.harzianum mRNA for imidazoleglycerolphosphate 38 1.8
 U32622, CTU32622 Comamonas testosteroni TsaR (tsaR), toluenes... 38 1.8
 U04102, POU04102 Pleurotus ostreatus D1743, Japan, mating gro... 38 1.8
 U04105, PFU04105 Pleurotus fossulatus D1821, mating group VI,... 38 1.8
 U04109, PEU04109 Pleurotus eryngii D1832, mating group VI rib... 38 1.8
 U65606, BSU65606 Basidiomycete from a bamboo (Phyllostachys p... 38 1.8

HUMAN ESTs

R49969, R49969 yj56c07.s1 Homo sapiens cDNA clone 152748 3' s... 523 e-147
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 W96422, W96422 ze43a05.s1 Soares retina N2b4HR Homo sapiens c... 315 2e-84
 R47821, R47821 yj56c07.r1 Homo sapiens cDNA clone 152748 5'. 214 7e-54
 AA761660, AA761660 nz24b09.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 212 3e-53
 AA887861, AA887861 nq99b07.s1 NCI_CGAP_Co10 Homo sapiens cDNA... 74 2e-11
 AA644044, AA644044 nm20b12.s1 NCI_CGAP_Co10 Homo sapiens cDNA... 72 6e-11

AA115963, AA115963 zm78d11.s1 Stratagene neuroepithelium (#93... 40 0.22
 AA779271, AA779271 zj43f02.s1 Soares fetal liver spleen 1NFLS... 40 0.22
 T65600, T65600 yc76a04.r1 Homo sapiens cDNA clone 21496 5'. 38 0.86
 AA515882, AA515882 nf67f10.s1 NCI_CGAP_Co3 Homo sapiens cDNA ... 38 0.86
 AA664812, AA664812 nu69b05.s1 NCI_CGAP_Alv1 Homo sapiens cDNA... 36 3.4
 T83365, T83365 ye03f05.s1 Homo sapiens cDNA clone 116673 3'. 36 3.4
 AA009773, AA009773 zi04d04.s1 Soares fetal liver spleen 1NFLS... 36 3.4
 AA916894, AA916894 og34g10.s1 NCI_CGAP_Br7 Homo sapiens cDNA ... 36 3.4
 N27865, N27865 yy02g03.s1 Homo sapiens cDNA clone 270100 3'. 36 3.4
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 AA505576, AA505576 nh93f03.s1 NCI_CGAP_Br2 Homo sapiens cDNA ... 36 3.4
 H30276, H30276 yp42f05.s1 Homo sapiens cDNA clone 190113 3'. 36 3.4
 AA699914, AA699914 zi61f08.s1 Soares fetal liver spleen 1NFLS... 36 3.4
 AA595583, AA595583 nk92c04.s1 NCI_CGAP_Co11 Homo sapiens cDNA... 36 3.4
 AA351139, AA351139 EST58769 Infant brain Homo sapiens cDNA 5'... 36 3.4
 AA810167, AA810167 ob88a03.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 36 3.4
 H50257, H50257 yo28a07.r1 Homo sapiens cDNA clone 179220 5'. 36 3.4
 W19939, W19939 zb37e09.r1 Soares parathyroid tumor NbHPA Homo... 36 3.4
 R19840, R19840 yg30e11.r1 Homo sapiens cDNA clone 33837 5'. 36 3.4
 AA514234, AA514234 nf56e10.s1 NCI_CGAP_Co3 Homo sapiens cDNA ... 36 3.4

AA183407, AA183407 ms
 AA821640, AA821640 vw
 AA289310, AA289310

AA900756, AA900756 UI-R-E0-di-d-04-0-UI.s1 UI-R-E0 Rattus nor... 46 0.001
 T18416, T18416 6c02e07t7 etiolated seedling Zea mays cDNA clo... 40 0.069
 AA817427, AA817427 LD22827.5prime LD Drosophila melanogaster ... 36 1.1
 AA274351, AA274351 TgESTzz25c09.s1 TgME49 invivo Bradyzoite c... 36 1.1
 AA391823, AA391823 LD10747.5prime LD Drosophila melanogaster ... 36 1.1
 AA274275, AA274275 TgESTzz24b02.s1 TgME49 invivo Bradyzoite c... 34 4.3
 R86490, R86490 RABEST068T Oryctolagus cuniculus cDNA clone pR... 34 4.3
 AA965817, AA965817 o5g08a1.r1 Aspergillus nidulans 24hr asexu... 34 4.3

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X81198, L35746, L49403, U21317, Z35640, AL010273, U09850, AF071771, Z96434,

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HUMAN ESTs

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 AA709149, AA709149 zf98g05.s1 Soares fetal heart NbHH19W Homo... 985 0.0
 AA428341, AA428341 zw18f09.s1 Soares ovary tumor NbHOT Homo s... 967 0.0
 AA043426, AA043426 zk54h09.r1 Soares pregnant uterus NbHPU Ho... 870 0.0
 AA878521, AA878521 oj19c01.s1 NCI_CGAP_Kid5 Homo sapiens cDNA... 844 0.0
 AA599696, AA599696 ag10h01.s1 Gessler Wilms tumor Homo sapien... 842 0.0
 W52304, W52304 zc47c08.r1 Soares senescent fibroblasts NbHSF ... 841 0.0
 AA043427, AA043427 zk54h09.s1 Soares pregnant uterus NbHPU Ho... 769 0.0
 N64314, N64314 yz46a12.s1 Homo sapiens cDNA clone 286078 3'. 763 0.0
 N52360, N52360 yz29g07.s1 Soares multiple sclerosis 2NbHMSP H... 753 0.0
 AA290863, AA290863 zt19a08.s1 Soares ovary tumor NbHOT Homo s... 747 0.0
 AA768023, AA768023 oa60e03.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 728 0.0
 AA872018, AA872018 oi05f08.s1 NCI_CGAP_GC4 Homo sapiens cDNA ... 718 0.0
 AA164765, AA164765 zp01g09.s1 Stratagene ovarian cancer (#937... 716 0.0
 AA814881, AA814881 oa75e02.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 708 0.0
 R86915, R86915 yq30f07.r1 Homo sapiens cDNA clone 197317 5'. 692 0.0
 W56703, W56703 zd14e01.r1 Soares fetal heart NbHH19W Homo sap... 642 0.0
 R84872, R84872 yq27e01.r1 Soares fetal liver spleen 1NFLS Hom... 636 0.0
 D79691, HUM307D10B Human aorta cDNA 5'-end GEN-307D10. 630 e-179
 AA025638, AA025638 ze90d11.s1 Soares fetal heart NbHH19W Homo... 626 e-178
 AA298883, AA298883 EST114512 Pancreas tumor I Homo sapiens cD... 624 e-177
 R86903, R86903 yq30d07.r1 Homo sapiens cDNA clone 197293 5'. 622 e-176
 AA033584, AA033584 zk21b12.s1 Soares pregnant uterus NbHPU Ho... 618 e-175
 AA633335, AA633335 nq58h09.s1 NCI_CGAP_Co9 Homo sapiens cDNA ... 611 e-173
 AA298894, AA298894 EST114513 Pancreas tumor I Homo sapiens cD... 599 e-169
 R85806, R85806 yq27e01.s1 Soares fetal liver spleen 1NFLS Hom... 595 e-168
 AA872617, AA872617 oi05g07.s1 NCI_CGAP_GC4 Homo sapiens cDNA ... 591 e-167
 H71458, H71458 yu71a06.s1 Homo sapiens cDNA clone 239218 3'. 587 e-166
 AA291045, AA291045 zt19a08.r1 Soares ovary tumor NbHOT Homo s... 563 e-159
 H71587, H71587 yu71a06.r1 Homo sapiens cDNA clone 239218 5'. 543 e-153
 AA035172, AA035172 zk28g05.s1 Soares pregnant uterus NbHPU Ho... 523 e-147
 AA164764, AA164764 zp01g09.r1 Stratagene ovarian cancer (#937... 517 e-145
 AA297001, AA297001 EST112550 Adipose tissue, white II Homo sa... 502 e-140
 AA296816, AA296816 EST112381 Aorta endothelial cells Homo sap... 500 e-139
 AA769090, AA769090 oa74e12.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 494 e-138
 H54447, H54447 yq91f04.s1 Homo sapiens cDNA clone 203167 3'. 438 e-121
 H54537, H54537 yq91f04.r1 Homo sapiens cDNA clone 203167 5'. 436 e-120
 AI049757, AI049757 an26g03.x1 Gessler Wilms tumor Homo sapien... 430 e-119

AA033583, AA033583 zk21b12.r1 Soares pregnant uterus NbHPU Ho... 422 e-116
D61748, HUM205G02B Human aorta cDNA 5'-end GEN-205G02. 412 e-113
AA148635, AA148635 zl26d10.r1 Soares pregnant uterus NbHPU Ho... 377 e-102
AA148636, AA148636 zl26d10.s1 Soares pregnant uterus NbHPU Ho... 373 e-101
AA025637, AA025637 ze90d11.r1 Soares fetal heart NbHH19W Homo... 371 e-101
AA932620, AA932620 oo61h04.s1 NCI_CGAP_Lu5 Homo sapiens cDNA ... 365 4e-99
AA385594, AA385594 EST99296 Thyroid Homo sapiens cDNA 5' end 339 2e-91
AA361957, AA361957 EST71295 T-cell lymphoma Homo sapiens cDNA... 289 2e-76
AA383998, AA383998 EST97483 Thyroid Homo sapiens cDNA 5' end ... 274 1e-71
H22175, H22175 yl38a03.r1 Homo sapiens cDNA clone 160492 5'. 256 3e-66
R50060, R50060 yj59c10.r1 Homo sapiens cDNA clone 153042 5'. 256 3e-66
AA229414, AA229414 nc47f12.r1 NCI_CGAP_Pr3 Homo sapiens cDNA ... 246 3e-63
D20466, HUMGS01440 Human HL60 3'directed MboI cDNA, HUMGS014... 208 6e-52
AA249061, AA249061 ll4438.seq.F Human fetal heart, Lambda ZAP... 168 5e-40
R86758, R86758 yq30f07.s1 Homo sapiens cDNA clone 197317 3'. 147 2e-33
R58025, R58025 F8018 Fetal heart Homo sapiens cDNA clone F801... 101 1e-19
AA371076, AA371076 EST82846 Prostate gland I Homo sapiens cDN... 42 0.081
AA977111, AA977111 oq24c03.s1 NCI_CGAP_GC4 Homo sapiens cDNA ... 40 0.32
AA608923, AA608923 af03b04.s1 Soares testis NHT Homo sapiens ... 38 1.3

gb|AA386999|AA386999 vc81b02.r1 Ko mouse embryo 11 5dpc Mus mus... 668 0.0
gb|AA589082|AA589082 vk24a08.r1 Knowles Solter mouse blastocyst... 658 0.0
gb|AA510881|AA510881 vh59c11.r1 Soares mouse mammary gland NbMM... 617 e-175
gb|AA763574|AA763574 vp07e08.r1 Soares mouse mammary gland NbMM... 615 e-174
gb|AA387423|AA387423 vc84b03.r1 Ko mouse embryo 11 5dpc Mus mus... 549 e-155
gb|AA915333|AA915333 vz28f05.r1 Soares 2NbMT Mus musculus cDNA ... 543 e-153
gb|AA816208|AA816208 vp43c10.r1 Barstead mouse irradiated colon... 444 e-123
gb|AA190043|AA190043 mt91h08.r1 Soares mouse lymph node NbMLN M... 424 e-117
gb|AA207393|AA207393 mv89c09.r1 GuayWoodford Beier mouse kidney... 394 e-108
emb|Z31258|MMTEST693 M.musculus expressed sequence tag MTEST693 309 8e-83
gb|AA930143|AA930143 vz52d11.s1 Soares 2NbMT Mus musculus cDNA ... 293 5e-78
gb|AA170612|AA170612 ms92c09.r1 Soares mouse 3NbMS Mus musculus... 287 3e-76
gb|AA762238|AA762238 vw58h02.r1 Soares mouse mammary gland NMLM... 266 1e-69
gb|AA689028|AA689028 vs02c12.r1 Barstead mouse irradiated colon... 264 4e-69
gb|AA959938|AA959938 vw58h02.s1 Soares mouse mammary gland NMLM... 240 6e-62
dbj|D18511|MUSGS01569 Mouse 3'-directed cDNA, MUSGS01569, clon... 172 1e-41
gb|AA474393|AA474393 vd57g07.r1 Knowles Solter mouse blastocyst... 100 1e-19
gb|W97165|W97165 mf90g05.r1 Soares mouse embryo NbME13.5 14.5 M... 74 8e-12
gb|AA512077|AA512077 vj43f05.r1 Stratagene mouse skin (#937313)... 62 3e-08
gb|AA794521|AA794521 vu68e07.r1 Stratagene mouse skin (#937313)... 54 8e-06
gb|AA155454|AA155454 mn38h12.r1 Beddington mouse embryonic regi... 48 5e-04
gb|W91000|W91000 mf83f06.r1 Soares mouse embryo NbME13.5 14.5 M... 40 0.12

gb|AA219917|AA219917 mv62f05.r1 Soares mouse 3NME12 5 Mus muscu... 38 0.45
 gb|AA529349|AA529349 vi35f08.r1 Beddington mouse embryonic regi... 36 1.8
 gb|AA754855|AA754855 vu51e08.r1 Soares mouse mammary gland NbMM... 36 1.8

gb|AA850379|AA850379 EST193146 Normalized rat ovary, Bento Soar... 569 e-161
 gb|W63375|W63375 TgESTzy68g02.r1 TgME49 Tachyzoite cDNA Toxopla... 394 e-108
 gb|AA946379|AA946379 EST201878 Normalized rat lung, Bento Soare... 353 5e-96
 gb|AA964427|AA964427 UI-R-E1-gp-a-08-0-UI.s1 UI-R-E1 Rattus nor... 335 1e-90
 gb|AA849599|AA849599 EST192366 Normalized rat muscle, Bento Soa... 307 3e-82
 gb|AA849595|AA849595 EST192362 Normalized rat muscle, Bento Soa... 307 3e-82
 gb|AA850378|AA850378 EST193145 Normalized rat ovary, Bento Soar... 278 3e-73
 gb|AA957389|AA957389 UI-R-E1-fu-b-04-0-UI.s1 UI-R-E1 Rattus nor... 157 6e-37
 gb|AI012981|AI012981 EST207432 Normalized rat spleen, Bento Soa... 147 6e-34
 dbj|C48357|C48357 C.elegans cDNA clone yk469b2 : 5' end, single... 40 0.10
 gb|AA440444|AA440444 LD15290.5prime LD Drosophila melanogaster ... 36 1.6
 dbj|C22690|C22690 Rice cDNA, partial sequence (S5274_4A) 36 1.6
 gb|AA697626|AA697626 HL02895.5prime HL Drosophila melanogaster ... 36 1.6
 gb|AA550136|AA550136 1244m3 gmbPfHB3.1, G. Roman Reddy Plasmodi... 36 1.6
 gb|T43579|T43579 6842 Lambda-PRL2 Arabidopsis thaliana cDNA clo... 36 1.6
 gb|AI030501|AI030501 UI-R-C0-jc-g-02-0-UI.s1 UI-R-C0 Rattus nor... 36 1.6
 gb|AA056876|AA056876 SWMFCA987SK Brugia malayi microfilaria cDN... 36 1.6
 gb|AA440689|AA440689 LD15550.5prime LD Drosophila melanogaster ... 36 1.6

SEQ ID NO:561

emb|Z47552|HSFMO3 H.sapiens mRNA for flavin-containing monooxyg... 44 0.10
 gb|U39966|HSFMO3G7 Homo sapiens flavin containing monooxygenase... 44 0.10
 emb|AL021026|HS127D3 Homo sapiens DNA sequence from PAC 127D3 o... 44 0.10
 gb|U35007|CPU35007 Carcharhinus plumbeus Ig lambda light chain ... 44 0.10
 gb|U35008|CPU35008 Carcharhinus plumbeus Ig lambda light chain ... 44 0.10
 dbj|D85068|RICT3A Rice transposable element T3 gene and ret... 42 0.40
 dbj|D63711|RICT3 Rice transposon T3 DNA, complete sequence 42 0.40
 gb|U01657|U01657 Carcharhinus plumbeus Ig lambda-chain gene, co... 42 0.40
 emb|Z92540|HS179I15A Human DNA sequence from PAC 179I15, BRCA2 ... 40 1.6
 dbj|AB001569|AB001569 Carrot DNA for transposon Tdc1 40 1.6
 gb|AE000613|HPAE000613 Helicobacter pylori section 91 of 134 of... 40 1.6
 emb|X07985|DMCUT Drosophila cut locus mRNA for homeodomain-cont... 40 1.6
 gb|AC005217|AC005217 Homo sapiens chromosome 5, P1 clone 1047D6... 40 1.6

HUMAN ESTs

gb|AA401219|AA401219 zv63a03.r1 Soares total fetus Nb2HF8 9w Ho... 993 0.0
 gb|H69371|H69371 yu19h09.r1 Homo sapiens cDNA clone 234305 5' s... 44 0.049
 gb|N62576|N62576 za13d10.s1 Homo sapiens cDNA clone 292435 3' s... 42 0.19
 gb|W77763|W77763 zd69c06.r1 Soares fetal heart NbHH19W Homo sap... 40 0.77
 gb|R14832|R14832 yf93g05.r1 Homo sapiens cDNA clone 30203 5'. 40 0.77
 gb|T90524|T90524 yd40a04.s1 Homo sapiens cDNA clone 110670 3' s... 38 3.0
 gb|R91887|R91887 yq04c09.r1 Homo sapiens cDNA clone 195952 5'. 38 3.0
 gb|AA586935|AA586935 nn68h03.s1 NCI_CGAP_Lar1 Homo sapiens cDNA... 38 3.0
 gb|T46987|T46987 yb12a07.s1 Homo sapiens cDNA clone 70932 3' co... 38 3.0
 gb|AA853975|AA853975 aj51f09.s1 Soares testis NHT Homo sapiens ... 38 3.0
 gb|T97059|T97059 ye50e01.r1 Homo sapiens cDNA clone 121176 5'. 38 3.0
 gb|AA883119|AA883119 am15h02.s1 Soares NFL T GBC S1 Homo sapien... 38 3.0
 gb|AA860074|AA860074 ak45b06.s1 Soares testis NHT Homo sapiens ... 38 3.0
 gb|AA889618|AA889618 ak28f06.s1 Soares_testis_NHT Homo sapiens ... 38 3.0

gb|AA230450|AA230450 mv73c06.r1 Soares mouse 3NME12 5 Mus muscu... 38 1.1
 gb|AA058041|AA058041 mj58e08.r1 Soares mouse embryo NbME13.5 14... 38 1.1
 gb|AA152953|AA152953 mq54a03.r1 Soares 2NbMT Mus musculus cDNA ... 38 1.1
 gb|W34414|W34414 ma98b07.r1 Soares mouse p3NMF19.5 Mus musculus... 38 1.1
 gb|AA465969|AA465969 ve90c06.s1 Knowles Solter mouse 2 cell Mus... 38 1.1
 gb|AA261173|AA261173 mz62b11.r1 Soares mouse lymph node NbMLN M... 38 1.1
 gb|AA238109|AA238109 mw97b05.r1 Soares mouse NML Mus musculus c... 38 1.1
 dbj|C86549|C86549 Mus musculus fertilized egg cDNA 3'-end seque... 38 1.1
 gb|AI048677|AI048677 ub29g09.r1 Soares 2NbMT Mus musculus cDNA ... 38 1.1
 dbj|D77921|MUSC1A08 Mouse embryonal carcinoma F9 cell cDNA, C1A08 38 1.1
 gb|AA396183|AA396183 vb45e04.r1 Soares mouse lymph node NbMLN M... 38 1.1
 gb|AA465898|AA465898 vc62f12.s1 Knowles Solter mouse 2 cell Mus... 36 4.3
 gb|AA041869|AA041869 mj05b12.r1 Soares mouse embryo NbME13.5 14... 36 4.3
 gb|AA637824|AA637824 vr21f11.r1 Barstead mouse myotubes MPLRB5 ... 36 4.3
 gb|W82563|W82563 mf05g06.r1 Soares mouse p3NMF19.5 Mus musculus... 36 4.3
 gb|AA389972|AA389972 vb30e03.r1 Soares mouse lymph node NbMLN M... 36 4.3
 gb|AA396253|AA396253 vb45f08.r1 Soares mouse lymph node NbMLN M... 36 4.3
 gb|AA920907|AA920907 vy84f04.r1 Stratagene mouse macrophage (#9... 36 4.3
 gb|AA517166|AA517166 vh98h05.r1 Barstead mouse myotubes MPLRB5 ... 36 4.3
 gb|AA433599|AA433599 vf47a05.r1 Soares mouse NbMH Mus musculus ... 36 4.3
 gb|AA867252|AA867252 vx25c01.r1 Soares 2NbMT Mus musculus cDNA ... 36 4.3
 dbj|C85619|C85619 Mus musculus fertilized egg cDNA 3'-end seque... 36 4.3
 gb|AA260277|AA260277 va93g05.r1 Soares mouse 3NME12 5 Mus muscu... 36 4.3
 gb|AA172548|AA172548 mt04g11.r1 Soares mouse 3NbMS Mus musculus... 36 4.3
 gb|AA266879|AA266879 mz96a02.r1 Soares mouse lymph node NbMLN M... 36 4.3
 gb|AA473019|AA473019 vd43e06.r1 Barstead MPLRB1 Mus musculus cD... 36 4.3

gb|R47549|R47549 SW3ICA119SK *Brugia malayi* infective larva cDNA... 40 0.24
 gb|H32651|H32651 EST107947 Rat PC-12 cells, untreated *Rattus* sp... 38 0.96
 gb|AA955987|AA955987 UI-R-E1-fb-f-06-0-UI.s1 UI-R-E1 *Rattus* nor... 38 0.96
 gb|AA819638|AA819638 UI-R-A0-an-f-03-0-UI.s1 UI-R-A0 *Rattus* nor... 38 0.96
 gb|AI010914|AI010914 EST205365 Normalized rat muscle, Bento Soa... 38 0.96
 gb|AA893199|AA893199 EST197002 Normalized rat kidney, Bento Soa... 38 0.96
 gb|AA945176|AA945176 EST200675 Normalized rat liver, Bento Soar... 38 0.96
 gb|R95272|R95272 SWOvL3CA167SK *Onchocerca volvulus* infective la... 36 3.8
 gb|AA917208|AA917208 ka05f02.s1 *Onchocerca volvulus* infective l... 36 3.8
 dbj|C62023|C62023 *C.elegans* cDNA clone yk249d5 : 5' end, single... 36 3.8
 gb|AI013322|AI013322 EST207997 Normalized rat spleen, Bento Soa... 36 3.8
 gb|AI043280|AI043280 TENU0920 *T. cruzi* epimastigote normalized ... 36 3.8
 gb|AI009422|AI009422 EST203873 Normalized rat heart, Bento Soar... 36 3.8
 gb|AI012655|AI012655 EST207106 Normalized rat placenta, Bento S... 36 3.8
 dbj|C62878|C62878 *C.elegans* cDNA clone yk296d4 : 5' end, single... 36 3.8
 gb|AA915818|AA915818 SWOvL3CA1269SK *Onchocerca volvulus* infecti... 36 3.8
 gb|W00009|W00009 TgESTzy75b07.r1 TgRH Tachyzoite cDNA *Toxoplasma*... 36 3.8
 gb|AA943503|AA943503 EST199002 Normalized rat brain, Bento Soar... 36 3.8
 gb|AA956933|AA956933 UI-R-E1-fl-b-08-0-UI.s1 UI-R-E1 *Rattus* nor... 36 3.8
 gb|H54977|H54977 HHU16a *Sorghum bicolor* cv. TX430 *Sorghum* bicol... 36 3.8

SEQ ID NO:562

gb|AC000112|HSAC000112 Human PAC clone DJ149P21, complete seque... 44 0.082
 gb|U50197|CEL25E2 *Caenorhabditis elegans* cosmid F25E2. 44 0.082
 dbj|AB007727|AB007727 *Arabidopsis thaliana* genomic DNA, chromos... 44 0.082
 gb|U02562|BSU02562 *Bacillus subtilis* N-acetylglucosaminidase (l... 42 0.32
 dbj|D45048|BACORFX *Bacillus subtilis* gene for beta-N-acetylgluc... 42 0.32
 emb|Z70683|CEF13B12 *Caenorhabditis elegans* cosmid F13B12, compl... 40 1.3
 emb|AL023828|CEY17G7B *Caenorhabditis elegans* cosmid Y17G7B, com... 40 1.3
 gb|U39740|CELZC64 *Caenorhabditis elegans* cosmid ZC64. 40 1.3
 gb|AF006490|AF006490 *Gossypium hirsutum* adenine nucleotide tran... 40 1.3
 emb|AL010170|PFSC03098 *Plasmodium falciparum* DNA *** SEQUENCING... 40 1.3
 gb|U53701|GHU53701 *Gossypium hirsutum* alcohol dehydrogenase 2d ... 40 1.3

HUMAN ESTs

gb|AA670455|AA670455 ae62h05.s1 Stratagene lung carcinoma 93721... 852 0.0
 gb|AA251062|AA251062 zs07c10.r1 NCI_CGAP_GCB1 *Homo sapiens* cDNA... 795 0.0

002090-6669460

gb|AA669916|AA669916 ag42h08.s1 Jia bone marrow stroma Homo sap... 638 0.0
 gb|AA300058|AA300058 EST12665 Uterus tumor I Homo sapiens cDNA ... 587 e-165
 gb|AA664277|AA664277 ac08c05.s1 Stratagene HeLa cell s3 937216 ... 549 e-154
 gb|AA373224|AA373224 EST85230 HSC172 cells I Homo sapiens cDNA ... 529 e-148
 gb|AA225705|AA225705 nc10b05.r1 NCI_CGAP_Pr1 Homo sapiens cDNA ... 515 e-144
 gb|W27883|W27883 39b10 Human retina cDNA randomly primed sublib... 484 e-134
 gb|R24643|R24643 yh36g05.r1 Homo sapiens cDNA clone 131864 5'. 438 e-121
 gb|N93137|N93137 zb28h06.s1 Homo sapiens cDNA clone 304955 3'. 432 e-119
 gb|AA250933|AA250933 zs07d01.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 426 e-117
 gb|AA216370|AA216370 nc10b05.s1 NCI_CGAP_Pr1 Homo sapiens cDNA ... 398 e-109
 gb|H26939|H26939 yl64g01.r1 Homo sapiens cDNA clone 163056 5'. 394 e-108
 gb|H30169|H30169 yo58g09.r1 Homo sapiens cDNA clone 182176 5'. 394 e-108
 gb|W38854|W38854 zb28h06.r1 Soares parathyroid tumor NbHPA Homo... 359 5e-97
 gb|AA602297|AA602297 np25a11.s1 NCI_CGAP_Pr22 Homo sapiens cDNA... 281 1e-73
 gb|AA167151|AA167151 zp06e09.r1 Stratagene ovarian cancer (#937... 256 6e-66
 gb|AA172387|AA172387 zo99d03.s1 Stratagene ovarian cancer (#937... 234 2e-59
 gb|AA173748|AA173748 zo99d03.r1 Stratagene ovarian cancer (#937... 224 2e-56
 gb|T83979|T83979 yd66a11.s1 Homo sapiens cDNA clone 113180 3'. 220 3e-55
 dbj|D61540|HUM415A08B Human fetal brain cDNA 5'-end GEN-415A08. 194 2e-47
 gb|N45148|N45148 yv25a05.r1 Homo sapiens cDNA clone 243728 5'. 165 2e-38
 gb|AA642960|AA642960 60f07.s1 NCI_CGAP_Lym3 Homo sapiens cDNA... 147 4e-33
 gb|R90980|R90980 yp93a03.r1 Homo sapiens cDNA clone 194956 5' s... 40 0.62
 gb|AA521500|AA521500 aa73h08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 40 0.62
 gb|H82921|H82921 yq46h10.s1 Homo sapiens cDNA clone 198883 3' s... 40 0.62
 gb|AA294871|AA294871 EST100023 Pancreas tumor I Homo sapiens cD... 38 2.4
 dbj|D63191|HUM503F11B Human placenta cDNA 5'-end GEN-503F11. 38 2.4
 gb|AA211096|AA211096 zq89g01.s1 Stratagene hNT neuron (#937233)... 38 2.4

gb|AA840137|AA840137 ud01e08.r1 Soares mouse uterus NMPu Mus mu... 383 e-104
 gb|AA145994|AA145994 mr13h04.r1 Soares mouse 3NbMS Mus musculus... 345 3e-93
 gb|AA146365|AA146365 mr05d05.r1 Soares mouse 3NbMS Mus musculus... 236 2e-60
 gb|AA203902|AA203902 mu60f02.r1 Soares mouse lymph node NbMLN M... 236 2e-60
 gb|AA204516|AA204516 mu66c10.r1 Soares mouse lymph node NbMLN M... 182 2e-44
 gb|AA137343|AA137343 mq80g08.r1 Stratagene mouse melanoma (#937... 52 6e-05
 gb|AA174717|AA174717 ms67a01.r1 Soares mouse 3NbMS Mus musculus... 48 0.001
 gb|W34073|W34073 ma85d10.r1 Soares mouse p3NMF19.5 Mus musculus... 48 0.001
 gb|AA289493|AA289493 vb36b01.r1 Soares mouse lymph node NbMLN M... 48 0.001
 gb|AA177700|AA177700 mt33e12.r1 Soares mouse 3NbMS Mus musculus... 48 0.001
 gb|AA146021|AA146021 mr13e03.r1 Soares mouse 3NbMS Mus musculus... 48 0.001
 gb|AA155352|AA155352 mn43d09.r1 Beddington mouse embryonic regi... 46 0.004
 gb|AA880874|AA880874 vx33b02.r1 Stratagene mouse lung 937302 Mu... 42 0.056

gb|AA590520|AA590520 vi54b08.r1 Beddington mouse embryonic regi... 38 0.88
 gb|AA596629|AA596629 vm56e06.r1 Stratagene mouse Tcell 937311 M... 38 0.88
 dbj|D76657|MUS75H09 Mouse embryonal carcinoma F9 cell cDNA, 75H09 38 0.88
 gb|AA050336|AA050336 mj12f05.r1 Soares mouse embryo NbME13.5 14... 38 0.88
 gb|AA120196|AA120196 mn35a12.r1 Beddington mouse embryonic regi... 38 0.88
 gb|W85267|W85267 mf42c06.r1 Soares mouse embryo NbME13.5 14.5 M... 36 3.5
 gb|AA239372|AA239372 my38f03.r1 Barstead mouse pooled organs MP... 36 3.5
 gb|AA497891|AA497891 vi73c07.r1 Stratagene mouse testis (#93730... 36 3.5
 gb|AA673053|AA673053 vn45e05.r1 Barstead mouse myotubes MPLRB5 ... 36 3.5
 emb|Z36324|MM224 M.musculus mRNA (clone 224) for expressed sequ... 36 3.5
 gb|AI021128|AI021128 ub01f06.r1 Soares mouse mammary gland NbMM... 36 3.5
 gb|AA403424|AA403424 mz56f07.r1 Barstead mouse pooled organs MP... 36 3.5
 gb|W66683|W66683 me23g11.r1 Soares mouse embryo NbME13.5 14.5 M... 36 3.5
 gb|AA689022|AA689022 vs02c03.r1 Barstead mouse irradiated colon... 36 3.5
 gb|AA574590|AA574590 vn63h11.r1 Barstead mouse proximal colon M... 36 3.5

dbj|C90696|C90696 Dictyostelium discoideum slug cDNA, clone SSJ634 38 0.78
 gb|AA269052|AA269052 MA1MA052.AA3 S. mansoni adult Lambda Zap S... 38 0.78
 gb|AA998786|AA998786 UI-R-C0-im-e-11-0-UI.s1 UI-R-C0 Rattus nor... 38 0.78
 gb|H33464|H33464 EST109494 Rat PC-12 cells, NGF-treated (9 days... 38 0.78
 gb|AA390721|AA390721 LD09459.5prime LD Drosophila melanogaster ... 36 3.1
 dbj|C83908|C83908 Dictyostelium discoideum slug cDNA, clone SSA567 36 3.1
 gb|AA202425|AA202425 LD02606.5prime LD Drosophila melanogaster ... 36 3.1
 gb|AI030951|AI030951 UI-R-C0-jf-d-04-0-UI.s1 UI-R-C0 Rattus nor... 36 3.1
 gb|N60251|N60251 TgESTzy11d04.r1 TgRH Tachyzoite cDNA Toxoplasm... 36 3.1
 gb|AA246875|AA246875 LD05855.5prime LD Drosophila melanogaster ... 36 3.1
 gb|AA803682|AA803682 GM13955.5prime GM Drosophila melanogaster ... 36 3.1
 gb|AA997528|AA997528 UI-R-C0-hw-h-11-0-UI.s1 UI-R-C0 Rattus nor... 36 3.1
 gb|AA695197|AA695197 GM02389.5prime GM Drosophila melanogaster ... 36 3.1
 gb|AA567339|AA567339 HL01077.5prime HL Drosophila melanogaster ... 36 3.1
 gb|AA950648|AA950648 LD30547.5prime LD Drosophila melanogaster ... 36 3.1

SEQ ID NO:563

substantially identical to D86956

SEQ ID NO:564

gb|AC004505|AC004505 Homo sapiens chromosome 20, P1 clone 86C1 ... 176 1e-41
 gb|S78798|S78798 1-phosphatidylinositol-4-phosphate 5-kinase is... 115 4e-23
 gb|U48696|HSU48696 Human mariner-like element-containing mRNA, ... 115 4e-23
 gb|U66300|LEU66300 Lycopersicon esculentum heat shock protein (... 115 4e-23
 gb|AF045432|AF045432 Danio rerio stem cell leukemia protein (ta... 111 6e-22
 emb|Z97178|BVRNAEF2 Beta vulgaris cDNA for elongation factor 2 107 9e-21
 gb|U39066|MMU39066 Murine MAP kinase kinase 6c mRNA, complete cds. 101 6e-19
 gb|U37573|XXU37573 Shuttle expression vector pBKCMV. 96 4e-17
 gb|AF033097|AF033097 Avena sativa nonphototropic hypocotyl 1 (N... 90 2e-15
 gb|AF027174|AF027174 Arabidopsis thaliana cellulose synthase ca... 86 3e-14
 gb|U65376|CFU65376 Canis familiaris rod photoreceptor transduci... 84 1e-13
 gb|AF033565|AF033565 Mus musculus cdc2/CDC28-like protein kinas... 82 5e-13
 emb|Z49980|HS2AMCP H.sapiens mRNA for ets-like protein (clone 7... 82 5e-13
 emb|AJ001103|LLARCAB Lactococcus lactis arcA and arcB genes 80 2e-12
 gb|U52868|CFU52868 Canis familiaris retinal cyclic-GMP phosphod... 80 2e-12
 gb|G29058|G29058 chicken STS ADL368 76 3e-11
 gb|G29060|G29060 chicken STS ADL352 76 3e-11
 gb|U34048|H DU34048 Haemophilus ducreyi hemoglobin-binding prote... 76 3e-11
 gb|U44386|SLU44386 Solanum lycopersicum heat shock protein (TFH... 68 8e-09
 gb|S83098|S83098 ribosomal protein S3 [Ambystoma mexicanum=Mexi... 66 3e-08
 gb|U48697|HSU48697 Human mariner-like element-containing mRNA, ... 60 2e-06
 gb|AF033096|AF033096 Avena sativa nonphototropic hypocotyl 1 (N... 60 2e-06
 emb|X99051|LLATTMSAT L.lagopus ATT microsatellite, locus LLST1 58 8e-06
 gb|U41811|HAU41811 Homarus americanus beta-I tubulin mRNA, comp... 46 0.029
 emb|X99055|LLCAMSAT1 L.lagopus CA microsatellite, locus LLSD5 44 0.12
 emb|X65215|BTMISATN B.taurus microsatellite DNA (624bp) 44 0.12
 gb|AE001023|AE001023 Archaeoglobus fulgidus section 84 of 172 o... 42 0.46
 emb|X80164|HSPDCM4 H.salinarium phage dcm4 Virus DNA 42 0.46
 emb|X87859|MTCMAJ12S C.major mitochondrial gene for 12S ribosom... 42 0.46
 emb|X87861|MTCPAL12S C.pallidus mitochondrial gene for 12S ribo... 42 0.46
 gb|L13767|STMSEC101A Streptomyces lividans sec101 gene, 5' end p... 42 0.46
 emb|Y08962|OSTRAMBPR O.sativa mRNA for transmembrane protein >g... 40 1.8
 gb|S65686|S65686 {multiple cloning sites, vector} [bacteriophag... 40 1.8
 gb|J02871|HUMCP45IV Human lung cytochrome P450 (IV subfamily) B... 40 1.8
 dbj|D10450|HUMRTVE Human genomic DNA, retrovirus-like element 40 1.8
 gb|S65683|S65683 {multiple cloning sites, vector} [bacteriophag... 40 1.8
 gb|L14950|PIGALDRED Sus scrofa aldose reductase mRNA, complete ... 40 1.8
 gb|S65693|S65693 {multiple cloning sites, vector} [bacteriophag... 40 1.8
 gb|S65694|S65694 {multiple cloning sites, vector} [bacteriophag... 40 1.8
 emb|AJ223292|SPAJ3292 Streptococcus pyogenes SOD gene, complete... 40 1.8
 gb|U25846|HAU25846 Homarus americanus clone LOB5 farnesoic acid... 40 1.8
 emb|X16699|HSP450P2 Human mRNA for cytochrome P-450HP 40 1.8
 gb|U37100|HSU37100 Homo sapiens aldose reductase-like peptide m... 40 1.8

HUMAN ESTs

gb|AA305996|AA305996 EST177003 Jurkat T-cells VI Homo sapiens c... 942 0.0
 gb|AA975279|AA975279 oq36e08.s1 NCI_CGAP_GC4 Homo sapiens cDNA ... 900 0.0
 gb|AA426359|AA426359 zw11b02.r1 Soares NhHMPu S1 Homo sapiens c... 868 0.0
 gb|AA424296|AA424296 zv90b08.r1 Soares NhHMPu S1 Homo sapiens c... 749 0.0
 gb|AA632259|AA632259 np67d04.s1 NCI_CGAP_Br2 Homo sapiens cDNA ... 730 0.0
 gb|H80377|H80377 yu59e01.r1 Homo sapiens cDNA clone 230424 5'. 658 0.0
 gb|AA515175|AA515175 ng68f10.s1 NCI_CGAP_Lip2 Homo sapiens cDNA... 615 e-174
 gb|AA351770|AA351770 EST59616 Infant brain Homo sapiens cDNA 5'... 611 e-172
 gb|AA426522|AA426522 zw11b02.s1 Soares NhHMPu S1 Homo sapiens c... 587 e-165
 gb|AA676220|AA676220 zi22a12.s1 Soares fetal liver spleen 1NFLS... 585 e-165
 gb|R35132|R35132 yg60e09.r1 Homo sapiens cDNA clone 36874 5'. 579 e-163
 gb|H80280|H80280 yu59e01.s1 Homo sapiens cDNA clone 230424 3'. 579 e-163
 gb|H81145|H81145 yu60e01.r1 Homo sapiens cDNA clone 230520 5'. 561 e-157
 gb|AA311105|AA311105 EST18187 Heart I Homo sapiens cDNA 5' end 533 e-149
 gb|AA380530|AA380530 EST93691 Supt cells Homo sapiens cDNA 5' end 527 e-147
 gb|H81050|H81050 yu60e01.s1 Homo sapiens cDNA clone 230520 3'. 500 e-139
 gb|AA460005|AA460005 zx49g07.s1 Soares testis NHT Homo sapiens ... 482 e-134
 gb|AA076450|AA076450 zm91d12.r1 Stratagene ovarian cancer (#937... 466 e-129
 gb|N43873|N43873 yy43e09.r1 Homo sapiens cDNA clone 274024 5'. 452 e-125
 gb|AA076451|AA076451 zm91d12.s1 Stratagene ovarian cancer (#937... 418 e-115
 gb|AA907095|AA907095 ol03b12.s1 NCI_CGAP_Lu5 Homo sapiens cDNA ... 414 e-113
 gb|W01027|W01027 za56g07.r1 Soares fetal liver spleen 1NFLS Hom... 262 1e-67
 gb|AA127183|AA127183 zn29d11.r1 Stratagene neuroepithelium NT2R... 222 1e-55
 gb|H65491|H65491 yr56a08.s1 Homo sapiens cDNA clone 209270 3'. 222 1e-55
 gb|N48543|N48543 yy49d08.r1 Homo sapiens cDNA clone 276879 5'. 210 4e-52
 gb|R32579|R32579 yh54h06.r1 Homo sapiens cDNA clone 133595 5'. 194 2e-47
 gb|AA247827|AA247827 j0778.seq.F Human fetal heart, Lambda ZAP ... 117 5e-24
 N84048, (many others similar, but smaller)

gb|AA589598|AA589598 vl49d08.s1 Stratagene mouse skin (#937313)... 398 e-109
 gb|AA647465|AA647465 vq82f02.s1 Knowles Solter mouse 2 cell Mus... 385 e-105
 gb|AA510284|AA510284 vh58f02.r1 Soares mouse mammary gland NbMM... 345 4e-93
 gb|AA028696|AA028696 mi12e12.r1 Soares mouse p3NMF19.5 Mus musc... 307 9e-82
 gb|N28081|N28081 MDB1409R Mouse brain, Stratagene Mus musculus ... 244 1e-62
 gb|AA177452|AA177452 mt24c12.r1 Soares mouse 3NbMS Mus musculus... 226 3e-57
 gb|N28080|N28080 MDB1409 Mouse brain, Stratagene Mus musculus c... 226 3e-57
 dbj|C88310|C88310 Mus musculus fertilized egg cDNA 3'-end seque... 226 3e-57
 gb|AA763786|AA763786 vo99g12.r1 Soares mouse mammary gland NbMM... 94 2e-17
 gb|AA667535|AA667535 vv18b12.r1 Stratagene mouse heart (#937316... 40 0.31
 gb|AA208274|AA208274 mv96a01.r1 GuayWoodford Beier mouse kidney... 38 1.2

gb AA955972 AA955972	UI-R-E1-ff-d-10-0-UI.s1	UI-R-E1 Rattus nor...	159	4e-37
gb AA957275 AA957275	UI-R-E1-fq-f-08-0-UI.s1	UI-R-E1 Rattus nor...	157	2e-36
emb Z84031 SSZ84031	S.scrofa mRNA; expressed sequence tag (5'; ...		111	9e-23
gb AF041408 AF041408	Fragaria x ananassa clone FA110b		96	5e-18
gb AA933116 AA933116	SWBmL3SA048T3	Brugia malayi L3 subtracted ...	58	1e-06
gb AA933363 AA933363	SWBmL3SA615T3	Brugia malayi L3 subtracted ...	52	7e-05
gb AA660164 AA660164	00001	MtRHE Medicago truncatula cDNA 5' si...	50	3e-04
gb N37420 N37420	18647	Lambda-PRL2 Arabidopsis thaliana cDNA cl...	44	0.018
gb H35981 H35981	14503	Lambda-PRL2 Arabidopsis thaliana cDNA cl...	44	0.018
gb AA882627 AA882627	TENS0198	T. cruzi epimastigote normalized ...	44	0.018
gb AI026481 AI026481	TENU0693	T. cruzi epimastigote normalized ...	42	0.070
gb AA946369 AA946369	EST201868	Normalized rat lung, Bento Soare...	42	0.070

gb|AI010371|AI010371 EST204822 Normalized rat lung, Bento Soare... 42 0.070
 gb|AI010257|AI010257 EST204708 Normalized rat lung, Bento Soare... 42 0.070
 dbj|D39318|RICR3325A Rice cDNA, partial sequence (R3325_1A). 40 0.28
 gb|U40140|OSU40140 Oryza sativa clone pFDRRC22 mRNA sequence. 40 0.28
 gb|AI009132|AI009132 EST203583 Normalized rat embryo, Bento Soa... 40 0.28
 dbj|D47291|RICS12574A Rice cDNA, partial sequence (S12574_1A). 40 0.28
 dbj|D47316|RICS12613A Rice cDNA, partial sequence (S12613_1A). 40 0.28
 gb|T42265|T42265 5528 Lambda-PRL2 Arabidopsis thaliana cDNA clo... 40 0.28
 dbj|D47631|RICS13239A Rice cDNA, partial sequence (S13239_1A). 40 0.28
 gb|AI013513|AI013513 EST208188 Normalized rat spleen, Bento Soa... 40 0.28
 gb|AA751980|AA751980 96AS0896 Rice Immature Seed Lambda ZAPII c... 40 0.28
 gb|AA660165|AA660165 00002 MtrHE Medicago truncatula cDNA 5' si... 40 0.28
 emb|Z34868|ATTS3597 A. thaliana transcribed sequence; clone FAF... 40 0.28
 dbj|D39131|RICR2302A Rice cDNA, partial sequence (R2302_1A). 40 0.28
 gb|AA963968|AA963968 UI-R-C0-gs-b-05-0-UI.s1 UI-R-C0 Rattus nor... 40 0.28
 gb|AA866346|AA866346 UI-R-A0-bm-a-05-0-UI.s1 UI-R-A0 Rattus nor... 40 0.28
 gb|AI044437|AI044437 UI-R-C1-js-e-06-0-UI.s1 UI-R-C1 Rattus nor... 40 0.28
 dbj|D41811|RICS4634A Rice cDNA, partial sequence (S4634_1A). 40 0.28
 dbj|C19261|C19261 Rice cDNA, partial sequence (E10176_1A) 40 0.28
 dbj|D48409|RICS14588A Rice cDNA, partial sequence (S14588_1A). 40 0.28
 dbj|C26556|C26556 Rice cDNA, partial sequence (C12586_1A) 40 0.28
 dbj|D47831|RICS13548A Rice cDNA, partial sequence (S13548_1A). 40 0.28
 dbj|C72152|C72152 Rice cDNA, partial sequence (E1094_3A) 40 0.28
 dbj|D46553|RICS11305A Rice cDNA, partial sequence (S11305_2A). 40 0.28
 gb|AI028926|AI0289 (and many others of similar score)

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emb|X68308|OOLPLIP O.ovis mRNA for lipoprotein lipase 40 1.2
 gb|AE000660|HUA000660 Homo sapiens T-cell receptor alpha delta... 40 1.2
 emb|AL022333|HS474I12 Human DNA sequence *** SEQUENCING IN PROG... 38 4.6
 emb|Z12618|CFTRG C.fasciculata gene encoding trypanothione redu... 38 4.6
 gb|M81651|HUMSEMIIB Human semenogelin II (SEMGII) gene, complet... 38 4.6
 gb|M96980|HUMMYT1A Homo sapiens myelin transcription factor 1 (... 38 4.6
 gb|U89688|ACU89688 Acanthamoeba castellanii myosin-I binding pr... 38 4.6
 gb|AC002497|AC002497 Human Cosmid g1940a142 from 7q31.3, comple... 38 4.6
 gb|M81652|HUMSMNGLN Homo sapiens semenogelin II mRNA, complete ... 38 4.6
 gb|M25665|HUMNCF1A Human neutrophil cytosol factor 1 (NCF-47k) ... 38 4.6
 gb|M73325|TRFTRPREDC Crithidia fasciculata trypanothione reduct... 38 4.6
 gb|M73324|TRFTRPREDB Crithidia fasciculata trypanothione reduct... 38 4.6
 emb|X92589|MMSEMIIGN M.mulatta semenogelin II gene 38 4.6
 emb|Z47556|HSSG1SG2 H.sapiens genes for semenogelin I and semen... 38 4.6
 gb|AC004753|AC004753 Homo sapiens chromosome 16, cosmid clone R... 38 4.6
 gb|M55067|HUMNADPHO Human 47-kD autosomal chronic granulomatous... 38 4.6

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gb|M73323|TRFTRPRED A Crithidia fasciculata trypanothione reduct... 38 4.6

HUMAN ESTs

gb|R11942|R11942 yf54c05.r1 Homo sapiens cDNA clone 25950 5'. 656 0.0
 gb|AA366384|AA366384 EST77326 Pancreas tumor III Homo sapiens c... 470 e-130
 gb|T12566|T12566 CHR90086 Homo sapiens genomic clone P94_24 5' ... 133 5e-29
 gb|R37032|R37032 yf54c05.s1 Homo sapiens cDNA clone 25950 3'. 44 0.036
 gb|AA661650|AA661650 nv02h12.s1 NCI_CGAP_Pr22 Homo sapiens cDNA... 38 2.2
 gb|AA261982|AA261982 zs20d03.r1 NCI_CGAP_GCB1 Homo sapiens cDNA... 38 2.2
 gb|AA588219|AA588219 no24c11.s1 NCI_CGAP_Pr22 Homo sapiens cDNA... 38 2.2
 gb|AA250891|AA250891 zs06c06.r1 NCI_CGAP_GCB1 Homo sapiens cDNA... 38 2.2
 gb|AA244177|AA244177 nc05a02.r1 NCI_CGAP_Pr1 Homo sapiens cDNA ... 38 2.2
 gb|AA715147|AA715147 nv10d05.s1 NCI_CGAP_Pr22 Homo sapiens cDNA... 38 2.2
 gb|AA659887|AA659887 nv03a10.s1 NCI_CGAP_Pr22 Homo sapiens cDNA... 38 2.2
 gb|AA627890|AA627890 nq70a08.s1 NCI_CGAP_Pr22 Homo sapiens cDNA... 38 2.2
 gb|AA603596|AA603596 np27b11.s1 NCI_CGAP_Pr22 Homo sapiens cDNA... 38 2.2
 gb|AA613738|AA613738 np25h09.s1 NCI_CGAP_Pr22 Homo sapiens cDNA... 38 2.2
 gb|AA715248|AA715248 nv10h06.s1 NCI_CGAP_Pr22 Homo sapiens cDNA... 38 2.2
 gb|AI038487|AI038487 ow25d12.x1 Soares parathyroid tumor NbHPA ... 38 2.2
 gb|AA252786|AA252786 zs26f10.r1 NCI_CGAP_GCB1 Homo sapiens cDNA... 38 2.2
 gb|AA287819|AA287819 zs50h04.r1 NCI_CGAP_GCB1 Homo sapiens cDNA... 38 2.2
 gb|AA564176|AA564176 nj04c08.s1 NCI_CGAP_Pr21 Homo sapiens cDNA... 38 2.2
 gb|AA643870|AA643870 np26h07.s1 NCI_CGAP_Pr22 Homo sapiens cDNA... 38 2.2
 gb|AA280371|AA280371 zt05f07.r1 NCI_CGAP_GCB1 Homo sapiens cDNA... 38 2.2
 gb|R00687|R00687 ye78h08.r1 Homo sapiens cDNA clone 123903 5' s... 38 2.2
 gb|AA587820|AA587820 nj06h05.s1 NCI_CGAP_Pr21 Homo sapiens cDNA... 38 2.2
 gb|AA588443|AA588443 no22c11.s1 NCI_CGAP_Pr22 Homo sapiens cDNA... 38 2.2
 gb|AA568385|AA568385 nl88f06.s1 NCI_CGAP_Co10 Homo sapiens cDNA... 38 2.2
 gb|AA281831|AA281831 zt06c08.r1 NCI_CGAP_GCB1 Homo sapiens cDNA... 38 2.2
 gb|AA700438|AA700438 zj74b08.s1 Soares fetal liver spleen 1NFLS... 38 2.2
 gb|AA689530|AA689530 ns66e07.r1 NCI_CGAP_Pr22 Homo sapiens cDNA... 38 2.2
 gb|AA688300|AA688300 nv14a09.s1 NCI_CGAP_Pr22 Homo sapiens cDNA... 38 2.2
 gb|AA687962|AA687962 nv13h04.s1 NCI_CGAP_Pr22 Homo sapiens cDNA... 38 2.2
 gb|AA526586|AA526586 ni96f11.s1 NCI_CGAP_Pr21 Homo sapiens cDNA... 38 2.2
 gb|AA642589|AA642589 nq73f04.s1 NCI_CGAP_Pr22 Homo sapiens cDNA... 38 2.2
 gb|AA541594|AA541594 ni89g07.s1 NCI_CGAP_Pr21 Homo sapiens cDNA... 38 2.2
 gb|AA278713|AA278713 zs76h02.r1 NCI_CGAP_GCB1 Homo sapiens cDNA... 38 2.2
 gb|T58661|T58661 ya94a07.r1 Homo sapiens cDNA clone 69300 5' si... 38 2.2
 gb|AA689473|AA689473 ns66e07.s1 NCI_CGAP_Pr22 Homo sapiens cDNA... 38 2.2
 gb|AA459023|AA459023 aa26a09.r1 NCI_CGAP_GCB1 Homo sapiens cDNA... 38 2.2

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dbj|C76752|C76752 Mus musculus 3.5-dpc blastocyst cDNA 3'-end s... 60 2e-07
gb|AA123048|AA123048 mn32g01.r1 Beddington mouse embryonic regi... 36 3.2
gb|AA616529|AA616529 vo10e01.r1 Barstead mouse myotubes MPLRB5 ... 36 3.2
gb|AA254370|AA254370 va13h09.r1 Soares mouse lymph node NbMLN M... 36 3.2
gb|AA537288|AA537288 vk46c04.r1 Soares mouse mammary gland NbMM... 36 3.2
gb|AA462365|AA462365 vg74c05.r1 Soares mouse NbMH Mus musculus ... 36 3.2
gb|AA589462|AA589462 vl47g07.s1 Stratagene mouse skin (#937313)... 36 3.2
gb|AA968017|AA968017 uh06h10.r1 Soares mouse hypothalamus NMHy ... 36 3.2

dbj|C93868|C93868 Dictyostelium discoideum slug cDNA, clone SSL809 36 2.8
gb|AA531984|AA531984 TgESTzz46b06.r1 TgME49 invivo Bradyzoite c... 36 2.8
gb|N60418|N60418 TgESTzy07a10.r1 TgRH Tachyzoite cDNA Toxoplasma... 36 2.8
gb|H32045|H32045 EST106774 Rat PC-12 cells, untreated Rattus sp... 36 2.8
gb|AA956789|AA956789 UI-R-E1-fr-h-01-0-UI.s1 UI-R-E1 Rattus nor... 36 2.8
gb|H33275|H33275 EST109117 Rat PC-12 cells, NGF-treated (9 days... 36 2.8
gb|AA531938|AA531938 TgESTzz45b08.r1 TgME49 invivo Bradyzoite c... 36 2.8
dbj|D41507|RICS4044A Rice cDNA, partial sequence (S4044_1A). 36 2.8
gb|AA799411|AA799411 EST188908 Normalized rat heart, Bento Soar... 36 2.8
gb|AA519671|AA519671 TgESTzz27c10.r1 TgME49 invivo Bradyzoite c... 36 2.8
dbj|D40678|RICS2786A Rice cDNA, partial sequence (S2786_1A). 36 2.8
gb|AA012430|AA012430 TgESTzz22b12.r1 TgME49cDNA Toxoplasma gond... 36 2.8
dbj|D40551|RICS2612A Rice cDNA, partial sequence (S2612_1A). 36 2.8
gb|AI008452|AI008452 EST202903 Normalized rat embryo, Bento Soa... 36 2.8
dbj|D41253|RICS3620A Rice cDNA, partial sequence (S3620_1A). 36 2.8
gb|AA923843|AA923843 UI-R-A1-dr-f-04-0-UI.s1 UI-R-A1 Rattus nor... 36 2.8
gb|AA799410|AA799410 EST188907 Normalized rat heart, Bento Soar... 36 2.8

1. A method of diagnosing a disorder characterized by expression of a human cancer associated antigen precursor coded for by a nucleic acid molecule, comprising:

contacting a biological sample isolated from a subject with an agent that specifically binds to the nucleic acid molecule, an expression product thereof, or a fragment of an expression product thereof complexed with an HLA molecule, wherein the nucleic acid molecule is a NA Group 1 nucleic acid molecule, and

determining the interaction between the agent and the nucleic acid molecule or the expression product as a determination of the disorder.

2. The method of claim 1, wherein the agent is selected from the group consisting of

(a)

a nucleotide acid molecule comprising NA group 1 nucleic acid molecules or a fragment thereof,

(b)

a nucleic acid molecule comprising NA group 3 nucleic acid molecules or a fragment thereof,

(c)

a nucleic acid molecule comprising NA group 17 nucleic acid molecules or a fragment thereof,

(d)

an antibody that binds to an expression product of NA group 1 nucleic acids,

(e)

an antibody that binds to an expression product of NA group 3 nucleic acids,

(f)

an antibody that binds to an expression product of NA group 17 nucleic acids,

5

(g)

and agent that binds to a complex of an HLA molecule and a fragment of an expression product of a NA group 1 nucleic acid,

10

(h)

an agent that binds to a complex of an HLA molecule and a fragment of an expression product of a NA group 3 nucleic acid, and

(I)

15

an agent that binds to a complex of an HLA molecule and a fragment of an expression product of a NA group 17 nucleic acid.

3. The method of claim 1, wherein the disorder is characterized by expression of a plurality of human cancer associated antigen precursors and wherein the agent is a plurality of agents, each of which is specific for a different human cancer associated antigen precursor, and wherein said plurality of agents is at least 2, at least 3, at least 4, at least 4, at least 6, at least 7, or at least 8, at least 9 or at least 10 such agents.

20

25 4.

The method of claims 1-3, wherein the agent is specific for a human cancer associated antigen precursor that is a breast, a gastric, a lung, a prostate, a renal or a colon cancer associated antigen precursor.

5.

30

A method for determining regression, progression or onset of a condition characterized by expression of abnormal levels of a protein encoded by a nucleic acid molecule that is a NA Group 1 molecule, comprising

monitoring a sample, from a patient who has or is suspected of having the condition, for a parameter selected from the group consisting of

(I)

5 the protein,

(ii)

a peptide derived from the protein,

(iii)

10 an antibody which selectively binds the protein or peptide, and

(iv)

15 protein and an MHC molecule,
as a determination of regression, progression or onset of said condition.

6. The method of claim 5, wherein the sample is a body fluid, a body effusion or a tissue.

20

7. The method of claim 5, wherein the step of monitoring comprises contacting the sample with a detectable agent selected from the group consisting of

(a)

25 an antibody which selectively binds the protein of (I), or the peptide of (ii),

(b)

a protein or peptide which binds the antibody of (iii), and

30

(c)

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a cell which presents the complex of the peptide and MHC molecule of (iv).

5

8. The method of claim 7, wherein the antibody, the protein, the peptide or the cell is labeled with a radioactive label or an enzyme.

9. The method of claim 5, comprising assaying the sample for the peptide.

10

10. The method of claim 5, wherein the nucleic acid molecule is a NA Group 3 molecule.

11. The method of claim 5, wherein the nucleic acid molecule is a NA Group 11 molecule.

15

12. The method of claim 5, wherein the nucleic acid molecule is a NA Group 12 molecule.

20

13. The method of claim 5, wherein the nucleic acid molecule is a NA Group 13 molecule.

14. The method of claim 5, wherein the nucleic acid molecule is a NA Group 14 molecule.

25

15. The method of claim 5, wherein the nucleic acid molecule is a NA Group 15 molecule.

16. The method of claim 5, wherein the nucleic acid molecule is a NA Group

30 16 molecule.

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17. The method of claim 5, wherein the protein is a plurality of proteins, the parameter is a plurality of parameters, each of the plurality of parameters being specific for a different of the plurality of proteins.

5 18. A pharmaceutical preparation for a human subject comprising
an agent which when administered to the subject enriches selectively the
presence of complexes of an HLA molecule and a human cancer associated antigen, and
a pharmaceutically acceptable carrier, wherein the human cancer
associated antigen is a fragment of a human cancer associated antigen precursor encoded by a
10 nucleic acid molecule comprises a NA Group 1 molecule.

19. The pharmaceutical preparation of claim 18, wherein the agent comprises
a plurality of agents, each of which enriches selectively in the subject complexes of an HLA
molecule and a different human cancer associated antigen.

15 20. The pharmaceutical preparation of claim 19, wherein the plurality is at
least two, at least three, at least four or at least 5 different such agents.

21. The pharmaceutical preparation of claim 18, wherein the nucleic acid
20 molecule is a NA Group 3 nucleic acid molecule.

22. The pharmaceutical preparation of claim 18, wherein the agent is selected
from the group consisting of

(1) an isolated polypeptide comprising the human cancer associated
25 antigen, or a functional variant thereof,

(2) an isolated nucleic acid operably linked to a promoter for expressing
the isolated polypeptide, or functional variant thereof,

(3) a host cell expressing the isolated polypeptide, or functional variant
thereof, and

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(4) isolated complexes of the polypeptide, or functional variant thereof, and an HLA molecule.

23. The pharmaceutical preparation of claims 18-22, further comprising an
5 adjuvant.

24. The pharmaceutical preparation of claim 18, wherein the agent is a cell expressing an isolated polypeptide comprising the human cancer associated antigen or a functional variant thereof, and wherein the cell is nonproliferative.

25. The pharmaceutical preparation of claim 18, wherein the agent is a cell expressing an isolated polypeptide comprising the human cancer associated antigen or a functional variant thereof, and wherein the cell expresses an HLA molecule that binds the polypeptide.

26. The pharmaceutical preparation of claim 18, wherein the agent is at least two, at least three, at least four or at least five different polypeptides, each coding for a different human cancer associated antigen or functional variant thereof.

27. The pharmaceutical preparation of claim 18, wherein the agent is a PP Group 2 polypeptide.

28. The pharmaceutical preparation of claim 18, wherein the agent is a PP Group 3 polypeptide or a PP Group 4 polypeptide.

29. The pharmaceutical preparation of claim 25, wherein the cell expresses one or both of the polypeptide and HLA molecule recombinantly.

30. The pharmaceutical preparation of claim 25, wherein the cell is nonproliferative.

41. The composition of claim 39, wherein the agent is an antibody.

42. A composition of matter comprising
a conjugate of the agent of claims 31-41 and a therapeutic or diagnostic
5 agent.

43. The composition of matter of claim 42, wherein the conjugate is of the
agent and a therapeutic or diagnostic that is a toxin.

10 44. A pharmaceutical composition comprising an isolated nucleic acid
molecule selected from the group consisting of:

(1)

NA Group 1 molecules, and

15 (2)

NA Group 2 molecules, and a pharmaceutically acceptable carrier.

45. The pharmaceutical composition of claim 44, wherein the isolated nucleic
acid molecule comprises a NA Group 3 or NA Group 4 molecule.

46. The pharmaceutical composition of claim 44, wherein the isolated nucleic
acid molecule comprises at least two isolated nucleic acid molecules coding for two different
polypeptides, each polypeptide comprising a different human cancer associated antigen.

25 47. The pharmaceutical composition of claims 44-46 further comprising an
expression vector with a promoter operably linked to the isolated nucleic acid molecule.

48. The pharmaceutical composition of claims 44-46 further comprising a host
cell recombinantly expressing the isolated nucleic acid molecule.

49. A pharmaceutical composition comprising
an isolated polypeptide comprising a PP Group 1 or a PP Group 2
polypeptide, and
a pharmaceutically acceptable carrier.

5

50. The pharmaceutical composition of claim 49, wherein the isolated
polypeptide comprises a PP Group 3 or a PP Group 4 polypeptide.

10 51. The pharmaceutical composition of claim 49, wherein the isolated
polypeptide comprises at least two different polypeptides, each comprising a different human
cancer associated antigen.

15 52. The pharmaceutical composition of claim 49, wherein the isolated
polypeptides are PP Group 11 polypeptides or HLA binding fragments thereof.

53. The pharmaceutical composition of claim 49, wherein the isolated
polypeptides are PP
Group 12 polypeptides or HLA binding fragments thereof.

20

54. The pharmaceutical composition of claim 49, wherein the isolated
polypeptides are PP Group 13 polypeptides or HLA binding fragments thereof.

25 55. The pharmaceutical composition of claim 49, wherein the isolated
polypeptides are PP Group 14 polypeptides or HLA binding fragments thereof.

56. The pharmaceutical composition of claim 49, wherein the isolated
polypeptides are PP Group 15 polypeptides or HLA binding fragments thereof.

30

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67. An isolated nucleic acid molecule selected from the group consisting of

(a)

a fragment of a nucleic acid selected from the group of nucleic acid
consisting of SEQ ID NOs presenting nucleic acid sequences among SEQ ID NOs. 1-816, of
5 sufficient length to represent a sequence unique within the human genome, and identifying a
nucleic acid encoding a human cancer associated antigen precursor,

(b)

complements of (a),

10 provided that the fragment includes a sequence of contiguous nucleotides
which is not identical to any sequence selected from the sequence group consisting of

(1) sequences having the GenBank accession numbers of Table 1

(correct?),

15 (2) complements of (1), and

(3) fragments of (1) and (2).

68. The isolated nucleic acid molecule of claim 67, wherein the sequence of
contiguous nucleotides is selected from the group consisting of:

20 (1)

at least two contiguous nucleotides nonidentical to the sequence group,

(2)

at least three contiguous nucleotides nonidentical to the sequence group,

(3)

25 at least four contiguous nucleotides nonidentical to the sequence group,

(4)

at least five contiguous nucleotides nonidentical to the sequence group,

(5)

30 at least six contiguous nucleotides nonidentical to the sequence group,

(6)

at least seven contiguous nucleotides nonidentical to the sequence group.

69. The isolated nucleic acid molecule of claim 67, wherein the fragment has a size selected from the group consisting of at least: 8 nucleotides, 10 nucleotides, 12 nucleotides, 14 nucleotides, 16 nucleotides, 18 nucleotides, 20, nucleotides, 22 nucleotides, 24 nucleotides, 26 nucleotides, 28 nucleotides, 30 nucleotides, 50 nucleotides, 75 nucleotides, 100 nucleotides, and 200 nucleotides.

70. The isolated nucleic acid molecule of claim 67, wherein the molecule encodes a polypeptide which, or a fragment of which, binds a human HLA receptor or a human antibody.

71. An expression vector comprising an isolated nucleic acid molecule of claims 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69 or 70 operably linked to a promoter.

72. An expression vector comprising a nucleic acid operably linked to a promoter, wherein the nucleic acid is a NA Group 2 molecule.

73. An expression vector comprising a NA Group 1 or Group 2 molecule and a nucleic acid encoding an HLA molecule.

74. A host cell transformed or transfected with an expression vector of claims 71, 72, or 73.

75. A host cell transformed or transfected with an expression vector of claim 71 or claim 72 and further comprising a nucleic acid encoding HLA.

76. An isolated polypeptide encoded by the isolated nucleic acid molecule of claims 59, 60, 61, 62, 63, 64, 65, or 66.

77. A fragment of the polypeptide of claim 76 which is immunogenic.

78. The fragment of claim 77, wherein the fragment, or a portion of the fragment, binds HLA or a human antibody.

5

79. An isolated fragment of a human cancer associated antigen precursor which, or portion of which, binds HLA or a human antibody, wherein the precursor is encoded by a nucleic acid molecule that is a NA Group 1 molecule.

10 80. The fragment of claim 79, wherein the fragment is part of a complex with HLA.

81. The fragment of claim 79, wherein the fragment is between 8 and 12 amino acids in length.

15

82. An isolated polypeptide comprising a fragment of the polypeptide of claim 76 of sufficient length to represent a sequence unique within the human genome and identifying a polypeptide that is a human cancer associated antigen precursor.

20 83. A kit for detecting the presence of the expression of a human cancer associated antigen precursor comprising
a pair of isolated nucleic acid molecules each of which consists essentially of a molecule selected from the group consisting of

25 (a) a 12-32 nucleotide contiguous segment of the nucleotide sequence of any of the NA Group 1 molecules and

(b) complements of ("a"), wherein the contiguous segments are nonoverlapping.

30

84. The kit of claim 83, wherein the pair of isolated nucleic acid molecules is constructed and arranged to selectively amplify an isolated nucleic acid molecule that is a NA Group 3 molecule.

5 85. A method for treating a subject with a disorder characterized by expression of a human cancer associated antigen precursor, comprising administering to the subject an amount of an agent, which enriches selectively in the subject the presence of complexes of an HLA molecule and a human cancer associated antigen, effective to ameliorate the disorder, wherein the human cancer associated antigen is a fragment of a human cancer associated antigen precursor encoded by a nucleic acid molecule selected from the group consisting of

(a)

a nucleic acid molecule comprising NA group 1 nucleic acid molecules,

(b)

a nucleic acid molecule comprising NA group 3 nucleic acid molecules,

(c)

a nucleic acid molecule comprising NA group 17 nucleic acid molecules.

86. The method of claim 85, wherein the disorder is characterized by expression of a plurality of human cancer associated antigen precursors and wherein the agent is a plurality of agents, each of which enriches selectively in the subject the presence of complexes of an HLA molecule and a different human cancer associated antigen.

87. The method of claim 86, wherein the plurality is at least 2, at least 3, at least 4, or at least 5 such agents.

88. The method of claims 85-87, wherein the agent is an isolated polypeptide selected from the group consisting of PP Group 1, PP Group 2, PP Group 3, PP Group 4, PP Group 5, PP Group 6, PP Group 7, PP Group 8, PP Group 9, PP Group 10, PP Group 11, PP Group 12, PP Group 13, PP Group 14, PP Group 15, PP Group 16 and PP Group 17 polypeptides.

89. The method of claims 85-88, wherein the disorder is cancer.

90. A method for treating a subject having a condition characterized by expression of a human cancer associated antigen precursor in cells of the subject, comprising:

(I)
removing an immunoreactive cell containing sample from the subject,

(ii)
contacting the immunoreactive cell containing sample to the host cell under conditions favoring production of cytolytic T cells against a human cancer associated antigen which is a fragment of the precursor,

(iii)
introducing the cytolytic T cells to the subject in an amount effective to lyse cells which express the human cancer associated antigen, wherein the host cell is transformed or transfected with an expression vector comprising an isolated nucleic acid molecule operably linked to a promoter, the isolated nucleic acid molecule being selected from the group of nucleic acid molecules consisting of NA Group 1, NA Group 2, NA Group 3, NA Group 4, NA Group 5, NA Group 6, NA Group 7, NA Group 8, NA Group 9, NA Group 10, NA Group 11, NA Group 12, NA Group 13, NA Group 14, NA Group 15, NA Group 16, and NA Group 17.

91. The method of claim 90, wherein the host cell recombinantly expresses an HLA molecule which binds the human cancer associated antigen.

92. The method of claim 90, wherein the host cell endogenously expresses an HLA molecule which binds the human cancer associated antigen.

93. A method for treating a subject having a condition characterized by expression of a human cancer associated antigen precursor in cells of the subject, comprising:

10 (I)
identifying a nucleic acid molecule expressed by the cells associated with said condition, wherein said nucleic acid molecule is a NA Group 1 molecule

15 (ii)
transfecting a host cell with a nucleic acid selected from the group consisting of

20 (a) the nucleic acid molecule identified,

25 (b)
a fragment of the nucleic acid identified which includes a segment coding for a human cancer associated antigen,

30 (c)
deletions, substitutions or additions to (a) or (b), and

(d)

degenerates of (a), (b), or (c);

(iii)

5 culturing said transfected host cells to express the transfected nucleic acid molecule, and;

(iv)

10 introducing an amount of said host cells or an extract thereof to the subject effective to increase an immune response against the cells of the subject associated with the condition.

94. The method of claim 93, further comprising:

(a)

15 identifying an MHC molecule which presents a portion of an expression product of the nucleic acid molecule,

20 wherein the host cell expresses the same MHC molecule as identified in (a) and wherein the host cell presents an MHC binding portion of the expression product of the nucleic acid molecule.

95. The method of claim 93, wherein the immune response comprises a B-cell
25 response or a T cell response.

96. The method of claim 95, wherein the response is a T-cell response which
comprises generation of cytolytic T-cells specific for the host cells presenting the portion of the
expression product of the nucleic acid molecule or cells of the subject expressing the human
30 cancer associated antigen.

97. The method of claim 93, wherein the nucleic acid molecule is a NA Group 3 molecule.

98. The method of claims 93 or 94, further comprising treating the host cells to render them non-proliferative.

99. A method for treating or diagnosing or monitoring a subject having a condition characterized by expression of an abnormal amount of a protein encoded by a nucleic acid molecule that is a NA Group 1 molecule, comprising

administering to the subject an antibody which specifically binds to the protein or a peptide derived therefrom, the antibody being coupled to a therapeutically useful agent, in an amount effective to treat the condition.

100. The method of claim 99, wherein the antibody is a monoclonal antibody.

101. The method of claim 100, wherein the monoclonal antibody is a chimeric antibody or a humanized antibody.

102. A method for treating a condition characterized by expression in a subject of abnormal amounts of a protein encoded by a nucleic acid molecule that is a NA Group 1 nucleic acid molecule, comprising

administering to a subject a pharmaceutical composition of any one of claims 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 47, and 58 in an amount effective to prevent, delay the onset of, or inhibit the condition in the subject.

103. The method of claim 102, wherein the condition is cancer.

104. The method of claims 102-103, further comprising first identifying that the subject expresses in a tissue abnormal amounts of the protein.

105. A method for treating a subject having a condition characterized by expression of abnormal amounts of a protein encoded by a nucleic acid molecule that is a NA Group 1 nucleic acid molecule, comprising

(i) identifying cells from the subject which express abnormal amounts of
5 the protein;
(ii) isolating a sample of the cells;
(iii) cultivating the cells, and
(iv) introducing the cells to the subject in an amount effective to provoke an immune response against the cells.

106. The method of claim 105, wherein the cells express a protein selected from the group consisting of a PP Group 11 protein, a PP Group 12 protein, a PP Group 13 protein, PP Group 14 protein, a PP Group 15 protein and a PP Group 16 protein.

107. The method of claim 105, further comprising rendering the cells non-proliferative, prior to introducing them to the subject.

108. A method for treating a pathological cell condition characterized by
20 aberrant expression of a protein encoded by a nucleic acid molecule that is a NA Group 1 nucleic acid molecule, comprising

administering to a subject in need thereof an effective amount of an agent which inhibits the expression or activity of the protein.

25 109. The method of claim 108, wherein the agent is an inhibiting antibody which selectively binds to the protein and wherein the antibody is a monoclonal antibody, a chimeric antibody or a humanized antibody.

110. The method of claim 108, wherein the agent is an antisense nucleic acid
30 molecule which selectively binds to the nucleic acid molecule which encodes the protein.

111. The method of claim 108, wherein the nucleic acid molecule is a NA Group 3 nucleic acid molecule.

112. A composition of matter useful in stimulating an immune response to a plurality of a protein encoded by nucleic acid molecules that are NA Group 1 molecules, comprising

a plurality of peptides derived from the amino acid sequences of the proteins, wherein the peptides bind to one or more MHC molecules presented on the surface of the cells which express an abnormal amount of the protein.

113. The composition of matter of claim 112, wherein at least a portion of the plurality of peptides bind to MHC molecules and elicit a cytolytic response thereto.

114. The composition of matter of claim 113, further comprising an adjuvant.

115. The composition of matter of claim 114, wherein said adjuvant is a saponin, GM-CSF, or an interleukin.

116. An isolated antibody which selectively binds to a complex of:

(i)

a peptide derived from a protein encoded by a nucleic acid molecule that is a NA Group 1 molecule and

(ii)

and an MHC molecule to which binds the peptide to form the complex, wherein the isolated antibody does not bind to (i) or (ii) alone.

117. The antibody of claim 116, wherein the antibody is a monoclonal antibody, a chimeric antibody or a humanized antibody.

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LUCA15

DX38237E

KEEPTPTPKYVUPPLIGLCEYGGSDYEEEEEETQPPPTAQIQKREEQTKKENEEDKLTWNKLACLRCRRQFFINKEVL 970
PELVNRNGDEEHPLKRGVAAAYSGSDHRE.....ELVERLESEEEKLADWKKMACLLCRRQFFPNKDAL 662
DLPKLASDDKPSFPRLVAAAYSGSDSEE.....EQERGGPEREEKLTDWQKLACLRCRRQFFPSKEAL 233

HY-10-13

LUCA15

DX38237F

TVHQQLSDLPKQHLETHRKTKQSEGLAYLERERE.CKFKCRGNDRRREKLQSFDSPEKRIKYSRETDSDRKLVDKEDID 1050
VARIHQQLSDLIHQNDIYRRGNLSEQLLEALELRERE.MKYRDRAAERREKYGIPEPPEPKRKKQFDAGTV..NVEQPTKDGID 742
TVHQQLSGLIHQNHLETHKRAHLSHIFTLEALKRIIDMEQMKYRDRAAERREKYGIPEPPEPKRKKYGGJSTASVDPEQPTKIDGLC 316

HY-10-14

LUCA15

DX38237E

TSSIGGAVQATGWRKGTGIGYCHPGLASSFEAEGRMRGFSVGASGKTSKRQSNETYRDVAVRRVMFARYKELD 1123
HENIGNKMLQAMGWREGSGIGRNGOCTTAPIEAQVRLKGCAGLCAKGSAYGLSGADSYKDAVRKAMFARFIEME 815
SDMIGSRMLQAMGWKEGSGIGRKKQGLVTPIEAQTVRUGSSGLGARGSSYGVTSTESYKETLHKTMVTRNEHAQ 389

Figure 1

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2851

792 (cont)

Fig 2 (cont'd)

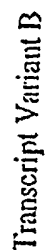
[illegible]

Fig. 3a

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Figure 3b.

227bp exon:

GACTGGGTGAAAGCTTTTCTGCAGCAGTCATGTTAAAAACCTTGTGTTGACTTTCCTCG
TGTCTGAAACTAAC
AGAACTGGACCTTTTCGGACTGGGTGAAAGCTTTTCTGCAGCAGTCATGTTGAAAACC
TTGTGTTGACTTTCCTT
CGTGTTCTGAAATGGGAGCATAAAAGTTTACTCCGCCACTTCGTCTTAAATAGCAAAAC
TTTGCTGTTTCTGCAG

137bp exon:

ATCTAGGACCTTGTTACAGAACTCTGCCAAAAAAAAAATGTTTACAGAAGAATGTGCTGT
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TGCTGGTGTGTAGATTTCAAACCTCTCTGGACAATA.TGAATAACACTGTCTTTGTTTCTAC
AG

0046265-050700

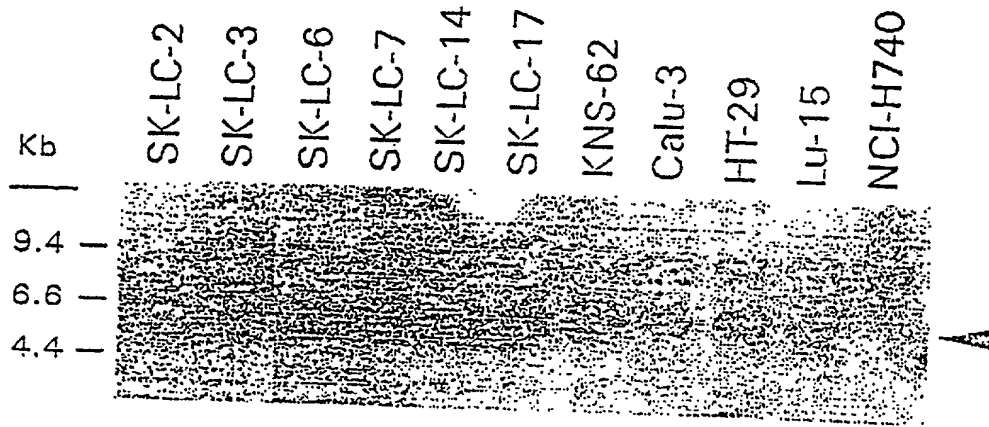


Figure 4

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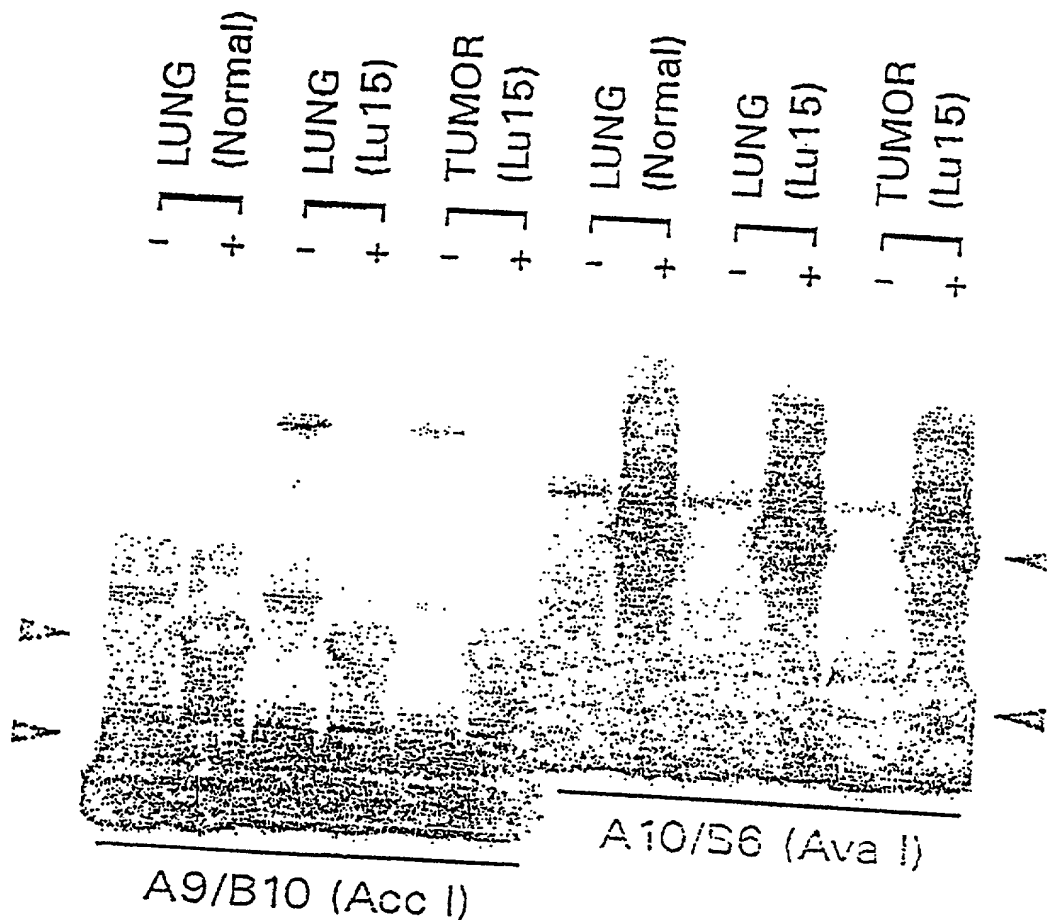


Figure 5

617 720 2441

LVD 5499-1 US

Attorney Docket No. L0461/7078

DECLARATION FOR PATENT APPLICATION

As a below named inventor, I hereby declare that:

My residence, post office address and citizenship are as stated below next to my name.

I believe I am the original, first and sole inventor (if only one name is listed below) or an original, first and joint inventor (if plural names are listed below) of the subject matter which is claimed and for which a patent is sought on the invention entitled

CANCER ASSOCIATED NUCLEIC ACIDS AND POLYPEPTIDES

the specification of which is attached hereto unless the following is checked:

☒ was filed on July 15, 1998, as PCT application no. PCT/US98/14679, now U.S. application no. 09/462,929, bearing attorney docket no. L0461/7078, and was amended on (if applicable).

I hereby state that I have reviewed and understand the contents of the above identified specification, including the claims, as amended by any amendment referred to above.

I acknowledge the duty to disclose information which is material to the examination of this application in accordance with Title 37, Code of Federal Regulations, §1.56.

I hereby claim foreign priority benefits under Title 35, United States Code, §119(a)-(d) or §365(b) of any foreign application(s) for patent or inventor's certificate, or section 365(a) of any PCT International application designating at least one country other than the United States listed below and have also identified below any foreign application for patent or inventor's certificate or PCT International application having a filing date before that of the application on which priority is claimed:

Prior Foreign PCT International Application(s) and any priority claims under 35 U.S.C. §§119 and 365(a),(b):

			Priority Claimed
<u>9721697.2</u>	<u>Great Britain</u>	<u>11 October 1997</u>	<input checked="" type="checkbox"/> <input type="checkbox"/>
(Number)	(Country- if PCT, so indicate)	(DD/MM/YY Filed)	YES NO
<u> </u>	<u> </u>	<u> </u>	<input type="checkbox"/> <input type="checkbox"/>
(Number)	(Country- if PCT, so indicate)	(DD/MM/YY Filed)	YES NO
<u> </u>	<u> </u>	<u> </u>	<input type="checkbox"/> <input type="checkbox"/>
(Number)	(Country- if PCT, so indicate)	(DD/MM/YY Filed)	YES NO

I hereby claim the benefit under Title 35, United States Code, §119(e) of any United States provisional application(s) listed below:

<u>60/061,599</u>	<u>10 October 1997</u>
(Application Number)	(filing date)
<u>60/061,765</u>	<u>10 October 1997</u>
(Application Number)	(filing date)

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I hereby claim the benefit under Title 35, United States Code, §120 of any United States application(s), or §365(c) of any PCT International application(s) designating the United States of America listed below and, insofar as the subject matter of each of the claims of this application is not disclosed in the prior United States or PCT International application in the manner provided by the first paragraph of Title 35, United States Code, §112, I acknowledge the duty to disclose material information as defined in Title 37, Code of Federal Regulations, §1.56, which became available between the filing date of the prior application and the national or PCT International filing date of this application:

<u>08/896,164</u>	<u>17 July 1997</u>	<u>Pending</u>
(Application No.)	(filing date)	(status-patented, pending, abandoned)
<u>08/948,705</u>	<u>10 October 1997</u>	<u>Pending</u>
(Application No.)	(filing date)	(status-patented, pending, abandoned)
<u>09/102,322</u>	<u>22 June 1998</u>	<u>Pending</u>
(Application No.)	(filing date)	(status-patented, pending, abandoned)

PCT International Applications designating the United States:

<u>(PCT Appl. No.)</u>	<u>(U.S. Ser. No.)</u>	<u>(PCT filing date)</u>	<u>(status-patented, pending, abandoned)</u>
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I hereby appoint the following attorney(s) and/or agent(s) to prosecute this application and to transact all business in the Patent and Trademark Office connected therewith:

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I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with

the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of the application or any patent issued thereon.

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Docket No.: L0461/7078

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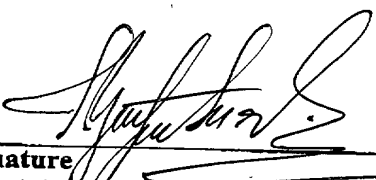
Homburg/Saar, Germany

Post Office Address:

Med. Klinik I, Universität des Saarlandes, D-66421 Homburg, Germany

Date

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Inventor's signature

Full name of sixth joint inventor:

Ivan Gout

Citizenship:

Ukraine

Residence:

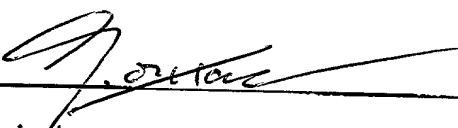
London, England

Post Office Address:

91 Riding House Street, London W1P 8BT, England

9.05.2000

Date


Inventor's signature

Full name of seventh joint inventor:

Michael O'Hare

Citizenship:

Great Britain

Residence:

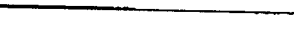
London, England

Post Office Address:

91 Riding House Street, London W1P 8BT, England

9/5/00

Date


Inventor's signature

Full name of eighth joint inventor:

Yuichi Obata

Citizenship:

Japan

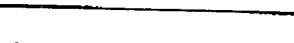
Residence:

Nagoya, Japan

Post Office Address:

Chikusa-ku, Nagoya 464, Japan

Date


Inventor's signature

Full name of ninth joint inventor:

Michael Pfreundschuh

Citizenship:

Germany


Residence:

Homburg/Saar, Germany

Post Office Address:

Med. Klinik I, Universitat des Saarlandes, D-66421 Homburg, Germany

Date


Inventor's signature

Full name of tenth joint inventor:

Özlem Türeci

Citizenship:

Germany


Residence:

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Post Office Address:

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Date


Inventor's signature

Full name of eleventh joint inventor:

Ugur Sahin

Citizenship:

Turkey

Residence:

Homburg/Saar, Germany

Post Office Address:

Med. Klinik I, Universitat des Saarlandes, D-66421 Homburg, Germany

Date

5. MAY. 2000 10:30

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NO. 2286

P. 5/7

Docket No.: E0461/7078

Page 4 of 4

Inventor's signature

Date

Full name of sixth joint inventor:

Ivan Gout

Citizenship:

Ukraine

Residence:

London, England

Post Office Address:

91 Riding House Street, London W1P 8BT, England

Inventor's signature

Date

Full name of seventh joint inventor:

Michael O'Hare

Citizenship:

Great Britain

Residence:

London, England

Post Office Address:

91 Riding House Street, London W1P 8BT, England

Inventor's signature

Date

Full name of eighth joint inventor:

Yuichi Obata

Citizenship:

Japan

Residence:

Nagoya, Japan

Post Office Address:

Chikusa-ku, Nagoya 464, Japan

Inventor's signature

Date

Full name of ninth joint inventor:

Michael Pfreundschuh

Citizenship:

Germany

Residence:

Homburg/Saar, Germany

Post Office Address:

Med. Klinik I, Universitat des Saarlandes, D-66421 Homburg, Germany

Inventor's signature

Date

Full name of tenth joint inventor:

Özlem Türeci

Citizenship:

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Residence:

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Inventor's signature

Date

Full name of eleventh joint inventor:

Ugur Sahin

Citizenship:

Turkey

Residence:

Homburg/Saar, Germany

Post Office Address:

Med. Klinik I, Universitat des Saarlandes, D-66421 Homburg, Germany

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Stockert, Elisabeth
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O'Hare, Michael
Obata, Yuichi
Pfreundschuh, Michael
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<211> 1113

<212> DNA

<213> Homo Sapiens

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<210> 17

<211> 731

<212> DNA

<213> Homo Sapiens

<400> 17

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<211> 1145
<212> DNA
<213> Homo Sapiens

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<211> 1106
<212> DNA
<213> Homo Sapiens

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 <211> 484
 <212> DNA
 <213> Homo Sapiens

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 <212> DNA
 <213> Homo Sapiens

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<210> 22
 <211> 1070
 <212> DNA
 <213> Homo Sapiens

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<210> 23

<211> 861

<212> DNA

<213> Homo Sapiens

<400> 23

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<210> 24

<211> 985

<212> DNA

<213> Homo Sapiens

<400> 24

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<210> 25

<211> 545

<212> DNA

<213> Homo Sapiens

<400> 25

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<210> 26

<211> 374

<212> DNA

<213> Homo Sapiens

<400> 26

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<210> 27

<211> 552

<212> DNA

<213> Homo Sapiens

<400> 27

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<210> 28

<211> 502

<212> DNA

<213> Homo Sapiens

<400> 28

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<210> 29

<211> 537
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 <213> Homo Sapiens

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<210> 30
 <211> 3872
 <212> DNA
 <213> Homo Sapiens

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<210> 31

<211> 655

<212> DNA

<213> Homo Sapiens

<400> 31

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 agatggaagg ccgccagagg aaagtgccca tgaatgatg gaggaggaag aggaaatccc 120
 aaaacctaag tctgtggttg caccgccagg tgctcctaag aaagagcatg taaatgtagt 180
 attcattggg cacgtanatg ctggcaagtc aaccattgga ggacaaataa tgtatttgac 240
 tggaatgggt gacaaaagga cgcttgaaaa gtatgaaaga gaagctaaag agaaaaacag 300
 agaaacttgg tacttgtctt gggccttaga cacaaatcag gaagaacgag acaagggtaa 360
 aacagtagaa gtgggtcgtg cctattttga aaccgaaaag aacatttcac aattctagat 420
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 aattccanga aggtgaggag atgcttctga accccgagga aaagatcctt tgaatatctc 540
 cgtaggagtt caccctctgg actccttcac tcaggggttt ggggagcacc cacaggggac 600
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<210> 32

<211> 466

<212> DNA

<213> Homo Sapiens

<400> 32

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accttctctga	agacctgctc	gcacactgca	tcccttgtag	tcagttccag	ctcgtgccga	180
attcgggcacg	agctcgtgcc	gaattcggca	cgagggaagc	actactccca	gcgctgggcc	240
caggaggacc	tgctggagga	gcagaaggat	ggggcccggg	cagcggctgt	ggctgacaag	300
aagaaaggcc	tcatggggcc	actgaccgaa	ctggacacta	aagatgtgga	tgccctgctg	360
aagaagtctg	aggcccagca	tgaacagccg	gaagatggat	gcccctttgg	tgccctgacg	420
cagcgcctcc	tgcaggccct	ggtggaggaa	aatattatct	tttccc		466

<210> 33

<211> 293

<212> DNA

<213> Homo Sapiens

<400> 33

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acagatgatg	ctgaatagcc	cgctgtttac	tgcaaactct	cagctgcagg	agcagatgag	120
gccacagctc	ccagccttcc	tgcagcagat	gcagaatcca	gacacactat	cagccatgtc	180
aaacccaaga	gcaatgcagg	ctttaatgca	gatccagcag	gggctacaga	cattagccac	240
tgaagcacct	ggcctgattc	cgagcttcac	tccaggtgtg	ggggtggggn	tct	293

<210> 34

<211> 456

<212> DNA

<213> Homo Sapiens

<400> 34

caaagcctta	agtcagagcc	tgctagaatg	tgtccagggt	tacagctata	ctgcacagca	60
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cattcaattg	aaatgcagga	tgggtgactg	ccattccaag	ttccatcttc	ctggcagatc	180
agcacagggt	tccccagaag	ttcatatcct	ggattacagg	tgtatgaaac	catggtacca	240
tacagaaaag	ttgatgaatg	tgtagcagga	gactcctttg	tattttccca	ggtttttagcc	300
actgctccca	aatgataagg	agggtgagga	gtcacatatg	gaacttccat	catgtcgtct	360
tcttgctcaa	aatatccctg	gtcatctttg	agtttagtac	agtctccaaa	atctatatga	420
ggagggaggc	cacagtctat	tggcatacca	aatttt			456

<210> 35

<211> 679

<212> DNA

<213> Homo Sapiens

<400> 35

ggcggcgctc	gtgtccgagg	tcactagttt	cccggtagtt	cagctgcaca	tgaatagaac	60
agcaatgaga	gccagtcaga	aggactttga	aaattcaata	aatcaagtga	aactcttgaa	120
aaaggatcca	ggaaacgaag	tgaagctaaa	actctacgag	ctatataagc	aggccactga	180
aggaccttgt	aacatgccca	aaccagggtg	atttgacttg	atcaacaagg	ccaaatggga	240
cgcattggaat	gcccttgcca	gcctgccccaa	ggaagctgcc	aggcagaact	atgtggattt	300
ggtgtccagt	ttgagtcctt	cattggaatc	ctctagtcag	gtggagcctg	gaacagacag	360
gaaatcaact	gggtttgaaa	ctctggtggt	gacctccgaa	gatggcatca	caaagatcat	420
gttcaaccgg	ccccaaaaaga	aaaatgccat	aaacactgag	atgtatcatg	aaattatgag	480
tgcaactaaa	gctgccagca	aggatgactc	aatcatcact	gttttaacag	gaaatggtga	540
ctattacagt	agtgggaatg	atctgactaa	cttcaactgat	attccccctg	gtggagtana	600
ggagaaaagc	aaaaataatg	ccgttttact	gaagggaatt	tgtgggctgt	tttatagaat	660
tctctaagcc	tctgattgc					679

<210> 36
 <211> 689
 <212> DNA
 <213> Homo Sapiens

<400> 36
 ctaaaccagt ggacatatca ggccatggtc cacgaactac taggcataaa caacaatcgg 60
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 tcaatagcag acatgaaggc gtttggtgag aattatccac agttcaagaa aatgtctggg 300
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 ctgctggagg tttcagaggt tgagcaagaa ctggcctgtc aaaatgacca ttctagtgtc 420
 ctccagaata taaaaaggct tctgcagaac cccaaagtga cagagtttga tgctgcccg 480
 ctggtgatgc tttatgcttt acattatgag cgacacagca gcaatagcct gccaggacta 540
 atgatgncc tcaggaataa aggtgtttct gagaagtatc gaaagctcgt gtctgcagtt 600
 gttgaatatg gtggtaaaac gagtcaaggg aagtgcctc ctcagcccca aagatgctgt 660
 tggctatcac caacaattc ctcaaaggg 689

<210> 37
 <211> 443
 <212> DNA
 <213> Homo Sapiens

<400> 37
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 tttattcctt ccggtgggtt cgcggtctag ctgaccaaga acggaactgg ggactttcgc 120
 agtgagagtt acagctctta aagatggcac cgaccaggc cgggcgcggt ggctcaggcc 180
 tgcaatccca gcactttggg aggcggaggc aggtgaatca cgaggtcagg aaatcgagac 240
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 tgggtggctgg cacctgtagt cccagctact tgggaggctg agccaggaaa gtggcatgaa 360
 cccgcgaggc agagcttgca ataagccgag atcgtgccaa tgcactccag cctgggcaac 420
 agaaggagac actgtctcaa aaa 443

<210> 38
 <211> 442
 <212> DNA
 <213> Homo Sapiens

<400> 38
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 acatttctga tgctcttagt gagcgggata aagtaaaatt cactgttcac acaaagattc 180
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 aatatttggc aatattcaag aagacagttg cgatgcatga agtgttcctg tgtcgtgtgg 360
 cagcacatcc tattttgaga agagatttaa atttccatgt cttcttggaa tataatcaag 420
 atttgagtgt gcgaggaaaa aa 442

<210> 39
 <211> 692
 <212> DNA
 <213> Homo Sapiens

<400> 39

cagggacagg ccctatctta tttttttttt catcttcatc atccacttct gcttacagtt 60
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 ataaccacagc ttttcttttt ggcttttagc ccattcagac tttgccagag tcaagccaag 360
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 tttgatagcc accaactgta cctgggtang caaagtcaga tttttgagaa nctttttcct 660
 gatttgaagt ttttaattacc ttaatttcct tt 692

<210> 40

<211> 619

<212> DNA

<213> Homo Sapiens

<400> 40

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 ccacttcagg agccactgga ggctgacagg acctcggaag agctgacaga ggccaagacc 180
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<210> 41

<211> 153

<212> PRT

<213> Homo Sapiens

<400> 41

Pro Glu Ser Lys Pro Ile Met Thr Ser Ser Glu Ala Phe Glu Pro Pro
 1 5 10 15
 Lys Tyr Leu Met Leu Gly Gln Gln Ala Val Gly Gly Val Pro Ile Gln
 20 25 30
 Pro Ser Val Arg Thr Gln Met Trp Leu Thr Glu Gln Leu Arg Thr Asn
 35 40 45
 Pro Leu Glu Gly Arg Asn Thr Glu Asp Ser Tyr Ser Leu Ala Pro Trp
 50 55 60
 Gln Gln Gln Gln Ile Glu Phe Arg Gln Gly Ser Glu Thr Pro Met Gln
 65 70 75 80
 Val Leu Thr Gly Ser Ser Arg Gln Ser Tyr Ser Pro Gly Tyr Gln Asp
 85 90 95
 Phe Ser Lys Trp Glu Ser Met Leu Lys Lys Glu Gly Leu Leu Arg Gln
 100 105 110
 Lys Glu Ile Val Asp Arg Gln Lys Gln Ile Thr His Leu Ile Arg Asp
 115 120 125
 Asn Glu Leu Pro Ala His Ala Met Leu Gly His Tyr Val Asn Cys Glu
 130 135 140

Asp Ser Tyr Val Ala Ser Leu His His
145 150

<210> 42
<211> 95
<212> PRT
<213> Homo Sapiens

<400> 42
Ile Leu Leu Glu Phe Tyr Leu Trp Gln Ile Gly Arg Tyr Ile Phe Val
1 5 10 15
His Val Asn Asn His Ile Tyr Ile Lys Leu Tyr Asn Cys Thr Phe Leu
20 25 30
Thr Ala Leu Ser Gln Val Ala Leu Ser Phe Pro Ser Ile Asn Gly Leu
35 40 45
Ile Phe Val Ser Phe Ala Phe Phe Arg Val Val Asn Ser Tyr Cys Pro
50 55 60
Leu Gln Phe Val Gln Phe Leu Arg Cys Leu Leu Leu Lys Arg Met
65 70 75 80
Leu Gly Glu Phe Ile Phe His Lys Glu Met Glu His Tyr Leu Lys
85 90 95

<210> 43
<211> 114
<212> PRT
<213> Homo Sapiens

<400> 43
Ser Lys Leu Leu Leu Ser Gly Thr Ala Asp Gly Ala Asp Leu Arg Thr
1 5 10 15
Val Asp Pro Glu Thr Gln Ala Arg Leu Glu Ala Leu Leu Glu Ala Ala
20 25 30
Gly Ile Gly Lys Leu Ser Thr Ala Asp Gly Lys Ala Phe Ala Asp Pro
35 40 45
Glu Val Leu Arg Arg Leu Thr Ser Ser Val Ser Cys Ala Leu Asp Glu
50 55 60
Ala Ala Ala Leu Thr Arg Met Arg Ala Glu Ser Thr Ala Asn Ala Gly
65 70 75 80
Gln Ser Asp Asn Arg Ser Leu Ala Glu Ala Cys Ser Gly Asp Val Ala
85 90 95
Val Arg Lys Leu Leu Ile Glu Gly Arg Ser Val Phe Glu Leu Pro Glu
100 105 110
Glu Gly

<210> 44
<211> 132
<212> PRT
<213> Homo Sapiens

<400> 44
Gly Glu Lys Glu Gln Asp Lys Pro Pro Asn Leu Val Leu Lys Asp Lys
1 5 10 15
Val Lys Pro Lys Gln Asp Thr Lys Tyr Asp Leu Ile Leu Asp Glu Gln
20 25 30

Ala Glu Asp Ser Lys Ser Ser His Ser His Thr Ser Lys His Lys Lys
 35 40 45
 Lys Thr His His Cys Ser Glu Glu Lys Glu Asp Glu Asp Tyr Met Pro
 50 55 60
 Ile Lys Asn Thr Asn Gln Asp Ile Tyr Arg Glu Met Gly Phe Gly His
 65 70 75 80
 Tyr Glu Glu Glu Glu Ser Cys Trp Glu Lys Gln Lys Ser Glu Lys Arg
 85 90 95
 Asp Arg Thr Gln Asn Arg Ser Arg Ser Arg Ser Arg Glu Arg Asp Gly
 100 105 110
 His Tyr Ser Asn Ser His Lys Ser Lys Tyr Gln Thr Asp Leu Tyr Glu
 115 120 125
 Arg Glu Arg Ser
 130

<210> 45
 <211> 214
 <212> PRT
 <213> Homo Sapiens

<400> 45
 Lys Thr Gln Glu Lys Pro Pro Lys Glu Leu Val Asn Glu Trp Ser Leu
 1 5 10 15
 Lys Ile Arg Lys Glu Met Arg Val Val Asp Arg Gln Ile Arg Asp Ile
 20 25 30
 Gln Arg Glu Glu Glu Lys Val Lys Arg Ser Val Lys Asp Ala Ala Lys
 35 40 45
 Lys Gly Gln Lys Asp Val Cys Ile Val Leu Ala Lys Glu Met Ile Arg
 50 55 60
 Ser Arg Lys Ala Val Ser Lys Leu Ala Ser Lys Ala His Met Asn Ser
 65 70 75 80
 Val Leu Met Gly Met Lys Asn Gln Leu Ala Val Leu Arg Val Ala Gly
 85 90 95
 Ser Leu Gln Lys Ser Thr Glu Val Met Lys Ala Met Gln Ser Leu Val
 100 105 110
 Lys Ile Pro Glu Ile Gln Ala Thr Met Arg Glu Leu Ser Lys Glu Met
 115 120 125
 Met Lys Ala Gly Ile Ile Glu Glu Met Leu Glu Asp Thr Phe Glu Ser
 130 135 140
 Met Asp Asp Gln Glu Glu Met Glu Glu Glu Ala Glu Met Glu Ile Asp
 145 150 155 160
 Arg Ile Leu Phe Glu Ile Thr Ala Gly Ala Leu Gly Lys Ala Pro Ser
 165 170 175
 Lys Val Thr Asp Ala Leu Pro Glu Pro Glu Pro Pro Gly Ala Met Ala
 180 185 190
 Ala Ser Glu Asp Glu Glu Glu Glu Glu Glu Leu Glu Ala Met Gln Ser
 195 200 205
 Arg Leu Ala Thr Arg Ser
 210

<210> 46
 <211> 248
 <212> PRT
 <213> Homo Sapiens

<400> 46

Gly Ser Arg Glu Thr Leu Ala Phe Val Pro Leu Leu Arg Leu Leu
 1 5 10 15
 Glu Ala Thr Leu Ser Pro Gly Arg Ala Phe Cys Ser Pro Ile Ser Ser
 20 25 30
 Lys Ile Gln Pro Ala Gln Val Ala Gly His Glu Leu Cys Ser Gly Ser
 35 40 45
 Trp Asn Leu Thr Leu Val Ala Ser Gly Pro Val Ser Met Ala Ala Glu
 50 55 60
 His Leu Leu Pro Gly Pro Pro Pro Ser Leu Ala Asp Phe Leu Glu Ala
 65 70 75 80
 Gly Gly Lys Gly Thr Glu Arg Gly Ser Gly Ser Ser Lys Pro Thr Gly
 85 90 95
 Ser Ser Gly Gly Pro Arg Met Ala Ser Phe Pro Lys Thr Lys Phe Asn
 100 105 110
 Glu Tyr Lys Asp Val Leu Pro Cys Met Thr Ser Ser Arg Gly Gly Lys
 115 120 125
 Ile Lys Ala Thr Asp Phe Met Val Ala Met Arg Cys Leu Gly Ala Ser
 130 135 140
 Pro Thr Pro Gly Glu Val Gln Arg His Leu Gln Thr His Gly Ile Asp
 145 150 155 160
 Gly Asn Gly Glu Leu Asp Phe Ser Thr Phe Leu Thr Ile Met His Met
 165 170 175
 Gln Ile Lys Gln Glu Asp Pro Lys Lys Glu Ile Leu Leu Ala Met Leu
 180 185 190
 Met Val Asp Lys Glu Lys Lys Gly Tyr Val Met Ala Ser Asp Leu Arg
 195 200 205
 Ser Lys Leu Thr Ser Gly Glu Lys Leu Thr His Lys Glu Val Asp Asp
 210 215 220
 Leu Phe Arg Glu Ala Asp Ile Glu Pro Asn Gly Lys Val Lys Tyr Asp
 225 230 235 240
 Glu Phe Ile His Lys Ile Thr Leu
 245

<210> 47

<211> 177

<212> PRT

<213> Homo Sapiens

<400> 47

Leu Cys Cys Met His Tyr Cys Cys Lys Ser Cys Trp Asn Glu Tyr Leu
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 Thr Thr Arg Ile Glu Gln Asn Leu Val Leu Asn Cys Thr Cys Pro Ile
 20 25 30
 Ala Asp Cys Pro Ala Gln Pro Thr Gly Ala Phe Ile Arg Ala Ile Val
 35 40 45
 Ser Ser Pro Glu Val Ile Ser Lys Tyr Lys Ala Leu Leu Arg Gly Tyr
 50 55 60
 Val Glu Ser Cys Ser Asn Leu Thr Trp Cys Thr Asn Pro Gln Gly Cys
 65 70 75 80
 Asp Arg Ile Leu Cys Arg Gln Gly Leu Gly Cys Gly Thr Thr Cys Ser
 85 90 95
 Lys Cys Gly Trp Ala Ser Cys Phe Asn Cys Ser Phe Pro Glu Ala His
 100 105 110
 Tyr Pro Ala Ser Cys Gly His Met Ser Gln Trp Val Asp Asp Gly Gly

115 120 125
 Tyr Tyr Asp Gly Met Ser Val Glu Ala Lys His Leu Ala Lys Leu Ile
 130 135 140
 Ser Lys Arg Cys Pro Ser Cys Gln Ala Pro Ile Glu Asn Glu Gly Cys
 145 150 155 160
 Leu His Met Thr Cys Ala Lys Cys Asn His Gly Phe Cys Trp Arg Cys
 165 170 175
 Leu

<210> 48
 <211> 102
 <212> PRT
 <213> Homo Sapiens

<400> 48
 Glu Lys Gly Leu His Ile Asp Gln Leu Val Cys Leu Val Leu Glu Ala
 1 5 10 15
 Gln Lys Gly Pro Asn Pro Pro Gly Thr Leu Gly His Thr Val Ala Gly
 20 25 30
 Gly Val Ala Cys Thr Thr Thr Val Leu Ser Cys Leu His Leu Leu Ser
 35 40 45
 Gln Gly Tyr Lys Arg Asp Arg Pro Gln Ile Leu Met Tyr Ala Ala Pro
 50 55 60
 Pro Met Gly Pro Cys Arg Gly Ala His Phe Cys Gly Ser Ser Gln Thr
 65 70 75 80
 Ser Pro Pro Lys Pro Val Ala Thr Leu Ser Leu Leu Pro Cys Pro Leu
 85 90 95
 Pro Pro Leu Lys Asn Gly
 100

<210> 49
 <211> 179
 <212> PRT
 <213> Homo Sapiens

<400> 49
 His Lys Pro Cys Asn Pro Arg Glu Lys Glu Arg Ile Gln Asn Ala Gly
 1 5 10 15
 Gly Ser Val Met Ile Gln Arg Val Asn Gly Ser Leu Ala Val Ser Arg
 20 25 30
 Ala Leu Gly Asp Tyr Asp Tyr Lys Cys Val Asp Gly Lys Gly Pro Thr
 35 40 45
 Glu Gln Leu Val Ser Pro Glu Pro Glu Val Tyr Glu Ile Leu Arg Ala
 50 55 60
 Glu Glu Asp Glu Phe Ile Ile Leu Ala Cys Asp Gly Ile Trp Asp Val
 65 70 75 80
 Met Ser Asn Glu Glu Leu Cys Glu Tyr Val Lys Ser Arg Leu Glu Val
 85 90 95
 Ser Asp Asp Leu Glu Asn Val Cys Asn Trp Val Val Asp Thr Cys Leu
 100 105 110
 His Lys Gly Ser Arg Asp Asn Met Ser Ile Val Leu Val Cys Phe Ser
 115 120 125
 Asn Ala Pro Lys Val Ser Asp Glu Ala Val Lys Lys Asp Ser Glu Leu
 130 135 140

Asp Lys His Leu Glu Ser Ile Met Glu Asn Leu Ala Lys Glu Cys Leu
 145 150 155 160
 Ile Leu Pro Met Ser Cys Ala Ser Cys Leu Gln Lys Ile Ser Gln Ile
 165 170 175
 Cys Leu Leu

<210> 50
 <211> 163
 <212> PRT
 <213> Homo Sapiens

<400> 50
 Asp Leu Pro Thr Leu Glu Asp His Gln Lys Gln Ser Gln Gln Leu Lys
 1 5 10 15
 Asp Ser Glu Leu Lys Ser Thr Glu Leu Gln Glu Lys Val Thr Glu Leu
 20 25 30
 Glu Ser Leu Leu Glu Glu Thr Gln Ala Ile Cys Arg Glu Lys Glu Ile
 35 40 45
 Gln Leu Glu Ser Leu Arg Gln Arg Glu Ala Glu Phe Ser Ser Ala Gly
 50 55 60
 His Ser Leu Gln Asp Lys Gln Ser Val Glu Glu Thr Ser Gly Glu Gly
 65 70 75 80
 Pro Glu Val Glu Met Glu Ser Trp Gln Lys Arg Tyr Asp Ser Leu Gln
 85 90 95
 Lys Ile Val Glu Lys Gln Gln Gln Lys Met Asp Gln Leu Arg Ser Gln
 100 105 110
 Val Gln Ser Leu Glu Gln Glu Val Ala Glu Glu Gly Thr Ser Gln Ala
 115 120 125
 Leu Arg Glu Glu Ala Gln Arg Arg Asp Ser Ala Leu Gln Gln Leu Arg
 130 135 140
 Thr Ala Val Lys Leu Ser Val Asn Gln Asp Leu Ile Glu Lys Asn Leu
 145 150 155 160
 Thr Leu Gln

<210> 51
 <211> 164
 <212> PRT
 <213> Homo Sapiens

<400> 51
 Phe Gly Asp Ser Val Asp Cys Ser Asp Cys Trp Leu Pro Val Val Lys
 1 5 10 15
 Phe Ile Glu Glu Gln Phe Glu Gln Tyr Leu Arg Asp Glu Ser Gly Leu
 20 25 30
 Asn Arg Lys Asn Ile Gln Asp Ser Arg Val His Cys Cys Leu Tyr Phe
 35 40 45
 Ile Ser Pro Phe Gly Arg Gly Leu Arg Pro Leu Ala Phe Leu Arg Ala
 50 55 60
 Val His Lys Val Asn Ile Ile Pro Val Ile Gly Lys Ala Asp Ala Leu
 65 70 75 80
 Met Pro Gln Glu Thr Gln Ala Leu Lys Gln Lys Ile Arg Asp Gln Leu
 85 90 95
 Lys Glu Glu Glu Ile His Ile Tyr Gln Phe Pro Glu Cys Asp Ser Asp

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<210> 52
<211> 600
<212> PRT
<213> Homo Sapiens
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[illegible][illegible][illegible]

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<210> 54
<211> 155
<212> PRT
<213> Homo Sapiens
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<210> 55
<211> 112
<212> PRT
<213> Homo Sapiens
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Met Gln Ala Leu Met Gln Ile Gln Gln Gly Leu Gln Thr Leu Ala Thr
 85 90 95
 Glu Ala Pro Gly Leu Ile Pro Ser Phe Thr Pro Gly Val Gly Val Gly
 100 105 110

<210> 56
 <211> 151
 <212> PRT
 <213> Homo Sapiens

<400> 56
 Lys Phe Gly Met Pro Ile Asp Cys Gly Leu Pro Pro His Ile Asp Phe
 1 5 10 15
 Gly Asp Cys Thr Lys Leu Lys Asp Asp Gln Gly Tyr Phe Glu Gln Glu
 20 25 30
 Asp Asp Met Met Glu Val Pro Tyr Val Thr Pro His Pro Pro Tyr His
 35 40 45
 Leu Gly Ala Val Ala Lys Thr Trp Glu Asn Thr Lys Glu Ser Pro Ala
 50 55 60
 Thr His Ser Ser Asn Phe Leu Tyr Gly Thr Met Val Ser Tyr Thr Cys
 65 70 75 80
 Asn Pro Gly Tyr Glu Leu Leu Gly Asn Pro Val Leu Ile Cys Gln Glu
 85 90 95
 Asp Gly Thr Trp Asn Gly Ser Ala Pro Ser Cys Ile Ser Ile Glu Cys
 100 105 110
 Asp Leu Pro Thr Ala Pro Glu Asn Gly Phe Leu Arg Phe Thr Glu Thr
 115 120 125
 Ser Met Gly Ser Ala Val Gln Tyr Ser Cys Lys Pro Gly His Ile Leu
 130 135 140
 Ala Gly Ser Asp Leu Arg Leu
 145 150

<210> 57
 <211> 220
 <212> PRT
 <213> Homo Sapiens

<400> 57
 Ala Ala Phe Val Ser Glu Val Thr Ser Phe Pro Val Val Gln Leu His
 1 5 10 15
 Met Asn Arg Thr Ala Met Arg Ala Ser Gln Lys Asp Phe Glu Asn Ser
 20 25 30
 Ile Asn Gln Val Lys Leu Leu Lys Lys Asp Pro Gly Asn Glu Val Lys
 35 40 45
 Leu Lys Leu Tyr Ala Leu Tyr Lys Gln Ala Thr Glu Gly Pro Cys Asn
 50 55 60
 Met Pro Lys Pro Gly Val Phe Asp Leu Ile Asn Lys Ala Lys Trp Asp
 65 70 75 80
 Ala Trp Asn Ala Leu Gly Ser Leu Pro Lys Glu Ala Ala Arg Gln Asn
 85 90 95
 Tyr Val Asp Leu Val Ser Ser Leu Ser Pro Ser Leu Glu Ser Ser Ser
 100 105 110
 Gln Val Glu Pro Gly Thr Asp Arg Lys Ser Thr Gly Phe Glu Thr Leu
 115 120 125
 Val Val Thr Ser Glu Asp Gly Ile Thr Lys Ile Met Phe Asn Arg Pro

130 135 140
 Lys Lys Lys Asn Ala Ile Asn Thr Glu Met Tyr His Glu Ile Met Arg
 145 150 155 160
 Ala Leu Lys Ala Ala Ser Lys Asp Asp Ser Ile Ile Thr Val Leu Thr
 165 170 175
 Gly Asn Gly Asp Tyr Tyr Ser Ser Gly Asn Asp Leu Thr Asn Phe Thr
 180 185 190
 Asp Ile Pro Pro Gly Gly Val Glu Lys Ala Lys Asn Asn Ala Val Leu
 195 200 205
 Leu Lys Gly Ile Cys Gly Leu Phe Tyr Arg Ile Ser
 210 215 220

<210> 58
 <211> 101
 <212> PRT
 <213> Homo Sapiens

<400> 58
 Trp Pro Asp Leu Val His Thr Trp Ser Ser Glu Glu Ala Met Gly Ser
 1 5 10 15
 Cys Cys Ser Cys Pro Asp Lys Asp Thr Val Pro Asp Asn His Arg Asn
 20 25 30
 Lys Phe Lys Val Ile Asn Val Asp Asp Asp Gly Asn Glu Leu Gly Ser
 35 40 45
 Gly Ile Met Glu Leu Thr Asp Thr Glu Leu Ile Leu Tyr Thr Arg Lys
 50 55 60
 Arg Asp Ser Val Lys Trp His Tyr Leu Cys Leu Arg Arg Tyr Gly Tyr
 65 70 75 80
 Asp Ser Asn Leu Phe Ser Phe Glu Ser Gly Pro Arg Cys Gln Thr Gly
 85 90 95
 Thr Arg Asn Leu Cys
 100

<210> 59
 <211> 43
 <212> PRT
 <213> Homo Sapiens

<400> 59
 Ala His Gly Pro Gly Val Glu Pro Thr Ser Arg His Gln Lys Asn Asn
 1 5 10 15
 Leu Ser Ser Ser His Thr Val Arg Leu Glu Thr Arg Gly Gln Thr Glu
 20 25 30
 Asn Gln Glu Cys Leu Leu Cys Pro His Glu Glu
 35 40

<210> 60
 <211> 210
 <212> PRT
 <213> Homo Sapiens

<400> 60
 Leu Asn Gln Trp Thr Tyr Gln Ala Met Val His Glu Leu Leu Gly Ile
 1 5 10 15
 Asn Asn Asn Arg Ile Asp Leu Ser Arg Val Pro Gly Ile Ser Lys Asp

20 25 30
 Leu Arg Glu Val Val Leu Ser Ala Glu Asn Asp Glu Phe Tyr Ala Asn
 35 40 45
 Asn Met Tyr Leu Asn Phe Ala Glu Ile Gly Ser Asn Ile Lys Asn Leu
 50 55 60
 Met Glu Asp Phe Gln Lys Lys Lys Pro Lys Glu Gln Gln Lys Leu Glu
 65 70 75 80
 Ser Ile Ala Asp Met Lys Ala Phe Val Glu Asn Tyr Pro Gln Phe Lys
 85 90 95
 Lys Met Ser Gly Thr Val Ser Lys His Val Thr Val Val Gly Glu Leu
 100 105 110
 Ser Arg Leu Val Ser Glu Arg Asn Leu Leu Glu Val Ser Glu Val Glu
 115 120 125
 Gln Glu Leu Ala Cys Gln Asn Asp His Ser Ser Ala Leu Gln Asn Ile
 130 135 140
 Lys Arg Leu Leu Gln Asn Pro Lys Val Thr Glu Phe Asp Ala Ala Arg
 145 150 155 160
 Leu Val Met Leu Tyr Ala Leu His Tyr Glu Arg His Ser Ser Asn Ser
 165 170 175
 Leu Pro Gly Leu Met Met Leu Arg Asn Lys Gly Val Ser Glu Lys Tyr
 180 185 190
 Arg Lys Leu Val Ser Ala Val Val Glu Tyr Gly Gly Lys Thr Ser Gln
 195 200 205
 Arg Lys
 210

<210> 61
 <211> 40
 <212> PRT
 <213> Homo Sapiens

<400> 61
 Thr Pro Gly Pro Gly Ala Gly Phe Tyr Ala Cys Pro Ala Arg Pro Leu
 1 5 10 15
 Val Ser Gly Ile Tyr Ser Phe Arg Trp Val Arg Gly Leu Ala Asp Gln
 20 25 30
 Glu Arg Asn Trp Gly Leu Ser Gln
 35 40

<210> 62
 <211> 238
 <212> PRT
 <213> Homo Sapiens

<400> 62
 His Glu Ala Arg Leu Lys Arg Ala Ser Ala Pro Thr Phe Asp Asn Asp
 1 5 10 15
 Tyr Ser Leu Ser Glu Leu Leu Ser Gln Leu Asp Ser Gly Val Ser Gln
 20 25 30
 Ala Val Glu Gly Pro Glu Glu Leu Ser Arg Ser Ser Ser Glu Ser Lys
 35 40 45
 Leu Pro Ser Ser Gly Ser Gly Lys Arg Leu Ser Gly Val Ser Ser Val
 50 55 60
 Asp Ser Ala Phe Ser Ser Arg Gly Ser Leu Ser Leu Ser Phe Glu Arg
 65 70 75 80

Glu Pro Ser Thr Ser Asp Leu Gly Thr Thr Asp Val Gln Lys Lys Lys
 85 90 95
 Leu Val Asp Ala Ile Val Ser Gly Asp Thr Ser Lys Leu Met Lys Ile
 100 105 110
 Leu Gln Pro Gln Asp Val Asp Leu Ala Leu Asp Ser Gly Ala Ser Leu
 115 120 125
 Leu His Leu Ala Val Glu Ala Gly Gln Glu Glu Cys Ala Lys Trp Leu
 130 135 140
 Leu Leu Asn Asn Ala Asn Pro Asn Leu Ser Asn Arg Arg Gly Ser Thr
 145 150 155 160
 Pro Leu His Met Ala Val Glu Arg Arg Val Arg Gly Val Val Glu Leu
 165 170 175
 Leu Leu Ala Arg Ile Ser Val Asn Ala Lys Asp Glu Asp Gln Trp Thr
 180 185 190
 Ala Leu His Phe Ala Asn Gly Gly Val His Thr Ala Ala Val Gly Glu
 195 200 205
 Arg Leu Gly Gln Thr Lys Val Asp Phe Glu Gly Arg Thr Pro Met Gln
 210 215 220
 Val Gly Leu Pro Thr Thr Gly Lys Asn Ile Leu Arg Ile Leu
 225 230 235

<210> 63
 <211> 146
 <212> PRT
 <213> Homo Sapiens

<400> 63
 Arg Leu Gly Ala Ala Met Met Glu Gly Leu Asp Asp Gly Pro Asp Phe
 1 5 10 15
 Leu Ser Glu Glu Asp Arg Gly Leu Lys Ala Ile Asn Val Asp Leu Gln
 20 25 30
 Ser Asp Ala Ala Leu Gln Val Asp Ile Ser Asp Ala Leu Ser Glu Arg
 35 40 45
 Asp Lys Val Lys Phe Thr Val His Thr Lys Ile Pro Pro Ala Pro Pro
 50 55 60
 Arg Pro Asp Phe Asp Ala Ser Arg Glu Lys Leu Gln Lys Leu Gly Glu
 65 70 75 80
 Gly Glu Gly Ser Met Thr Lys Glu Glu Phe Thr Lys Met Lys Gln Glu
 85 90 95
 Leu Glu Ala Glu Tyr Leu Ala Ile Phe Lys Lys Thr Val Ala Met His
 100 105 110
 Glu Val Phe Leu Cys Arg Val Ala Ala His Pro Ile Leu Arg Arg Asp
 115 120 125
 Leu Asn Phe His Val Phe Leu Glu Tyr Asn Gln Asp Leu Ser Val Arg
 130 135 140
 Gly Lys
 145

<210> 64
 <211> 63
 <212> PRT
 <213> Homo Sapiens

<400> 64
 Glu Arg Gly His Ser Ile Lys Asp Phe Val Ser Phe Ala Arg His Phe

1	5	10	15
Ser Pro Asn	Pro Arg Ile Val Ser	Val Asn Ala Ser Tyr	Ser Leu Ser
	20	25	30
Asn Glu Ser	Ser Leu Glu Gln Val Tyr Thr	Leu Lys Met Ser	Phe Ile
	35	40	45
Ala Ser Asn	Thr Tyr His Asn Gln Leu Tyr Lys	Glu Gly Phe Leu	
50	55	60	

<210> 65

<211> 199

<212> PRT

<213> Homo Sapiens

<400> 65

Glu Ala Pro	Asp Ser Ala Glu Gly Thr Thr	Leu Thr Val Leu Pro Glu
1	5	10
Gly Glu Glu	Leu Pro Leu Cys Val Ser Glu Ser	Asn Gly Leu Glu Leu
	20	30
Pro Pro Ser	Ala Ala Ser Asp Glu Pro Leu Gln Glu	Pro Leu Glu Ala
	35	45
Asp Arg Thr	Ser Glu Glu Leu Thr Glu Ala Lys Thr	Pro Thr Ser Ser
50	55	60
Pro Glu Lys	Pro Gln Glu Leu Val Thr Ala Glu Val	Ala Ala Pro Ser
65	70	75
Thr Ser Ser	Ser Ala Thr Ser Ser Pro Glu Gly	Pro Ser Pro Ala Arg
	85	90
Pro Pro Arg	Arg Arg Thr Ser Ala Asp Val Glu Ile Arg	Gly Gln Gly
	100	105
Thr Gly Arg	Pro Gly Gln Pro Pro Gly Pro Lys Val	Leu Arg Lys Leu
	115	120
Pro Gly Arg	Leu Val Thr Val Val Glu Glu Lys Glu	Leu Val Arg Arg
	130	135
Arg Arg Gln	Gln Arg Gly Ala Ala Ser Thr Leu Val	Pro Gly Val Ser
145	150	155
Glu Thr Ser	Ala Ser Pro Gly Ser Pro Ser Val Arg	Ser Met Ser Gly
	165	170
Pro Glu Ser	Ser Pro Pro Ile Gly Gly Pro Cys Glu Ala	Ala Pro Ser
	180	185
Ser Ser Leu	Pro Thr Pro Pro	
195		

<210> 66

<211> 1599

<212> DNA

<213> Homo Sapiens

<400> 66

ttctttgaaa	cattattatt	cagaacgaag	gagaatgata	cagatacact	ggctgaggtg	60
ttttgaggtg	cattgaaatg	ttccatgctg	ttacttaggt	taacatgttc	ttgaggtacc	120
atgccatgga	ttaaaaggaa	atttggtgaag	tggtctccac	ctaaacgact	tactagggaa	180
gctatgcgaa	attattttaa	agggtgaagg	gatcaaatag	tacttatacct	tcatgcaaaa	240
gttgtacaga	agtcatatgg	caatcaaaaa	atTTTTTTTT	gccctcccc	ttgtgtatat	300
cttatgggca	gtggatggaa	gaaaaaaaa	gaacaaatga	aatgcatgg	ttgttctgaa	360
cacagctctc	atccatgtgc	atTTATTGGG	ataggaaata	gtgaccaaga	aatgcagcag	420
ctaaacttgg	aaggaaagaa	ctattgcaca	gccaaaacat	tgtacatatc	tgattcagac	480

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aagcaaaagc acttcatttt ttctgtaaag gtgttctatg gcaacggtga tgacattggt 540
gtgttcctca gcaagtagat aaaagtcac tccaaacctt ccaaaaagaa gcagtcattg 600
aaaaatgctg acttatgcat tgtctcagga acaaagggtg ctctgtttaa tcgactacga 660
tcccagacag ttagtaccag atacttgcac gtagaaggag gtaattttca tgccagttca 720
cagcagtggt gagcatttta cattcaattc ttggatgatg atggatcaga aggagaagaa 780
ttcacagtct gagatgccta cattcattat ggacaaacat gcaaacttgt gtgctcagtt 840
actggcatgg cactcccaag attgataatt atgaaagttg ataagcatac cgcattattg 900
gatgcagatg atcctgtgtc acaactccat aaatgtgcat ttaccttaa ggatacagaa 960
agaatgtatt tgtgcctttc tcaagaaaga ataattcaat ttcaggccac tccatgtcca 1020
agagaaccaa ataaagagat gataaatgat ggcgcttctt ggacaatcat tagcacagat 1080
aaggcagggt atacatttta tgagggaatg ggccctgtcc ttgccccagt cactcctgtg 1140
cctgtggtag agagccttca gttgaatggc ggtggggacg tagcaatgct tgaacttaca 1200
ggacagaatt tcaactccaa tttacgagtg tggtttgggg gggtagaagc tgaaactatg 1260
tacaggtgtg gagagagtat gctctgtgtc gtcccagaca tttctgcatt ccgagaaggt 1320
tggagatggg tccggcaacc agtccagggt ccagtaactt tgggtccgaa tgatggaatc 1380
atttattcca ccagccttac ctttacctac acaccagaac cagggccgcg gccacattgc 1440
agtgcagcag gagcaatcct tctagccaat tcaagccagg tgccccctaa cgaatcaaac 1500
acaaacagcg aggggaagta cacaaacgcc agcacaaatt caaccagtgt cacatcatct 1560
acagccacag tggtatccta actaccgtct ttttgtctag 1599

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<210> 67

<211> 729

<212> PRT

<213> Homo Sapiens

<400> 67

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Met Gly Lys Lys Tyr Lys Asn Ile Val Leu Leu Lys Gly Leu Glu Val
 1          5          10          15
Ile Asn Asp Tyr His Phe Arg Met Val Lys Ser Leu Leu Ser Asn Asp
          20          25          30
Leu Lys Leu Asn Leu Lys Met Arg Glu Glu Tyr Asp Lys Ile Gln Ile
          35          40          45
Ala Asp Leu Met Glu Glu Lys Phe Arg Gly Asp Ala Gly Leu Gly Lys
          50          55          60
Leu Ile Lys Ile Phe Glu Asp Ile Pro Thr Leu Glu Asp Leu Ala Glu
65          70          75          80
Thr Leu Lys Lys Glu Lys Leu Lys Val Lys Gly Pro Ala Leu Ser Arg
          85          90          95
Lys Arg Lys Lys Glu Val His Ala Thr Ser Pro Ala Pro Ser Thr Ser
          100          105          110
Ser Thr Val Lys Thr Glu Gly Ala Glu Ala Thr Pro Gly Ala Gln Lys
          115          120          125
Arg Lys Lys Ser Thr Lys Glu Lys Ala Gly Pro Lys Gly Ser Lys Val
          130          135          140
Ser Glu Glu Gln Thr Gln Pro Pro Ser Pro Ala Gly Ala Gly Met Ser
          145          150          155          160
Thr Ala Met Gly Arg Ser Pro Ser Pro Lys Thr Ser Leu Ser Ala Pro
          165          170          175
Pro Asn Ser Ser Ser Thr Glu Asn Pro Lys Thr Val Ala Lys Cys Gln
          180          185          190
Val Thr Pro Arg Arg Asn Val Leu Gln Lys Arg Pro Val Ile Val Lys
          195          200          205
Val Leu Ser Thr Thr Lys Pro Phe Glu Tyr Glu Thr Pro Glu Met Glu
          210          215          220
Lys Lys Ile Met Phe His Ala Thr Val Ala Thr Gln Thr Gln Phe Phe

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225					230					235					240
His	Val	Lys	Val	Leu	Asn	Thr	Ser	Leu	Lys	Glu	Lys	Phe	Asn	Gly	Lys
				245						250					255
Lys	Ile	Ile	Ile	Ile	Ser	Asp	Tyr	Leu	Glu	Tyr	Asp	Ser	Leu	Leu	Glu
			260					265					270		
Val	Asn	Glu	Glu	Ser	Thr	Val	Ser	Glu	Ala	Gly	Pro	Asn	Gln	Thr	Phe
		275					280					285			
Glu	Val	Pro	Asn	Lys	Ile	Ile	Asn	Arg	Ala	Lys	Glu	Thr	Leu	Lys	Ile
	290					295					300				
Asp	Ile	Leu	His	Lys	Gln	Ala	Ser	Gly	Asn	Ile	Val	Tyr	Gly	Val	Phe
305					310				315						320
Met	Leu	His	Lys	Lys	Thr	Val	Asn	Gln	Lys	Thr	Thr	Ile	Tyr	Glu	Ile
				325					330					335	
Gln	Asp	Asp	Arg	Gly	Lys	Met	Asp	Val	Val	Gly	Thr	Gly	Gln	Cys	His
		340					345						350		
Asn	Ile	Pro	Cys	Glu	Glu	Gly	Asp	Lys	Leu	Gln	Leu	Phe	Cys	Phe	Arg
	355						360					365			
Leu	Arg	Lys	Lys	Asn	Gln	Met	Ser	Lys	Leu	Ile	Ser	Glu	Met	His	Ser
	370					375					380				
Phe	Ile	Gln	Ile	Lys	Lys	Thr	Asn	Pro	Arg	Asn	Asn	Asp	Pro	Lys	
385				390					395					400	
Ser	Met	Lys	Leu	Pro	Gln	Glu	Gln	Arg	Gln	Leu	Pro	Tyr	Pro	Ser	Glu
			405						410					415	
Ala	Ser	Thr	Thr	Phe	Pro	Glu	Ser	His	Leu	Arg	Thr	Pro	Gln	Met	Pro
		420						425					430		
Pro	Thr	Thr	Pro	Ser	Ser	Ser	Phe	Phe	Thr	Lys	Lys	Ser	Glu	Asp	Thr
	435					440						445			
Ile	Ser	Lys	Met	Asn	Asp	Phe	Met	Arg	Met	Gln	Ile	Leu	Lys	Glu	Gly
	450				455					460					
Ser	His	Phe	Pro	Gly	Pro	Phe	Met	Thr	Ser	Ile	Gly	Pro	Ala	Glu	Ser
465					470				475					480	
His	Pro	His	Thr	Pro	Gln	Met	Pro	Pro	Ser	Thr	Pro	Ser	Ser	Ser	Phe
			485					490						495	
Leu	Thr	Thr	Leu	Lys	Pro	Arg	Leu	Lys	Thr	Glu	Pro	Glu	Glu	Val	Ser
		500						505					510		
Ile	Glu	Asp	Ser	Ala	Gln	Ser	Asp	Leu	Lys	Glu	Val	Met	Val	Leu	Asn
	515						520					525			
Ala	Thr	Glu	Ser	Phe	Val	Tyr	Glu	Pro	Lys	Glu	Gln	Lys	Lys	Met	Phe
	530					535				540					
His	Ala	Thr	Val	Ala	Thr	Glu	Asn	Glu	Val	Phe	Arg	Val	Lys	Val	Phe
545					550				555						560
Asn	Ile	Asp	Leu	Lys	Glu	Lys	Phe	Thr	Pro	Lys	Lys	Ile	Ile	Ala	Ile
			565					570						575	
Ala	Asn	Tyr	Val	Cys	Arg	Asn	Gly	Phe	Leu	Glu	Val	Tyr	Pro	Phe	Thr
		580					585					590			
Leu	Val	Ala	Asp	Val	Asn	Ala	Asp	Ala	Asn	Met	Glu	Ile	Pro	Lys	Gly
	595					600					605				
Leu	Ile	Arg	Ser	Ala	Ser	Val	Thr	Pro	Lys	Ile	Asn	Gln	Leu	Cys	Ser
	610					615					620				
Gln	Thr	Lys	Gly	Ser	Phe	Val	Asn	Gly	Val	Phe	Glu	Val	His	Lys	Lys
625					630				635						640
Asn	Val	Arg	Gly	Glu	Phe	Thr	Tyr	Tyr	Glu	Ile	Gln	Asp	Asn	Thr	Gly
			645					650						655	
Lys	Met	Glu	Val	Val	His	Gly	Arg	Leu	Asn	Thr	Ile	Asn	Cys	Glu	
		660					665						670		

Glu Gly Asp Lys Leu Lys Leu Thr Ser Phe Glu Leu Ala Pro Lys Ser
 675 680 685
 Gly Asn Thr Gly Glu Leu Arg Ser Val Ile His Ser His Ile Lys Val
 690 695 700
 Ile Lys Thr Lys Lys Asn Lys Lys Asp Ile Leu Asn Pro Asp Ser Ser
 705 710 715 720
 Met Glu Thr Ser Pro Asp Phe Phe Phe
 725

<210> 68

<211> 754

<212> PRT

<213> Homo Sapiens

<400> 68

Met Ala Ser Val Pro Ala Leu Gln Leu Thr Pro Ala Asn Pro Pro Pro
 1 5 10 15
 Pro Glu Val Ser Asn Pro Lys Lys Pro Gly Arg Val Thr Asn Gln Leu
 20 25 30
 Gln Tyr Leu His Lys Val Val Met Lys Ala Leu Trp Lys His Gln Phe
 35 40 45
 Ala Trp Pro Phe Arg Gln Pro Val Asp Ala Val Lys Leu Gly Leu Pro
 50 55 60
 Asp Tyr His Lys Ile Ile Lys Gln Pro Met Asp Met Gly Thr Ile Lys
 65 70 75 80
 Arg Arg Leu Glu Asn Asn Tyr Tyr Trp Ala Ala Ser Glu Cys Met Gln
 85 90 95
 Asp Phe Asn Thr Met Phe Thr Asn Cys Tyr Ile Tyr Asn Lys Pro Thr
 100 105 110
 Asp Asp Ile Val Leu Met Ala Gln Thr Leu Glu Lys Ile Phe Leu Gln
 115 120 125
 Lys Val Ala Ser Met Pro Gln Glu Glu Gln Glu Leu Val Val Thr Ile
 130 135 140
 Pro Lys Asn Ser His Lys Lys Gly Ala Lys Leu Ala Ala Leu Gln Gly
 145 150 155 160
 Ser Val Thr Ser Ala His Gln Val Pro Ala Val Ser Ser Val Ser His
 165 170 175
 Thr Ala Leu Tyr Thr Pro Pro Pro Glu Ile Pro Thr Thr Val Leu Asn
 180 185 190
 Ile Pro His Pro Ser Val Ile Ser Ser Pro Leu Leu Lys Ser Leu His
 195 200 205
 Ser Ala Gly Pro Pro Leu Leu Ala Val Thr Ala Ala Pro Pro Ala Gln
 210 215 220
 Pro Leu Ala Lys Lys Lys Gly Val Lys Arg Lys Ala Asp Thr Thr Thr
 225 230 235 240
 Pro Thr Pro Thr Ala Ile Leu Ala Pro Gly Ser Pro Ala Ser Pro Pro
 245 250 255
 Gly Ser Leu Glu Pro Lys Ala Ala Arg Leu Pro Pro Met Arg Arg Glu
 260 265 270
 Ser Gly Arg Pro Ile Lys Pro Pro Arg Lys Asp Leu Pro Asp Ser Gln
 275 280 285
 Gln Gln His Gln Ser Ser Lys Lys Gly Lys Leu Ser Glu Gln Leu Lys
 290 295 300
 His Cys Asn Gly Ile Leu Lys Glu Leu Leu Ser Lys Lys His Ala Ala
 305 310 315 320

Tyr Ala Trp Pro Phe Tyr Lys Pro Val Asp Ala Ser Ala Leu Gly Leu
 325 330 335
 His Asp Tyr His Asp Ile Ile Lys His Pro Met Asp Leu Ser Thr Val
 340 345 350
 Lys Arg Lys Met Glu Asn Arg Asp Tyr Arg Asp Ala Gln Glu Phe Ala
 355 360 365
 Ala Asp Val Arg Leu Met Phe Ser Asn Cys Tyr Lys Tyr Asn Pro Pro
 370 375 380
 Asp His Asp Val Val Ala Met Ala Arg Lys Leu Gln Asp Val Phe Glu
 385 390 395 400
 Phe Arg Tyr Ala Lys Met Pro Asp Glu Pro Leu Glu Pro Gly Pro Leu
 405 410 415
 Pro Val Ser Thr Ala Met Pro Pro Gly Leu Ala Lys Ser Ser Ser Glu
 420 425 430
 Ser Ser Ser Glu Glu Ser Ser Ser Glu Ser Ser Ser Glu Glu Glu Glu
 435 440 445
 Glu Glu Asp Glu Glu Asp Glu Glu Glu Glu Ser Glu Ser Ser Asp
 450 455 460
 Ser Glu Glu Glu Arg Ala His Arg Leu Ala Glu Leu Gln Glu Gln Leu
 465 470 475 480
 Arg Ala Val His Glu Gln Leu Ala Ala Leu Ser Gln Gly Pro Ile Ser
 485 490 495
 Lys Pro Lys Arg Lys Arg Glu Lys Lys Glu Lys Lys Lys Lys Arg Lys
 500 505 510
 Ala Glu Lys His Arg Gly Arg Ala Gly Ala Asp Glu Asp Asp Lys Gly
 515 520 525
 Pro Arg Ala Pro Arg Pro Pro Gln Pro Lys Lys Ser Lys Lys Ala Ser
 530 535 540
 Gly Ser Gly Gly Gly Ser Ala Ala Leu Gly Pro Ser Gly Phe Gly Pro
 545 550 555 560
 Ser Gly Gly Ser Gly Thr Lys Leu Pro Lys Lys Ala Thr Lys Thr Ala
 565 570 575
 Pro Pro Ala Leu Pro Thr Gly Tyr Asp Ser Glu Glu Glu Glu Glu Ser
 580 585 590
 Arg Pro Met Ser Tyr Asp Glu Lys Arg Gln Leu Ser Leu Asp Ile Asn
 595 600 605
 Lys Leu Pro Gly Glu Lys Leu Gly Arg Val Val His Ile Ile Gln Ala
 610 615 620
 Arg Glu Pro Ser Leu Arg Asp Ser Asn Pro Glu Glu Ile Glu Ile Asp
 625 630 635 640
 Phe Glu Thr Leu Lys Pro Ser Thr Leu Arg Glu Leu Glu Arg Tyr Val
 645 650 655
 Leu Ser Cys Leu Arg Lys Lys Pro Arg Lys Pro Tyr Thr Ile Lys Lys
 660 665 670
 Pro Val Gly Lys Thr Lys Glu Glu Leu Ala Leu Glu Lys Lys Arg Glu
 675 680 685
 Leu Glu Lys Arg Leu Gln Asp Val Ser Gly Gln Leu Asn Ser Thr Lys
 690 695 700
 Lys Pro Pro Lys Lys Ala Asn Glu Lys Thr Glu Ser Ser Ser Ala Gln
 705 710 715 720
 Gln Val Ala Val Ser Arg Leu Ser Ala Ser Ser Ser Ser Asp Ser
 725 730 735
 Ser Ser Ser Ser Ser Ser Ser Ser Ser Asp Thr Ser Asp Ser Asp
 740 745 750
 Ser Gly

<210> 69
 <211> 210
 <212> PRT
 <213> Homo Sapiens

<400> 69
 Met Asp Asp Glu Glu Glu Thr Tyr Arg Leu Trp Lys Ile Arg Lys Thr
 1 5 10 15
 Ile Met Gln Leu Cys His Asp Arg Gly Tyr Leu Val Thr Gln Asp Glu
 20 25 30
 Leu Asp Gln Thr Leu Glu Glu Phe Lys Ala Gln Phe Gly Asp Lys Pro
 35 40 45
 Ser Glu Gly Arg Pro Arg Arg Thr Asp Leu Thr Val Leu Val Ala His
 50 55 60
 Asn Asp Asp Pro Thr Asp Gln Met Phe Val Phe Phe Pro Glu Glu Pro
 65 70 75 80
 Lys Val Gly Ile Lys Thr Ile Lys Val Tyr Cys Gln Arg Met Gln Glu
 85 90 95
 Glu Asn Ile Thr Arg Ala Leu Ile Val Val Gln Gln Gly Met Thr Pro
 100 105 110
 Ser Ala Lys Gln Ser Leu Val Asp Met Ala Pro Lys Tyr Ile Leu Glu
 115 120 125
 Gln Phe Leu Gln Gln Glu Leu Leu Ile Asn Ile Thr Glu His Glu Leu
 130 135 140
 Val Pro Glu His Val Val Met Thr Lys Glu Glu Val Thr Glu Leu Leu
 145 150 155 160
 Ala Arg Tyr Lys Leu Arg Glu Asn Gln Leu Pro Arg Ile Gln Ala Gly
 165 170 175
 Asp Pro Val Ala Arg Tyr Phe Gly Ile Lys Arg Gly Gln Val Val Lys
 180 185 190
 Ile Ile Arg Pro Ser Glu Thr Ala Gly Arg Tyr Ile Thr Tyr Arg Leu
 195 200 205
 Val Gln
 210

<210> 70
 <211> 621
 <212> PRT
 <213> Homo Sapiens

<400> 70
 Met Leu Leu Leu Pro Ser Ala Ala Glu Gly Gln Gly Thr Ala Ile Thr
 1 5 10 15
 His Ala Leu Thr Ser Ala Ser Ser Val Cys Gln Val Glu Pro Val Gly
 20 25 30
 Arg Trp Phe Glu Ala Phe Val Lys Arg Arg Asn Arg Asn Ala Ser Thr
 35 40 45
 Ser Phe Gln Glu Leu Glu Asp Lys Lys Glu Leu Ser Glu Glu Ser Glu
 50 55 60
 Asp Glu Glu Leu Gln Leu Glu Glu Phe Pro Met Leu Lys Thr Leu Asp
 65 70 75 80
 Pro Lys Asp Trp Lys Asn Gln Asp His Tyr Ala Val Leu Gly Leu Gly
 85 90 95

His Val Arg Tyr Thr Ala Thr Gln Arg Gln Ile Lys Ala Ala His Lys
 100 105 110
 Ala Met Val Leu Lys His His Pro Asp Lys Arg Lys Ala Ala Gly Glu
 115 120 125
 Pro Ile Lys Glu Gly Asp Asn Asp Tyr Phe Thr Cys Ile Thr Lys Ala
 130 135 140
 Tyr Glu Met Leu Ser Asp Pro Val Lys Arg Arg Ala Phe Asn Ser Val
 145 150 155 160
 Asp Pro Thr Phe Asp Asn Ser Val Pro Ser Lys Ser Glu Ala Lys Asp
 165 170 175
 Asn Phe Phe Gln Val Phe Ser Pro Val Phe Glu Arg Asn Ser Arg Trp
 180 185 190
 Ser Asn Lys Lys Asn Val Pro Lys Leu Gly Asp Met Asn Ser Ser Phe
 195 200 205
 Glu Asp Val Asp Ala Phe Tyr Ser Phe Trp Tyr Asn Phe Asp Ser Trp
 210 215 220
 Arg Glu Phe Ser Tyr Leu Asp Glu Glu Glu Lys Glu Lys Ala Glu Cys
 225 230 235 240
 Arg Asp Glu Arg Lys Trp Ile Glu Lys Gln Asn Arg Ala Thr Arg Ala
 245 250 255
 Gln Arg Lys Lys Glu Glu Met Asn Arg Ile Arg Thr Leu Val Asp Asn
 260 265 270
 Ala Tyr Ser Cys Asp Pro Arg Ile Lys Lys Phe Lys Glu Glu Glu Lys
 275 280 285
 Ala Lys Lys Glu Ala Glu Lys Lys Ala Lys Ala Glu Ala Arg Arg Lys
 290 295 300
 Glu Gln Glu Ala Lys Glu Lys Gln Arg Gln Ala Glu Leu Glu Ala Val
 305 310 315 320
 Arg Leu Ala Lys Glu Lys Glu Glu Glu Glu Val Arg Gln Gln Ala Leu
 325 330 335
 Leu Ala Lys Lys Glu Lys Asp Ile Gln Lys Lys Ala Ile Lys Lys Glu
 340 345 350
 Arg Gln Lys Leu Arg Asn Ser Cys Lys Ser Trp Asn His Phe Ser Asp
 355 360 365
 Asn Glu Ala Asp Arg Val Lys Met Met Glu Glu Val Glu Lys Leu Cys
 370 375 380
 Asp Arg Leu Glu Leu Ala Ser Leu Gln Gly Leu Asn Glu Ile Leu Ala
 385 390 395 400
 Ser Ser Thr Arg Glu Val Gly Lys Ala Ala Leu Glu Lys Gln Ile Glu
 405 410 415
 Glu Val Asn Glu Gln Met Arg Arg Glu Lys Glu Glu Ala Asp Ala Arg
 420 425 430
 Met Arg Gln Ala Ser Lys Asn Ala Glu Lys Ser Thr Gly Gly Ser Gly
 435 440 445
 Ser Gly Ser Lys Asn Trp Ser Glu Asp Asp Leu Gln Leu Leu Ile Lys
 450 455 460
 Ala Val Asn Leu Phe Pro Ala Gly Thr Asn Ser Arg Trp Glu Val Ile
 465 470 475 480
 Ala Asn Tyr Met Asn Ile His Ser Ser Ser Gly Val Lys Arg Thr Ala
 485 490 495
 Lys Asp Val Ile Ser Lys Ala Lys Ser Leu Gln Lys Leu Asp Pro His
 500 505 510
 Gln Lys Asp Asp Ile Asn Lys Lys Ala Phe Asp Lys Phe Lys Lys Glu
 515 520 525
 His Gly Val Ala Ser Gln Ala Asp Ser Ala Ala Pro Ser Glu Arg Phe

530		535		540
Glu Gly Pro Cys Ile Asp Ser Thr Pro Trp Thr Thr Glu Glu Gln Lys				
545		550		555
Leu Leu Glu Gln Ala Leu Lys Thr Tyr Pro Val Asn Thr Pro Glu Arg				
	565		570	575
Trp Glu Lys Ile Ala Glu Ala Val Pro Gly Arg Thr Lys Lys Asp Cys				
	580		585	590
Met Arg Arg Tyr Lys Glu Leu Val Glu Met Val Lys Ala Lys Lys Ala				
	595		600	605
Ala Gln Glu Gln Val Leu Asn Ala Ser Arg Ala Arg Lys				
610		615		620

<210> 71

<211> 267

<212> PRT

<213> Homo Sapiens

<400> 71

Met Ala Ser Leu Leu Lys Val Asp Gln Glu Val Lys Leu Lys Val Asp				
1	5	10	15	
Ser Phe Arg Glu Arg Ile Thr Ser Lys Ala Glu Asp Leu Val Ala Asn				
	20	25	30	
Phe Phe Pro Lys Lys Leu Leu Glu Leu Asp Ser Phe Leu Lys Glu Pro				
	35	40	45	
Ile Leu Asn Ile His Asp Leu Thr Gln Ile His Ser Asp Met Asn Leu				
	50	55	60	
Pro Val Pro Asp Pro Ile Leu Leu Thr Asn Ser His Asp Gly Leu Asp				
65	70	75	80	
Gly Pro Thr Tyr Lys Lys Arg Arg Leu Asp Glu Cys Glu Glu Ala Phe				
	85	90	95	
Gln Gly Thr Lys Val Phe Val Met Pro Asn Gly Met Leu Lys Ser Asn				
	100	105	110	
Gln Gln Leu Val Asp Ile Ile Glu Lys Val Lys Pro Glu Ile Arg Leu				
	115	120	125	
Leu Ile Glu Lys Cys Asn Thr Pro Ser Gly Lys Gly Pro His Ile Cys				
	130	135	140	
Phe Asp Leu Gln Val Lys Met Trp Val Gln Leu Leu Ile Pro Arg Ile				
145	150	155	160	
Glu Asp Gly Asn Asn Phe Gly Val Ser Ile Gln Glu Glu Thr Val Ala				
	165	170	175	
Glu Leu Arg Thr Val Glu Ser Glu Ala Ala Ser Tyr Leu Asp Gln Ile				
	180	185	190	
Ser Arg Tyr Tyr Ile Thr Arg Ala Lys Leu Val Ser Lys Ile Ala Lys				
	195	200	205	
Tyr Pro His Val Glu Asp Tyr Arg Arg Thr Val Thr Glu Ile Asp Glu				
	210	215	220	
Lys Glu Tyr Ile Ser Leu Arg Leu Ile Ile Ser Glu Leu Arg Asn Gln				
225	230	235	240	
Tyr Val Thr Leu His Asp Met Ile Leu Lys Asn Ile Glu Lys Ile Lys				
	245	250	255	
Arg Pro Arg Ser Ser Asn Ala Glu Thr Leu Tyr				
	260	265		

<210> 72

<211> 1752

<212> PRT

<213> Homo Sapiens

<400> 72

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Arg Glu Lys Arg Arg Arg Lys Ser Val Glu Asp Arg Phe Asp Gln Gln
 1           5           10           15
Lys Asn Asp Tyr Asp Gln Leu Gln Lys Ala Arg Gln Cys Glu Lys Glu
          20           25           30
Asn Leu Gly Trp Gln Lys Leu Glu Ser Glu Lys Ala Ile Lys Glu Lys
          35           40           45
Glu Tyr Glu Ile Glu Arg Leu Arg Val Leu Leu Gln Glu Glu Gly Thr
          50           55           60
Arg Lys Arg Glu Tyr Glu Asn Glu Leu Ala Lys Val Arg Asn His Tyr
65           70           75           80
Asn Glu Glu Met Ser Asn Leu Arg Asn Lys Tyr Glu Thr Glu Ile Asn
          85           90           95
Ile Thr Lys Thr Thr Ile Lys Glu Ile Ser Met Gln Lys Glu Asp Asp
          100          105          110
Ser Lys Asn Leu Arg Asn Gln Leu Asp Arg Leu Ser Arg Glu Asn Arg
          115          120          125
Asp Leu Lys Asp Glu Ile Val Arg Leu Asn Asp Ser Ile Leu Gln Ala
          130          135          140
Thr Glu Gln Arg Arg Arg Ala Glu Glu Asn Ala Leu Gln Gln Lys Ala
145          150          155          160
Cys Gly Ser Glu Ile Met Gln Lys Lys Gln His Leu Glu Ile Glu Leu
          165          170          175
Lys Gln Val Met Gln Gln Arg Ser Glu Asp Asn Ala Arg His Lys Gln
          180          185          190
Ser Leu Glu Glu Ala Ala Lys Thr Ile Gln Asp Lys Asn Lys Glu Ile
          195          200          205
Glu Arg Leu Lys Ala Glu Phe Gln Glu Glu Ala Lys Arg Arg Trp Glu
          210          215          220
Tyr Glu Asn Glu Leu Ser Lys Val Arg Asn Asn Tyr Asp Glu Glu Ile
225          230          235          240
Ile Ser Leu Lys Asn Gln Phe Glu Thr Glu Ile Asn Ile Thr Lys Thr
          245          250          255
Thr Ile His Gln Leu Thr Met Gln Lys Glu Glu Asp Thr Ser Gly Tyr
          260          265          270
Arg Ala Gln Ile Asp Asn Leu Thr Arg Glu Asn Arg Ser Leu Ser Glu
          275          280          285
Glu Ile Lys Arg Leu Lys Asn Thr Leu Thr Gln Thr Thr Glu Asn Leu
          290          295          300
Arg Arg Val Glu Glu Asp Ile Gln Gln Gln Lys Ala Thr Gly Ser Glu
305          310          315          320
Val Ser Gln Arg Lys Gln Gln Leu Glu Val Glu Leu Arg Gln Val Thr
          325          330          335
Gln Met Arg Thr Glu Glu Ser Val Arg Tyr Lys Gln Ser Leu Asp Asp
          340          345          350
Ala Ala Lys Thr Ile Gln Asp Lys Asn Lys Glu Ile Glu Arg Leu Lys
          355          360          365
Gln Leu Ile Asp Lys Glu Thr Asn Asp Arg Lys Cys Leu Glu Asp Glu
          370          375          380
Asn Ala Arg Leu Gln Arg Val Gln Tyr Asp Leu Gln Lys Ala Asn Ser
385          390          395          400
Ser Ala Thr Glu Thr Ile Asn Lys Leu Lys Val Gln Glu Gln Glu Leu

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405 410 415
 Thr Arg Leu Arg Ile Asp Tyr Glu Arg Val Ser Gln Glu Arg Thr Val
 420 425 430
 Lys Asp Gln Asp Ile Thr Arg Phe Gln Asn Ser Leu Lys Glu Leu Gln
 435 440 445
 Leu Gln Lys Gln Lys Val Glu Glu Glu Leu Asn Arg Leu Lys Arg Thr
 450 455 460
 Ala Ser Glu Asp Ser Cys Lys Arg Lys Lys Leu Glu Glu Glu Leu Glu
 465 470 475 480
 Gly Met Arg Arg Ser Leu Lys Glu Gln Ala Ile Lys Ile Thr Asn Leu
 485 490 495
 Thr Gln Gln Leu Glu Gln Ala Ser Ile Val Lys Lys Arg Ser Glu Asp
 500 505 510
 Asp Leu Arg Gln Gln Arg Asp Val Leu Asp Gly His Leu Arg Glu Lys
 515 520 525
 Gln Arg Thr Gln Glu Glu Leu Arg Arg Leu Ser Ser Glu Val Glu Ala
 530 535 540
 Leu Arg Arg Gln Leu Leu Gln Glu Gln Glu Ser Val Lys Gln Ala His
 545 550 555 560
 Leu Arg Asn Glu His Phe Gln Lys Ala Ile Glu Asp Lys Ser Arg Ser
 565 570 575
 Leu Asn Glu Ser Lys Ile Glu Ile Glu Arg Leu Gln Ser Leu Thr Glu
 580 585 590
 Asn Leu Thr Lys Glu His Leu Met Leu Glu Glu Glu Leu Arg Asn Leu
 595 600 605
 Arg Leu Glu Tyr Asp Asp Leu Arg Arg Gly Arg Ser Glu Ala Asp Ser
 610 615 620
 Asp Lys Asn Ala Thr Ile Leu Glu Leu Arg Ser Gln Leu Gln Ile Ser
 625 630 635 640
 Asn Asn Arg Thr Leu Glu Leu Gln Gly Leu Ile Asn Asp Leu Gln Arg
 645 650 655
 Glu Arg Glu Asn Leu Arg Gln Glu Ile Glu Lys Phe Gln Lys Gln Ala
 660 665 670
 Leu Glu Ala Ser Asn Arg Ile Gln Glu Ser Lys Asn Gln Cys Thr Gln
 675 680 685
 Val Val Gln Glu Arg Glu Ser Leu Leu Val Lys Ile Lys Val Leu Glu
 690 695 700
 Gln Asp Lys Ala Arg Leu Gln Arg Leu Glu Asp Glu Leu Asn Arg Ala
 705 710 715 720
 Lys Ser Thr Leu Glu Ala Glu Thr Arg Val Lys Gln Arg Leu Glu Cys
 725 730 735
 Glu Lys Gln Gln Ile Gln Asn Asp Leu Asn Gln Trp Lys Thr Gln Tyr
 740 745 750
 Ser Arg Lys Glu Glu Ala Ile Arg Lys Ile Glu Ser Glu Arg Glu Lys
 755 760 765
 Ser Glu Arg Glu Lys Asn Ser Leu Arg Ser Glu Ile Glu Arg Leu Gln
 770 775 780
 Ala Glu Ile Lys Arg Ile Glu Glu Arg Cys Arg Arg Lys Leu Glu Asp
 785 790 795 800
 Ser Thr Arg Glu Thr Gln Ser Gln Leu Glu Thr Glu Arg Ser Arg Tyr
 805 810 815
 Gln Arg Glu Ile Asp Lys Leu Arg Gln Arg Pro Tyr Gly Ser His Arg
 820 825 830
 Glu Thr Gln Thr Glu Cys Glu Trp Thr Val Asp Thr Ser Lys Leu Val
 835 840 845

Phe Asp Gly Leu Arg Lys Lys Val Thr Ala Met Gln Leu Tyr Glu Cys
 850 855 860
 Gln Leu Ile Asp Lys Thr Thr Leu Asp Lys Leu Leu Lys Gly Lys Lys
 865 870 875 880
 Ser Val Glu Glu Val Ala Ser Glu Ile Gln Pro Phe Leu Arg Gly Ala
 885 890 895
 Gly Ser Ile Ala Gly Ala Ser Ala Ser Pro Lys Glu Lys Tyr Ser Leu
 900 905 910
 Val Glu Ala Lys Arg Lys Lys Leu Ile Ser Pro Glu Ser Thr Val Met
 915 920 925
 Leu Leu Glu Ala Gln Ala Ala Thr Gly Gly Ile Ile Asp Pro His Arg
 930 935 940
 Asn Glu Lys Leu Thr Val Asp Ser Ala Ile Ala Arg Asp Leu Ile Asp
 945 950 955 960
 Phe Asp Asp Arg Gln Gln Ile Tyr Ala Ala Glu Lys Ala Ile Thr Gly
 965 970 975
 Phe Asp Asp Pro Phe Ser Gly Lys Thr Val Ser Val Ser Glu Ala Ile
 980 985 990
 Lys Lys Asn Leu Ile Asp Arg Glu Thr Gly Met Arg Leu Leu Glu Ala
 995 1000 1005
 Gln Ile Ala Ser Gly Gly Val Val Asp Pro Val Asn Ser Val Phe Leu
 1010 1015 1020
 Pro Lys Asp Val Ala Leu Ala Arg Gly Leu Ile Asp Arg Asp Leu Tyr
 1025 1030 1035 104
 Arg Ser Leu Asn Asp Pro Arg Asp Ser Gln Lys Asn Phe Val Asp Pro
 1045 1050 1055
 Val Thr Lys Lys Lys Val Ser Tyr Val Gln Leu Lys Glu Arg Cys Arg
 1060 1065 1070
 Ile Glu Pro His Thr Gly Leu Leu Leu Leu Ser Val Gln Lys Arg Ser
 1075 1080 1085
 Met Ser Phe Gln Gly Ile Arg Gln Pro Val Thr Val Thr Glu Leu Val
 1090 1095 1100
 Asp Ser Gly Ile Leu Arg Pro Ser Thr Val Asn Glu Leu Glu Ser Gly
 1105 1110 1115 112
 Gln Ile Ser Tyr Asp Glu Val Gly Glu Arg Ile Lys Asp Phe Leu Gln
 1125 1130 1135
 Gly Ser Ser Cys Ile Ala Gly Ile Tyr Asn Glu Thr Thr Lys Gln Lys
 1140 1145 1150
 Leu Gly Ile Tyr Glu Ala Met Lys Ile Gly Leu Val Arg Pro Gly Thr
 1155 1160 1165
 Ala Leu Glu Leu Leu Glu Ala Gln Ala Ala Thr Gly Phe Ile Val Asp
 1170 1175 1180
 Pro Val Ser Asn Leu Arg Leu Pro Val Glu Glu Ala Tyr Lys Arg Gly
 1185 1190 1195 120
 Leu Val Gly Ile Glu Phe Lys Glu Lys Leu Leu Ser Ala Glu Arg Ala
 1205 1210 1215
 Val Thr Gly Tyr Asn Asp Pro Glu Thr Gly Asn Ile Ile Ser Leu Phe
 1220 1225 1230
 Gln Ala Met Asn Lys Glu Leu Ile Glu Lys Gly His Gly Ile Arg Leu
 1235 1240 1245
 Leu Glu Ala Gln Ile Ala Thr Gly Gly Ile Ile Asp Pro Lys Glu Ser
 1250 1255 1260
 His Arg Leu Pro Val Asp Ile Ala Tyr Lys Arg Gly Tyr Phe Asn Glu
 1265 1270 1275 128
 Glu Leu Ser Glu Ile Leu Ser Asp Pro Ser Asp Asp Thr Lys Gly Phe

1285 1290 1295
 Phe Asp Pro Asn Thr Glu Glu Asn Leu Thr Tyr Leu Gln Leu Lys Glu
 1300 1305 1310
 Arg Cys Ile Lys Asp Glu Glu Thr Gly Leu Cys Leu Leu Pro Leu Lys
 1315 1320 1325
 Glu Lys Lys Lys Gln Val Gln Thr Ser Gln Lys Asn Thr Leu Arg Lys
 1330 1335 1340
 Arg Arg Val Val Ile Val Asp Pro Glu Thr Asn Lys Glu Met Ser Val
 1345 1350 1355 136
 Gln Glu Ala Tyr Lys Lys Gly Leu Ile Asp Tyr Glu Thr Phe Lys Glu
 1365 1370 1375
 Leu Cys Glu Gln Glu Cys Glu Trp Glu Glu Ile Thr Ile Thr Gly Ser
 1380 1385 1390
 Asp Gly Ser Thr Arg Val Val Leu Val Asp Arg Lys Thr Gly Ser Gln
 1395 1400 1405
 Tyr Asp Ile Gln Asp Ala Ile Asp Lys Gly Leu Val Asp Arg Lys Phe
 1410 1415 1420
 Phe Asp Gln Tyr Arg Ser Gly Ser Leu Ser Leu Thr Gln Phe Ala Asp
 1425 1430 1435 144
 Met Ile Ser Leu Lys Asn Gly Val Gly Thr Ser Ser Ser Met Gly Ser
 1445 1450 1455
 Gly Val Ser Asp Asp Val Phe Ser Ser Ser Arg His Glu Ser Val Ser
 1460 1465 1470
 Lys Ile Ser Thr Ile Ser Ser Val Arg Asn Leu Thr Ile Arg Ser Ser
 1475 1480 1485
 Ser Phe Ser Asp Thr Leu Glu Glu Ser Ser Pro Ile Ala Ala Ile Phe
 1490 1495 1500
 Asp Thr Glu Asn Leu Glu Lys Ile Ser Ile Thr Glu Gly Ile Glu Arg
 1505 1510 1515 152
 Gly Ile Val Asp Ser Ile Thr Gly Gln Arg Leu Leu Glu Ala Gln Ala
 1525 1530 1535
 Cys Thr Gly Gly Ile Ile His Pro Thr Thr Gly Gln Lys Leu Ser Leu
 1540 1545 1550
 Gln Asp Ala Val Ser Gln Gly Val Ile Asp Gln Asp Met Ala Thr Ser
 1555 1560 1565
 Val Lys Pro Ala Gln Lys Ala Phe Ile Gly Phe Glu Gly Val Lys Gly
 1570 1575 1580
 Lys Lys Lys Met Ser Ala Ala Glu Ala Val Lys Glu Lys Trp Leu Pro
 1585 1590 1595 160
 Tyr Glu Ala Gly Gln Arg Phe Leu Glu Phe Gln Tyr Leu Thr Gly Gly
 1605 1610 1615
 Leu Val Asp Pro Glu Val His Gly Arg Ile Ser Thr Glu Glu Ala Ile
 1620 1625 1630
 Arg Lys Gly Phe Ile Asp Gly Arg Ala Ala Gln Arg Leu Gln Asp Thr
 1635 1640 1645
 Ser Ser Tyr Ala Lys Ile Leu Thr Cys Pro Lys Thr Lys Leu Lys Ile
 1650 1655 1660
 Ser Tyr Lys Asp Ala Ile Asn Arg Ser Met Val Glu Asp Ile Thr Gly
 1665 1670 1675 168
 Leu Arg Leu Leu Glu Ala Ala Ser Val Ser Ser Lys Gly Leu Pro Ser
 1685 1690 1695
 Pro Tyr Asn Met Ser Ser Ala Pro Gly Ser Arg Ser Gly Ser Arg Ser
 1700 1705 1710
 Gly Ser Arg Ser Gly Ser Arg Ser Gly Ser Arg Ser Gly Ser Arg Arg
 1715 1720 1725

Gly Ser Phe Asp Ala Thr Gly Asn Ser Ser Tyr Ser Tyr Ser Tyr Ser
 1730 1735 1740
 Phe Ser Ser Ser Ser Ile Gly His
 1745 1750

<210> 73
 <211> 1978
 <212> PRT
 <213> Homo Sapiens

<400> 73
 Met Ser Arg Pro Arg Phe Asn Pro Arg Gly Asp Phe Pro Leu Gln Arg
 1 5 10 15
 Pro Arg Ala Pro Asn Pro Ser Gly Met Arg Pro Pro Gly Pro Phe Met
 20 25 30
 Arg Pro Gly Ser Met Gly Leu Pro Arg Phe Tyr Pro Ala Gly Arg Ala
 35 40 45
 Arg Gly Ile Pro His Arg Phe Ala Gly Leu Glu Ser Tyr Gln Asn Met
 50 55 60
 Gly Pro Gln Arg Met Asn Val Gln Val Thr Gln His Arg Thr Asp Pro
 65 70 75 80
 Arg Leu Thr Lys Glu Lys Leu Asp Phe His Glu Ala Gln Gln Lys Lys
 85 90 95
 Gly Lys Pro His Gly Ser Arg Trp Asp Asp Glu Pro His Ile Ser Ala
 100 105 110
 Ser Val Ala Val Lys Gln Ser Ser Val Thr Gln Val Thr Glu Gln Ser
 115 120 125
 Pro Lys Val Gln Ser Arg Tyr Thr Lys Glu Ser Ala Ser Ser Ile Leu
 130 135 140
 Ala Ser Phe Gly Leu Ser Asn Glu Asp Leu Glu Glu Leu Ser Arg Tyr
 145 150 155 160
 Pro Asp Glu Gln Leu Thr Pro Glu Asn Met Pro Leu Ile Leu Arg Asp
 165 170 175
 Ile Arg Met Arg Lys Met Gly Arg Arg Leu Pro Asn Leu Pro Ser Gln
 180 185 190
 Ser Arg Asn Lys Glu Thr Leu Gly Ser Glu Ala Val Ser Ser Asn Val
 195 200 205
 Ile Asp Tyr Gly His Ala Ser Lys Tyr Gly Tyr Thr Glu Asp Pro Leu
 210 215 220
 Glu Val Arg Ile Tyr Asp Pro Glu Ile Pro Thr Asp Glu Val Glu Asn
 225 230 235 240
 Glu Phe Gln Ser Gln Gln Asn Ile Ser Ala Ser Val Pro Asn Pro Asn
 245 250 255
 Val Ile Cys Asn Ser Met Phe Pro Val Glu Asp Val Phe Arg Gln Met
 260 265 270
 Asp Phe Pro Gly Glu Ser Ser Asn Asn Arg Ser Phe Phe Ser Val Glu
 275 280 285
 Ser Gly Thr Lys Met Ser Gly Leu His Ile Ser Gly Gly Gln Ser Val
 290 295 300
 Leu Glu Pro Ile Lys Ser Val Asn Gln Ser Ile Asn Gln Thr Val Ser
 305 310 315 320
 Gln Thr Met Ser Gln Ser Leu Ile Pro Pro Ser Met Asn Gln Gln Pro
 325 330 335
 Phe Ser Ser Glu Leu Ile Ser Ser Val Ser Gln Gln Glu Arg Ile Pro
 340 345 350

His Glu Pro Val Ile Asn Ser Ser Asn Val His Val Gly Ser Arg Gly
 355 360 365
 Ser Lys Lys Asn Tyr Gln Ser Gln Ala Asp Ile Pro Ile Arg Ser Pro
 370 375 380
 Phe Gly Ile Val Lys Ala Ser Trp Leu Pro Lys Phe Ser His Ala Asp
 385 390 395 400
 Ala Gln Lys Met Lys Arg Leu Pro Thr Pro Ser Met Met Asn Asp Tyr
 405 410 415
 Tyr Ala Ala Ser Pro Arg Ile Phe Pro His Leu Cys Ser Leu Cys Asn
 420 425 430
 Val Glu Cys Ser His Leu Lys Asp Trp Ile Gln His Gln Asn Thr Ser
 435 440 445
 Thr His Ile Glu Ser Cys Arg Gln Leu Arg Gln Gln Tyr Pro Asp Trp
 450 455 460
 Asn Pro Glu Ile Leu Pro Ser Arg Arg Asn Glu Gly Asn Arg Lys Glu
 465 470 475 480
 Asn Glu Thr Pro Arg Arg Arg Ser His Ser Pro Ser Pro Arg Arg Ser
 485 490 495
 Arg Arg Ser Ser Ser His Arg Phe Arg Arg Ser Arg Ser Pro Met
 500 505 510
 His Tyr Met Tyr Arg Pro Arg Ser Arg Ser Pro Arg Ile Cys His Arg
 515 520 525
 Phe Ile Ser Arg Tyr Arg Ser Arg Ser Arg Ser Arg Ser Pro Tyr Arg
 530 535 540
 Ile Arg Asn Pro Phe Arg Gly Ser Pro Lys Cys Phe Arg Ser Val Ser
 545 550 555 560
 Pro Glu Arg Met Ser Arg Arg Ser Val Arg Ser Ser Asp Arg Lys Lys
 565 570 575
 Ala Leu Glu Asp Val Val Gln Arg Ser Gly His Gly Thr Glu Phe Asn
 580 585 590
 Lys Gln Lys His Leu Glu Ala Ala Asp Lys Gly His Ser Pro Ala Gln
 595 600 605
 Lys Pro Lys Thr Ser Ser Gly Thr Lys Pro Ser Val Lys Pro Thr Ser
 610 615 620
 Ala Thr Lys Ser Asp Ser Asn Leu Gly Gly His Ser Ile Arg Cys Lys
 625 630 635 640
 Ser Lys Asn Leu Glu Asp Asp Thr Leu Ser Glu Cys Lys Gln Val Ser
 645 650 655
 Asp Lys Ala Val Ser Leu Gln Arg Lys Leu Arg Lys Glu Gln Ser Leu
 660 665 670
 His Tyr Gly Ser Val Leu Leu Ile Thr Glu Leu Pro Glu Asp Gly Cys
 675 680 685
 Thr Glu Glu Asp Val Arg Lys Leu Phe Gln Pro Phe Gly Lys Val Asn
 690 695 700
 Asp Val Leu Ile Val Pro Tyr Arg Lys Glu Ala Tyr Leu Glu Met Glu
 705 710 715 720
 Phe Lys Glu Ala Ile Thr Ala Ile Met Lys Tyr Ile Glu Thr Thr Pro
 725 730 735
 Leu Thr Ile Lys Gly Lys Ser Val Lys Ile Cys Val Pro Gly Lys Lys
 740 745 750
 Lys Ala Gln Asn Lys Glu Val Lys Lys Lys Thr Leu Glu Ser Lys Lys
 755 760 765
 Val Ser Ala Ser Thr Leu Lys Arg Asp Ala Asp Ala Ser Lys Ala Val
 770 775 780
 Glu Ile Val Thr Ser Thr Ser Ala Ala Lys Thr Gly Gln Ala Lys Ala

785		790		795		800
Cys Val Ala Lys	Val Asn Lys Ser Thr Gly Lys Ser Ala Ser Ser Val					
	805		810		815	
Lys Ser Val Val Thr Val Ala Val Lys Gly Asn Lys Ala Ser Ile Lys						
	820		825		830	
Thr Ala Lys Ser Gly Gly Lys Lys Ser Leu Glu Ala Lys Lys Thr Gly						
	835		840		845	
Asn Val Lys Asn Lys Asp Ser Asn Lys Pro Val Thr Ile Pro Glu Asn						
	850		855		860	
Ser Glu Ile Lys Thr Ser Ile Glu Val Lys Ala Thr Glu Asn Cys Ala						
	865		870		875	
Lys Glu Ala Ile Ser Asp Ala Ala Leu Glu Ala Thr Glu Asn Glu Pro						
	885		890		895	
Leu Asn Lys Glu Thr Glu Glu Met Cys Val Met Leu Val Ser Asn Leu						
	900		905		910	
Pro Asn Lys Gly Tyr Ser Val Glu Glu Val Tyr Asp Leu Ala Lys Pro						
	915		920		925	
Phe Gly Gly Leu Lys Asp Ile Leu Ile Leu Ser Ser His Lys Lys Ala						
	930		935		940	
Tyr Ile Glu Ile Asn Arg Lys Ala Ala Glu Ser Met Val Lys Phe Tyr						
	945		950		955	
Thr Cys Phe Pro Val Leu Met Asp Gly Asn Gln Leu Ser Ile Ser Met						
	965		970		975	
Ala Pro Glu Asn Met Asn Ile Lys Asp Glu Glu Ala Ile Phe Ile Thr						
	980		985		990	
Leu Val Lys Glu Asn Asp Pro Glu Ala Asn Ile Asp Thr Ile Tyr Asp						
	995		1000		1005	
Arg Phe Val His Leu Asp Asn Leu Pro Glu Asp Gly Leu Gln Cys Val						
	1010		1015		1020	
Leu Cys Val Gly Leu Gln Phe Gly Lys Val Asp His His Val Phe Ile						
	1025		1030		1035	
Ser Asn Arg Asn Lys Ala Ile Leu Gln Leu Asp Ser Pro Glu Ser Ala						
	1045		1050		1055	
Gln Ser Met Tyr Ser Phe Leu Lys Gln Asn Pro Gln Asn Ile Gly Asp						
	1060		1065		1070	
His Met Leu Thr Cys Ser Leu Ser Pro Lys Ile Asp Leu Pro Glu Val						
	1075		1080		1085	
Gln Ile Glu His Asp Pro Glu Leu Glu Lys Glu Ser Pro Gly Leu Lys						
	1090		1095		1100	
Asn Ser Pro Ile Asp Glu Ser Glu Val Gln Thr Ala Thr Asp Ser Pro						
	1105		1110		1115	
Ser Val Lys Pro Asn Glu Leu Glu Glu Glu Ser Thr Pro Ser Ile Gln						
	1125		1130		1135	
Thr Glu Thr Leu Val Gln Gln Glu Glu Pro Cys Glu Glu Glu Ala Glu						
	1140		1145		1150	
Lys Ala Thr Cys Asp Ser Asp Phe Ala Val Glu Thr Leu Glu Leu Glu						
	1155		1160		1165	
Thr Gln Gly Glu Glu Val Lys Glu Glu Ile Pro Leu Val Ala Ser Ala						
	1170		1175		1180	
Ser Val Ser Ile Glu Gln Phe Thr Glu Asn Ala Glu Glu Cys Ala Leu						
	1185		1190		1195	
Asn Gln Gln Met Phe Asn Ser Asp Leu Glu Lys Lys Gly Ala Glu Ile						
	1205		1210		1215	
Ile Asn Pro Lys Thr Ala Leu Leu Pro Ser Asp Ser Val Phe Ala Glu						
	1220		1225		1230	

Glu Arg Asn Leu Lys Gly Ile Leu Glu Glu Ser Pro Ser Glu Ala Glu
 1235 1240 1245
 Asp Phe Ile Ser Gly Ile Thr Gln Thr Met Val Glu Ala Val Ala Glu
 1250 1255 1260
 Val Glu Lys Asn Glu Thr Val Ser Glu Ile Leu Pro Ser Thr Cys Ile
 1265 1270 1275 128
 Val Thr Leu Val Pro Gly Ile Pro Thr Gly Asp Glu Lys Thr Val Asp
 1285 1290 1295
 Lys Lys Asn Ile Ser Glu Lys Lys Gly Asn Met Asp Glu Lys Glu Glu
 1300 1305 1310
 Lys Glu Phe Asn Thr Lys Glu Thr Arg Met Asp Leu Gln Ile Gly Thr
 1315 1320 1325
 Glu Lys Ala Glu Lys Asn Glu Gly Arg Met Asp Ala Glu Lys Val Glu
 1330 1335 1340
 Lys Met Ala Ala Met Lys Glu Lys Pro Ala Glu Asn Thr Leu Phe Lys
 1345 1350 1355 136
 Ala Tyr Pro Asn Lys Gly Val Gly Gln Ala Asn Lys Pro Asp Glu Thr
 1365 1370 1375
 Ser Lys Thr Ser Ile Leu Ala Val Ser Asp Val Ser Ser Ser Lys Pro
 1380 1385 1390
 Ser Ile Lys Ala Val Ile Val Ser Ser Pro Lys Ala Lys Ala Thr Val
 1395 1400 1405
 Ser Lys Thr Glu Asn Gln Lys Ser Phe Pro Lys Ser Val Pro Arg Asp
 1410 1415 1420
 Gln Ile Asn Ala Glu Lys Lys Leu Ser Ala Lys Glu Phe Gly Leu Leu
 1425 1430 1435 144
 Lys Pro Thr Ser Ala Arg Ser Gly Leu Ala Glu Ser Ser Ser Lys Phe
 1445 1450 1455
 Lys Pro Thr Gln Ser Ser Leu Thr Arg Gly Gly Ser Gly Arg Ile Ser
 1460 1465 1470
 Ala Leu Gln Gly Lys Leu Ser Lys Leu Asp Tyr Arg Asp Ile Thr Lys
 1475 1480 1485
 Gln Ser Gln Glu Thr Glu Ala Arg Pro Ser Ile Met Lys Arg Asp Asp
 1490 1495 1500
 Ser Asn Asn Lys Thr Leu Ala Glu Gln Asn Thr Lys Asn Pro Lys Ser
 1505 1510 1515 152
 Thr Thr Gly Arg Ser Ser Lys Ser Lys Glu Pro Leu Phe Pro Phe
 1525 1530 1535
 Asn Leu Asp Glu Phe Val Thr Val Asp Glu Val Ile Glu Glu Val Asn
 1540 1545 1550
 Pro Ser Gln Ala Lys Gln Asn Pro Leu Lys Gly Lys Arg Lys Glu Thr
 1555 1560 1565
 Leu Lys Asn Val Pro Phe Ser Glu Leu Asn Leu Lys Lys Lys Lys Gly
 1570 1575 1580
 Lys Thr Ser Thr Pro Arg Gly Val Glu Gly Glu Leu Ser Phe Val Thr
 1585 1590 1595 160
 Leu Asp Glu Ile Gly Glu Glu Glu Asp Ala Ala Ala His Leu Ala Gln
 1605 1610 1615
 Ala Leu Val Thr Val Asp Glu Val Ile Asp Glu Glu Glu Leu Asn Met
 1620 1625 1630
 Glu Glu Met Val Lys Asn Ser Asn Ser Leu Phe Thr Leu Asp Glu Leu
 1635 1640 1645
 Ile Asp Gln Asp Asp Cys Ile Ser His Ser Glu Pro Lys Asp Val Thr
 1650 1655 1660
 Val Leu Ser Val Ala Glu Glu Gln Asp Leu Leu Lys Gln Glu Arg Leu

1665 1670 1675 168
 Val Thr Val Asp Glu Ile Gly Glu Val Glu Glu Leu Pro Leu Asn Glu
 1685 1690 1695
 Ser Ala Asp Ile Thr Phe Ala Thr Leu Asn Thr Lys Gly Asn Glu Gly
 1700 1705 1710
 Asp Ile Val Arg Asp Ser Ile Gly Phe Ile Ser Ser Gln Val Pro Glu
 1715 1720 1725
 Asp Pro Ser Thr Leu Val Thr Val Asp Glu Ile Gln Asp Asp Ser Ser
 1730 1735 1740
 Asp Leu His Leu Val Thr Leu Asp Glu Val Thr Glu Glu Asp Glu Asp
 1745 1750 1755 176
 Ser Leu Ala Asp Phe Asn Asn Leu Lys Glu Glu Leu Asn Phe Val Thr
 1765 1770 1775
 Val Asp Glu Val Gly Glu Glu Glu Asp Gly Asp Asn Asp Leu Lys Val
 1780 1785 1790
 Glu Leu Ala Gln Ser Lys Asn Asp His Pro Thr Asp Lys Lys Gly Asn
 1795 1800 1805
 Arg Lys Lys Arg Ala Val Asp Thr Lys Lys Thr Lys Leu Glu Ser Leu
 1810 1815 1820
 Ser Gln Val Gly Pro Val Asn Glu Asn Val Met Glu Glu Asp Leu Lys
 1825 1830 1835 184
 Thr Met Ile Glu Arg His Leu Thr Ala Lys Thr Pro Thr Lys Arg Val
 1845 1850 1855
 Arg Ile Gly Lys Thr Leu Pro Ser Glu Lys Ala Val Val Thr Glu Pro
 1860 1865 1870
 Ala Lys Gly Glu Glu Ala Phe Gln Met Ser Glu Val Asp Glu Glu Ser
 1875 1880 1885
 Gly Leu Lys Asp Ser Glu Pro Glu Arg Lys Arg Lys Lys Thr Glu Asp
 1890 1895 1900
 Ser Ser Ser Gly Lys Ser Val Ala Ser Asp Val Pro Glu Glu Leu Asp
 1905 1910 1915 192
 Phe Leu Val Pro Lys Ala Gly Phe Phe Cys Pro Ile Cys Ser Leu Phe
 1925 1930 1935
 Tyr Ser Gly Glu Lys Ala Met Thr Asn His Cys Lys Ser Thr Arg His
 1940 1945 1950
 Lys Gln Asn Thr Glu Lys Phe Met Ala Lys Gln Arg Lys Glu Lys Glu
 1955 1960 1965
 Gln Asn Glu Ala Glu Glu Arg Ser Ser Arg
 1970 1975

<210> 74
 <211> 366
 <212> PRT
 <213> Homo Sapiens

<400> 74
 Met Arg Val Met Ala Pro Arg Thr Leu Ile Leu Leu Leu Ser Gly Ala
 1 5 10 15
 Leu Ala Leu Thr Glu Thr Trp Ala Gly Ser His Ser Met Arg Tyr Phe
 20 25 30
 Tyr Thr Ala Val Ser Arg Pro Gly Arg Gly Glu Pro His Phe Ile Ala
 35 40 45
 Val Gly Tyr Val Asp Asp Thr Gln Phe Val Arg Phe Asp Ser Asp Ala
 50 55 60
 Ala Ser Pro Arg Gly Glu Pro Arg Ala Pro Trp Val Glu Gln Glu Gly

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65          70          75          80
Pro Glu Tyr Trp Asp Arg Glu Thr Gln Lys Tyr Lys Arg Gln Ala Gln
      85          90          95
Thr Asp Arg Val Ser Leu Arg Asn Leu Arg Gly Tyr Tyr Asn Gln Ser
      100         105         110
Glu Ala Gly Ser His Ile Ile Gln Arg Met Tyr Gly Cys Asp Val Gly
      115         120         125
Pro Asp Gly Arg Leu Leu Arg Gly Tyr Asp Gln Tyr Ala Tyr Asp Gly
      130         135         140
Lys Asp Tyr Ile Ala Leu Asn Glu Asp Leu Arg Ser Trp Thr Ala Ala
145         150         155         160
Asp Thr Ala Ala Gln Ile Thr Gln Arg Lys Trp Glu Ala Ala Arg Glu
      165         170         175
Ala Glu Gln Leu Arg Ala Tyr Leu Glu Gly Leu Cys Val Glu Trp Leu
      180         185         190
Arg Arg Tyr Leu Lys Asn Gly Lys Glu Thr Leu Gln Arg Ala Glu His
      195         200         205
Pro Lys Thr His Val Thr His His Pro Val Ser Asp His Glu Ala Thr
      210         215         220
Leu Arg Cys Trp Ala Leu Gly Phe Tyr Pro Ala Glu Ile Thr Leu Thr
225         230         235         240
Trp Gln Trp Asp Gly Glu Asp Gln Thr Gln Asp Thr Glu Leu Val Glu
      245         250         255
Thr Arg Pro Ala Gly Asp Gly Thr Phe Gln Lys Trp Ala Ala Val Val
      260         265         270
Val Pro Ser Gly Glu Glu Gln Arg Tyr Thr Cys His Val Gln His Glu
      275         280         285
Gly Leu Pro Glu Pro Leu Thr Leu Arg Trp Glu Pro Ser Ser Gln Pro
      290         295         300
Thr Ile Pro Ile Val Gly Ile Val Ala Gly Leu Ala Val Leu Ala Val
305         310         315         320
Leu Ala Val Leu Gly Ala Val Val Ala Val Val Met Cys Arg Arg Lys
      325         330         335
Ser Ser Gly Gly Lys Gly Gly Ser Cys Ser Gln Ala Ala Ser Ser Asn
      340         345         350
Ser Ala Gln Gly Ser Asp Glu Ser Leu Ile Ala Cys Lys Ala
      355         360         365

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<210> 75

<211> 240

<212> PRT

<213> Homo Sapiens

<400> 75

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Met Gly Leu Glu Leu Tyr Leu Asp Leu Leu Ser Gln Pro Cys Arg Ala
 1          5          10          15
Val Tyr Ile Phe Ala Lys Lys Asn Asp Ile Pro Phe Glu Leu Arg Ile
      20         25         30
Val Asp Leu Ile Lys Gly Gln His Leu Ser Asp Ala Phe Ala Gln Val
      35         40         45
Asn Pro Leu Lys Lys Val Pro Ala Leu Lys Asp Gly Asp Phe Thr Leu
      50         55         60
Thr Glu Ser Val Ala Ile Leu Leu Tyr Leu Thr Arg Lys Tyr Lys Val
65          70          75          80
Pro Asp Tyr Trp Tyr Pro Gln Asp Leu Gln Ala Arg Ala Arg Val Asp

```

				85						90					95				
Glu	Tyr	Leu	Ala	Trp	Gln	His	Thr	Thr	Leu	Arg	Arg	Ser	Cys	Leu	Arg				
			100						105				110						
Ala	Leu	Trp	His	Lys	Val	Met	Phe	Pro	Val	Phe	Leu	Gly	Gly	Pro	Val				
		115					120					125							
Ser	Pro	Gln	Thr	Leu	Ala	Ala	Thr	Leu	Ala	Glu	Leu	Asp	Val	Thr	Leu				
		130				135					140								
Gln	Leu	Leu	Glu	Asp	Lys	Phe	Leu	Gln	Asn	Lys	Ala	Phe	Leu	Thr	Gly				
145					150				155					160					
Pro	His	Ile	Ser	Leu	Ala	Asp	Leu	Val	Ala	Ile	Thr	Glu	Leu	Met	His				
				165				170						175					
Pro	Val	Gly	Ala	Gly	Cys	Gln	Val	Phe	Glu	Gly	Arg	Pro	Lys	Leu	Ala				
		180					185						190						
Thr	Trp	Arg	Gln	Arg	Val	Glu	Ala	Ala	Val	Gly	Glu	Asp	Leu	Phe	Gln				
		195				200						205							
Glu	Ala	His	Glu	Val	Ile	Leu	Lys	Ala	Lys	Asp	Phe	Pro	Pro	Ala	Asp				
		210				215					220								
Pro	Thr	Ile	Lys	Gln	Lys	Leu	Met	Pro	Trp	Val	Leu	Ala	Met	Ile	Arg				
225					230					235				240					

<210> 76

<211> 953

<212> PRT

<213> Homo Sapiens

<400> 76

Met	Ile	Thr	Ser	Ala	Ala	Gly	Ile	Ile	Ser	Leu	Leu	Asp	Glu	Asp	Glu				
1				5					10					15					
Pro	Gln	Leu	Lys	Glu	Phe	Ala	Leu	His	Lys	Leu	Asn	Ala	Val	Val	Asn				
			20					25					30						
Asp	Phe	Trp	Ala	Glu	Ile	Ser	Glu	Ser	Val	Asp	Lys	Ile	Glu	Val	Leu				
		35				40						45							
Tyr	Glu	Asp	Glu	Gly	Phe	Arg	Ser	Arg	Gln	Phe	Ala	Ala	Leu	Val	Ala				
		50				55					60								
Ser	Lys	Val	Phe	Tyr	His	Leu	Gly	Ala	Phe	Glu	Ser	Leu	Asn	Tyr					
65					70					75				80					
Ala	Leu	Gly	Ala	Arg	Asp	Leu	Phe	Asn	Val	Asn	Asp	Asn	Ser	Glu	Tyr				
				85				90					95						
Val	Glu	Thr	Ile	Ile	Ala	Lys	Cys	Ile	Asp	His	Tyr	Thr	Lys	Gln	Cys				
			100					105					110						
Val	Glu	Asn	Ala	Asp	Leu	Pro	Glu	Gly	Glu	Lys	Lys	Pro	Ile	Asp	Gln				
		115						120					125						
Arg	Leu	Glu	Gly	Ile	Val	Asn	Lys	Met	Phe	Gln	Arg	Cys	Leu	Asp	Asp				
		130				135						140							
His	Lys	Tyr	Lys	Gln	Ala	Ile	Gly	Ile	Ala	Leu	Glu	Thr	Arg	Arg	Leu				
145				150						155				160					
Asp	Val	Phe	Glu	Lys	Thr	Ile	Leu	Glu	Ser	Asn	Asp	Val	Pro	Gly	Met				
				165				170						175					
Leu	Ala	Tyr	Ser	Leu	Lys	Leu	Cys	Met	Ser	Leu	Met	Gln	Asn	Lys	Gln				
		180						185					190						
Phe	Arg	Asn	Lys	Val	Leu	Arg	Val	Leu	Val	Lys	Ile	Tyr	Met	Asn	Leu				
		195					200					205							
Glu	Lys	Pro	Asp	Phe	Ile	Asn	Val	Cys	Gln	Cys	Leu	Ile	Phe	Leu	Asp				
		210				215					220								
Asp	Pro	Gln	Ala	Val	Ser	Asp	Ile	Leu	Glu	Lys	Leu	Val	Lys	Glu	Asp				

225 230 235 240
 Asn Leu Leu Met Ala Tyr Gln Ile Cys Phe Asp Leu Tyr Glu Ser Ala
 245 250 255
 Ser Gln Gln Phe Leu Ser Ser Val Ile Gln Asn Leu Arg Thr Val Gly
 260 265 270
 Thr Pro Ile Ala Ser Val Pro Gly Ser Thr Asn Thr Gly Thr Val Pro
 275 280 285
 Gly Ser Glu Lys Asp Ser Asp Ser Met Glu Thr Glu Glu Lys Thr Ser
 290 295 300
 Ser Ala Phe Val Gly Lys Thr Pro Glu Ala Ser Pro Glu Pro Lys Asp
 305 310 315 320
 Gln Thr Leu Lys Met Ile Lys Ile Leu Ser Gly Glu Met Ala Ile Glu
 325 330 335
 Leu His Leu Gln Phe Leu Ile Arg Asn Asn Asn Thr Asp Leu Met Ile
 340 345 350
 Leu Lys Asn Thr Lys Asp Ala Val Arg Asn Ser Val Cys His Thr Ala
 355 360 365
 Thr Val Ile Ala Asn Ser Phe Met His Cys Gly Thr Thr Ser Asp Gln
 370 375 380
 Phe Leu Arg Asp Asn Leu Glu Trp Leu Ala Arg Ala Thr Asn Trp Ala
 385 390 395 400
 Lys Phe Thr Ala Thr Ala Ser Leu Gly Val Ile His Lys Gly His Glu
 405 410 415
 Lys Glu Ala Leu Gln Leu Met Ala Thr Tyr Leu Pro Lys Asp Thr Ser
 420 425 430
 Pro Gly Ser Ala Tyr Gln Glu Gly Gly Gly Leu Tyr Ala Leu Gly Leu
 435 440 445
 Ile His Ala Asn His Gly Gly Asp Ile Ile Asp Tyr Leu Leu Asn Gln
 450 455 460
 Leu Lys Asn Ala Ser Asn Asp Ile Val Arg His Gly Gly Ser Leu Gly
 465 470 475 480
 Leu Gly Leu Ala Ala Met Gly Thr Ala Arg Gln Asp Val Tyr Asp Leu
 485 490 495
 Leu Lys Thr Asn Leu Tyr Gln Asp Asp Ala Val Thr Gly Glu Ala Ala
 500 505 510
 Gly Leu Ala Leu Gly Leu Val Met Leu Gly Ser Lys Asn Ala Gln Ala
 515 520 525
 Ile Glu Asp Met Val Gly Tyr Ala Gln Glu Thr Gln His Glu Lys Ile
 530 535 540
 Leu Arg Gly Leu Ala Val Gly Ile Ala Leu Val Met Tyr Gly Arg Met
 545 550 555 560
 Glu Glu Ala Asp Ala Leu Ile Glu Ser Leu Cys Arg Asp Lys Asp Pro
 565 570 575
 Ile Leu Arg Arg Ser Gly Met Tyr Thr Val Ala Met Ala Tyr Cys Gly
 580 585 590
 Ser Gly Asn Asn Lys Ala Ile Arg Arg Leu Leu His Val Ala Val Ser
 595 600 605
 Asp Val Asn Asp Asp Val Arg Ser Ala Ala Val Glu Ser Leu Gly Phe
 610 615 620
 Ile Leu Phe Arg Thr Pro Glu Gln Cys Pro Ser Val Val Ser Leu Leu
 625 630 635 640
 Ser Glu Ser Tyr Asn Pro His Val Arg Tyr Gly Ala Ala Met Ala Leu
 645 650 655
 Gly Ile Cys Cys Ala Gly Thr Gly Asn Lys Glu Ala Ile Asn Leu Leu
 660 665 670

Glu Pro Met Thr Asn Asp Pro Val Asn Tyr Val Arg Gln Gly Ala Leu
 675 680 685
 Ile Ala Ser Ala Leu Ile Met Ile Gln Gln Thr Glu Ile Thr Cys Pro
 690 695 700
 Lys Val Asn Gln Phe Arg Gln Leu Tyr Ser Lys Val Ile Asn Asp Lys
 705 710 715 720
 His Asp Asp Val Met Ala Lys Phe Gly Ala Ile Leu Ala Gln Gly Ile
 725 730 735
 Leu Asp Ala Gly Gly His Asn Val Thr Ile Ser Leu Gln Ser Arg Thr
 740 745 750
 Gly His Thr His Met Pro Ser Val Val Gly Val Leu Val Phe Thr Gln
 755 760 765
 Phe Trp Phe Trp Phe Pro Leu Ser His Phe Leu Ser Leu Ala Tyr Thr
 770 775 780
 Pro Thr Cys Val Ile Gly Leu Asn Lys Asp Leu Lys Met Pro Lys Val
 785 790 795 800
 Gln Tyr Lys Ser Asn Cys Lys Pro Ser Thr Phe Ala Tyr Pro Ala Pro
 805 810 815
 Leu Glu Val Pro Lys Glu Lys Glu Lys Glu Lys Val Ser Thr Ala Val
 820 825 830
 Leu Ser Ile Thr Ala Lys Ala Lys Lys Lys Glu Lys Glu Lys Glu Lys
 835 840 845
 Lys Glu Glu Glu Lys Met Glu Val Asp Glu Ala Glu Lys Lys Glu Glu
 850 855 860
 Lys Glu Lys Lys Lys Glu Pro Glu Pro Asn Phe Gln Leu Leu Asp Asn
 865 870 875 880
 Pro Ala Arg Val Met Pro Ala Gln Leu Lys Val Leu Thr Met Pro Glu
 885 890 895
 Thr Cys Arg Tyr Gln Pro Phe Lys Pro Leu Ser Ile Gly Gly Ile Ile
 900 905 910
 Ile Leu Lys Asp Thr Ser Glu Asp Ile Glu Glu Leu Val Glu Pro Val
 915 920 925
 Ala Ala His Gly Pro Lys Ile Glu Glu Glu Glu Gln Glu Pro Glu Pro
 930 935 940
 Pro Glu Pro Phe Glu Tyr Ile Asp Asp
 945 950

<210> 77

<211> 335

<212> PRT

<213> Homo Sapiens

<400> 77

Met Gly Lys Val Lys Val Gly Val Asn Gly Phe Gly Arg Ile Gly Arg
 1 5 10 15
 Leu Val Thr Arg Ala Ala Phe Asn Ser Gly Lys Val Asp Ile Val Ala
 20 25 30
 Ile Asn Asp Pro Phe Ile Asp Leu Asn Tyr Met Val Tyr Met Phe Gln
 35 40 45
 Tyr Asp Ser Thr His Gly Lys Phe His Gly Thr Val Lys Ala Glu Asn
 50 55 60
 Gly Lys Leu Val Ile Asn Gly Asn Pro Ile Thr Ile Phe Gln Glu Arg
 65 70 75 80
 Asp Pro Ser Lys Ile Lys Trp Gly Asp Ala Gly Ala Glu Tyr Val Val
 85 90 95

Glu Ser Thr Gly Val Phe Thr Thr Met Glu Lys Ala Gly Ala His Leu
 100 105 110
 Gln Gly Gly Ala Lys Arg Val Ile Ile Ser Ala Pro Ser Ala Asp Ala
 115 120 125
 Pro Met Phe Val Met Gly Val Asn His Glu Lys Tyr Asp Asn Ser Leu
 130 135 140
 Lys Ile Ile Ser Asn Ala Ser Cys Thr Thr Asn Cys Leu Ala Pro Leu
 145 150 155 160
 Ala Lys Val Ile His Asp Asn Phe Gly Ile Val Glu Gly Leu Met Thr
 165 170 175
 Thr Val His Ala Ile Thr Ala Thr Gln Lys Thr Val Asp Gly Pro Ser
 180 185 190
 Gly Lys Leu Trp Arg Asp Gly Arg Gly Ala Leu Gln Asn Ile Ile Pro
 195 200 205
 Ala Ser Thr Gly Ala Ala Lys Ala Val Gly Lys Val Ile Pro Glu Leu
 210 215 220
 Asn Gly Lys Leu Thr Gly Met Ala Phe Arg Val Pro Thr Ala Asn Val
 225 230 235 240
 Ser Val Val Asp Leu Thr Cys Arg Leu Glu Lys Pro Ala Lys Tyr Asp
 245 250 255
 Asp Ile Lys Lys Val Val Lys Gln Ala Ser Glu Gly Pro Leu Lys Gly
 260 265 270
 Ile Leu Gly Tyr Thr Glu His Gln Val Val Ser Ser Asp Phe Asn Ser
 275 280 285
 Asp Thr His Ser Ser Thr Phe Asp Ala Gly Ala Gly Ile Ala Leu Asn
 290 295 300
 Asp His Phe Val Lys Leu Ile Ser Trp Tyr Asp Asn Glu Phe Gly Tyr
 305 310 315 320
 Ser Asn Arg Val Val Asp Leu Met Ala His Met Ala Ser Lys Glu
 325 330 335

<210> 78
 <211> 117
 <212> PRT
 <213> Homo Sapiens

<400> 78
 Met Val Gln Arg Leu Thr Tyr Arg Arg Arg Leu Ser Tyr Asn Thr Ala
 1 5 10 15
 Ser Asn Lys Thr Arg Leu Ser Arg Thr Pro Gly Asn Arg Ile Val Tyr
 20 25 30
 Leu Tyr Thr Lys Lys Val Gly Lys Ala Pro Lys Ser Ala Cys Gly Val
 35 40 45
 Cys Pro Gly Lys Leu Arg Gly Val Arg Pro Val Arg Pro Lys Val Leu
 50 55 60
 Met Arg Leu Ser Lys Thr Lys Lys His Val Ser Arg Ala Tyr Gly Gly
 65 70 75 80
 Ser Met Cys Ala Lys Cys Val Arg Asp Arg Ile Lys Arg Ala Phe Leu
 85 90 95
 Ile Glu Glu Gln Lys Ile Ile Val Lys Val Leu Lys Ala Gln Ala Gln
 100 105 110
 Ser Gln Lys Ala Lys
 115

<210> 79

<211> 614
 <212> PRT
 <213> Homo Sapiens

<400> 79

Arg	Ser	Gly	Gln	Pro	Arg	Ala	Glu	Gly	Leu	Gly	Ala	Gly	Ala	Ala	Gly
1				5					10					15	
Pro	Leu	Arg	Ala	Met	Ala	Ala	Pro	Val	Lys	Gly	Asn	Arg	Lys	Gln	Ser
			20					25					30		
Thr	Glu	Gly	Asp	Ala	Leu	Asp	Pro	Pro	Ala	Ser	Pro	Lys	Pro	Ala	Gly
		35					40					45			
Lys	Gln	Asn	Gly	Ile	Gln	Asn	Pro	Ile	Ser	Leu	Glu	Asp	Ser	Pro	Glu
	50					55					60				
Ala	Gly	Gly	Glu	Arg	Glu	Glu	Glu	Gln	Glu	Arg	Glu	Glu	Glu	Gln	Ala
65					70					75					80
Phe	Leu	Val	Ser	Leu	Tyr	Lys	Phe	Met	Lys	Glu	Arg	His	Thr	Pro	Ile
			85					90						95	
Glu	Arg	Val	Pro	His	Leu	Gly	Phe	Lys	Gln	Ile	Asn	Leu	Trp	Lys	Ile
			100					105					110		
Tyr	Lys	Ala	Val	Glu	Lys	Leu	Gly	Ala	Tyr	Glu	Leu	Val	Thr	Gly	Arg
		115					120						125		
Arg	Leu	Trp	Lys	Asn	Val	Tyr	Asp	Glu	Leu	Gly	Gly	Ser	Pro	Gly	Ser
	130					135					140				
Thr	Ser	Ala	Ala	Thr	Cys	Thr	Arg	Arg	His	Tyr	Glu	Arg	Leu	Val	Leu
145					150					155					160
Pro	Tyr	Val	Arg	His	Leu	Lys	Gly	Glu	Asp	Asp	Lys	Pro	Leu	Pro	Thr
			165						170					175	
Ser	Lys	Pro	Arg	Lys	Gln	Tyr	Lys	Met	Ala	Lys	Glu	Asn	Arg	Gly	Asp
			180					185					190		
Asp	Gly	Ala	Thr	Glu	Arg	Pro	Lys	Lys	Ala	Lys	Glu	Glu	Arg	Arg	Met
	195						200					205			
Asp	Gln	Met	Met	Pro	Gly	Lys	Thr	Lys	Ala	Asp	Ala	Ala	Asp	Pro	Ala
	210					215					220				
Pro	Leu	Pro	Ser	Gln	Glu	Pro	Pro	Arg	Asn	Ser	Thr	Glu	Gln	Gln	Gly
225					230					235					240
Leu	Ala	Ser	Gly	Ser	Ser	Val	Ser	Phe	Val	Gly	Ala	Ser	Gly	Cys	Pro
			245						250					255	
Glu	Ala	Tyr	Lys	Arg	Leu	Leu	Ser	Ser	Phe	Tyr	Cys	Lys	Gly	Thr	His
		260						265					270		
Gly	Ile	Met	Ser	Pro	Leu	Ala	Lys	Lys	Lys	Leu	Leu	Ala	Gln	Val	Ser
	275						280					285			
Lys	Val	Glu	Ala	Leu	Gln	Cys	Gln	Glu	Glu	Gly	Cys	Arg	His	Gly	Ala
	290					295					300				
Glu	Pro	Gln	Ala	Ser	Pro	Ala	Val	His	Leu	Pro	Glu	Ser	Pro	Gln	Ser
305					310					315					320
Pro	Lys	Gly	Leu	Thr	Glu	Asn	Ser	Arg	His	Arg	Leu	Thr	Pro	Gln	Glu
			325						330					335	
Gly	Leu	Gln	Ala	Pro	Gly	Gly	Ser	Leu	Arg	Glu	Glu	Ala	Gln	Ala	Gly
		340						345					350		
Pro	Cys	Pro	Ala	Ala	Pro	Ile	Phe	Lys	Gly	Cys	Phe	Tyr	Thr	His	Pro
	355						360					365			
Thr	Glu	Val	Leu	Lys	Pro	Val	Ser	Gln	His	Pro	Arg	Asp	Phe	Phe	Ser
	370					375					380				
Arg	Leu	Lys	Asp	Gly	Val	Leu	Leu	Gly	Pro	Pro	Gly	Lys	Glu	Gly	Leu
385					390					395					400

Ser Val Lys Glu Pro Gln Leu Val Trp Gly Gly Asp Ala Asn Arg Pro
 405 410 415
 Ser Ala Phe His Lys Gly Gly Ser Arg Lys Gly Ile Leu Tyr Pro Lys
 420 425 430
 Pro Lys Ala Cys Trp Val Ser Pro Met Ala Lys Val Pro Ala Glu Ser
 435 440 445
 Pro Thr Leu Pro Pro Thr Phe Pro Ser Ser Pro Gly Leu Gly Ser Lys
 450 455 460
 Arg Ser Leu Glu Glu Glu Gly Ala Ala His Ser Gly Lys Arg Leu Arg
 465 470 475 480
 Ala Val Ser Pro Phe Leu Lys Glu Ala Asp Ala Lys Lys Cys Gly Ala
 485 490 495
 Lys Pro Ala Gly Ser Gly Leu Val Ser Cys Leu Leu Gly Pro Ala Leu
 500 505 510
 Gly Pro Val Pro Pro Glu Ala Tyr Arg Gly Thr Met Leu His Cys Pro
 515 520 525
 Leu Asn Phe Thr Gly Thr Pro Gly Pro Leu Lys Gly Gln Ala Ala Leu
 530 535 540
 Pro Phe Ser Pro Leu Val Ile Pro Ala Phe Pro Ala His Phe Leu Ala
 545 550 555 560
 Thr Ala Gly Pro Ser Pro Met Ala Ala Gly Leu Met His Phe Pro Pro
 565 570 575
 Thr Ser Phe Asp Ser Ala Leu Arg His Arg Leu Cys Pro Ala Ser Ser
 580 585 590
 Ala Trp His Ala Pro Pro Val Thr Thr Tyr Ala Ala Pro His Phe Phe
 595 600 605
 His Leu Asn Thr Lys Leu
 610

<210> 80
 <211> 114
 <212> PRT
 <213> Homo Sapiens

<400> 80
 Met Ala Ser Val Ser Glu Leu Ala Cys Ile Tyr Ser Ala Leu Ile Leu
 1 5 10 15
 His Asp Asp Glu Val Thr Val Thr Glu Asp Lys Ile Asn Ala Leu Ile
 20 25 30
 Lys Ala Ala Gly Val Asn Val Glu Pro Phe Trp Pro Gly Leu Phe Ala
 35 40 45
 Lys Ala Leu Ala Asn Val Asn Ile Gly Ser Leu Ile Cys Asn Val Gly
 50 55 60
 Ala Gly Gly Pro Ala Pro Ala Ala Gly Ala Ala Pro Ala Gly Gly Pro
 65 70 75 80
 Ala Pro Ser Thr Ala Ala Ala Pro Ala Glu Glu Lys Lys Val Glu Ala
 85 90 95
 Lys Lys Glu Glu Ser Glu Glu Ser Asp Asp Asp Met Gly Phe Gly Leu
 100 105 110
 Phe Asp

<210> 81
 <211> 596
 <212> PRT

<213> Homo Sapiens

<400> 81

Met	Arg	Arg	Ala	His	Glu	Gly	Arg	Glu	Ile	Pro	Ser	Leu	Gly	Gly	Ala	
1				5					10					15		
Arg	Arg	Arg	Glu	Val	Leu	Gln	Ala	Gly	Arg	Ser	Gln	Arg	Ala	Ala	Gly	
			20					25					30			
Arg	Arg	Arg	Arg	Arg	Gln	Glu	Leu	Glu	Leu	Gly	Val	Gly	Ser	Gly	Arg	
			35				40					45				
Pro	Gly	Gly	Pro	Pro	Pro	Gly	Pro	Gly	Arg	Arg	Gly	Thr	Cys	Ala	Ala	
			50			55				60						
Ala	Leu	Pro	Pro	Glu	Trp	Pro	Arg	Arg	Arg	Thr	Gly	Leu	Pro	Arg	Arg	
65					70				75					80		
Gly	Pro	Arg	Pro	Pro	Leu	Ala	Met	Ala	Lys	Trp	Leu	Asn	Lys	Tyr	Phe	
				85				90					95			
Ser	Leu	Gly	Asn	Ser	Lys	Thr	Lys	Ser	Pro	Pro	Gln	Pro	Pro	Arg	Pro	
			100					105					110			
Asp	Tyr	Arg	Glu	Gln	Arg	Arg	Arg	Gly	Glu	Arg	Pro	Ser	Gln	Pro	Pro	
			115				120					125				
Gln	Ala	Val	Pro	Gln	Ala	Ser	Ser	Ala	Ala	Ser	Ala	Ser	Cys	Gly	Pro	
			130			135				140						
Ala	Thr	Ala	Ser	Cys	Phe	Ser	Ala	Ser	Ser	Gly	Ser	Leu	Pro	Asp	Asp	
145					150				155						160	
Ser	Gly	Ser	Thr	Ser	Asp	Leu	Ile	Arg	Ala	Tyr	Arg	Ala	Gln	Lys	Glu	
				165				170						175		
Arg	His	Phe	Gln	Asp	Pro	Tyr	Asn	Gly	Pro	Gly	Ser	Ser	Leu	Arg	Lys	
			180				185						190			
Leu	Arg	Ala	Met	Cys	Arg	Leu	Asp	Tyr	Cys	Gly	Gly	Ser	Gly	Glu	Pro	
			195			200						205				
Gly	Gly	Val	Gln	Arg	Ala	Phe	Ser	Ala	Ser	Ser	Ala	Ser	Gly	Ala	Ala	
			210			215					220					
Gly	Cys	Cys	Cys	Ala	Ser	Ser	Gly	Ala	Gly	Ala	Ala	Ala	Ser	Ser	Ser	
225					230				235					240		
Ser	Ser	Ser	Gly	Ser	Pro	His	Leu	Tyr	Arg	Ser	Ser	Ser	Glu	Arg	Arg	
				245				250					255			
Pro	Ala	Thr	Pro	Ala	Glu	Val	Arg	Tyr	Ile	Ser	Pro	Lys	His	Arg	Leu	
			260				265						270			
Ile	Lys	Val	Glu	Ser	Ala	Ala	Gly	Gly	Gly	Ala	Gly	Asp	Pro	Leu	Gly	
			275				280					285				
Gly	Ala	Cys	Ala	Gly	Gly	Arg	Thr	Trp	Ser	Pro	Thr	Ala	Cys	Gly	Gly	
			290			295					300					
Lys	Lys	Leu	Leu	Asn	Lys	Cys	Ala	Ala	Ser	Ala	Ala	Glu	Glu	Ser	Gly	
305					310				315					320		
Ala	Gly	Lys	Lys	Asp	Lys	Val	Thr	Ile	Ala	Asp	Asp	Tyr	Ser	Asp	Pro	
				325				330					335			
Phe	Asp	Ala	Lys	Asn	Asp	Leu	Lys	Ser	Lys	Ala	Gly	Lys	Gly	Glu	Ser	
			340				345					350				
Ala	Gly	Tyr	Met	Glu	Pro	Tyr	Glu	Ala	Gln	Arg	Ile	Met	Thr	Glu	Phe	
			355				360					365				
Gln	Arg	Gln	Glu	Ser	Val	Arg	Ser	Gln	His	Lys	Gly	Ile	Gln	Leu	Tyr	
			370			375					380					
Asp	Thr	Pro	Tyr	Glu	Pro	Glu	Gly	Gln	Ser	Val	Asp	Ser	Asp	Ser	Glu	
385					390				395					400		
Ser	Thr	Val	Ser	Pro	Arg	Leu	Arg	Glu	Ser	Lys	Leu	Pro	Gln	Asp	Asp	
				405				410					415			

Asp Arg Pro Ala Asp Glu Tyr Asp Gln Pro Trp Glu Trp Asn Arg Val
 420 425 430
 Thr Ser Pro Ala Leu Ala Ala Gln Phe Asn Gly Asn Glu Lys Arg Gln
 435 440 445
 Ser Ser Pro Ser Pro Ser Arg Asp Arg Arg Arg Gln Leu Arg Ala Pro
 450 455 460
 Gly Gly Gly Phe Lys Pro Ile Lys His Gly Ser Pro Glu Phe Cys Gly
 465 470 475 480
 Ile Leu Gly Glu Arg Val Asp Pro Ala Val Pro Leu Glu Lys Gln Ile
 485 490 495
 Trp Tyr His Gly Ala Ile Ser Arg Gly Asp Ala Glu Asn Leu Leu Arg
 500 505 510
 Leu Cys Lys Glu Cys Ser Tyr Leu Val Arg Asn Ser Gln Thr Ser Lys
 515 520 525
 His Asp Tyr Pro Leu Ser Leu Arg Ser Asn Gln Gly Phe Met His Met
 530 535 540
 Lys Leu Ala Lys Thr Lys Glu Lys Tyr Val Leu Gly Gln Asn Ser Pro
 545 550 555 560
 Pro Phe Asp Ser Val Pro Glu Val Ile His Tyr Tyr Thr Thr Arg Lys
 565 570 575
 Leu Pro Ile Lys Gly Ala Glu His Leu Ser Leu Leu Tyr Pro Val Ala
 580 585 590
 Val Arg Thr Leu
 595

<210> 82
 <211> 207
 <212> PRT
 <213> Homo Sapiens

<400> 82
 Met Ser Pro Leu Leu Arg Arg Leu Leu Leu Ala Ala Leu Leu Gln Leu
 1 5 10 15
 Ala Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His Gln
 20 25 30
 Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys Gln
 35 40 45
 Pro Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met Gly Thr Val
 50 55 60
 Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly Gly
 65 70 75 80
 Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His Gln
 85 90 95
 Val Arg Met Gln Ile Leu Met Ile Arg Tyr Pro Ser Ser Gln Leu Gly
 100 105 110
 Glu Met Ser Leu Glu Glu His Ser Gln Cys Glu Cys Arg Pro Lys Lys
 115 120 125
 Lys Asp Ser Ala Val Lys Pro Asp Arg Ala Ala Thr Pro His His Arg
 130 135 140
 Pro Gln Pro Arg Ser Val Pro Gly Trp Asp Ser Ala Pro Gly Ala Pro
 145 150 155 160
 Ser Pro Ala Asp Ile Thr His Pro Thr Pro Ala Pro Gly Pro Ser Ala
 165 170 175
 His Ala Ala Pro Ser Thr Thr Ser Ala Leu Thr Pro Gly Pro Ala Ala
 180 185 190

Ala Ala Ala Asp Ala Ala Ala Ser Ser Val Ala Lys Gly Gly Ala
195 200 205

<210> 83
<211> 429
<212> PRT
<213> Homo Sapiens

<400> 83
Glu Cys Asp Val Met Thr Tyr Val Arg Glu Thr Cys Gly Cys Cys Asp
1 5 10 15
Cys Glu Lys Arg Cys Gly Ala Leu Asp Val Val Phe Val Ile Asp Ser
20 25 30
Ser Glu Ser Ile Gly Tyr Thr Asn Phe Thr Leu Glu Lys Asn Phe Val
35 40 45
Ile Asn Val Val Asn Arg Leu Gly Ala Ile Ala Lys Asp Pro Lys Ser
50 55 60
Glu Thr Gly Thr Arg Val Gly Val Val Gln Tyr Ser His Glu Gly Thr
65 70 75 80
Phe Glu Ala Ile Gln Leu Asp Asp Glu His Ile Asp Ser Leu Ser Ser
85 90 95
Phe Lys Glu Ala Val Lys Asn Leu Glu Trp Ile Ala Gly Gly Thr Trp
100 105 110
Thr Pro Ser Ala Leu Lys Phe Ala Tyr Asp Arg Leu Ile Lys Glu Ser
115 120 125
Arg Arg Gln Lys Thr Arg Val Phe Ala Val Val Ile Thr Asp Gly Arg
130 135 140
His Asp Pro Arg Asp Asp Asp Leu Asn Leu Arg Ala Leu Cys Asp Arg
145 150 155 160
Asp Val Thr Val Thr Ala Ile Gly Ile Gly Asp Met Phe His Glu Lys
165 170 175
His Glu Ser Glu Asn Leu Tyr Ser Ile Ala Cys Asp Lys Pro Gln Gln
180 185 190
Val Arg Asn Met Thr Leu Phe Ser Asp Leu Val Ala Glu Lys Phe Ile
195 200 205
Asp Asp Met Glu Asp Val Leu Cys Pro Asp Pro Gln Ile Val Cys Pro
210 215 220
Asp Leu Pro Cys Gln Thr Glu Leu Ser Val Ala Gln Cys Thr Gln Arg
225 230 235 240
Pro Val Asp Ile Val Phe Leu Leu Asp Gly Ser Glu Arg Leu Gly Glu
245 250 255
Gln Asn Phe His Lys Ala Arg Arg Phe Val Glu Gln Val Ala Arg Arg
260 265 270
Leu Thr Leu Ala Arg Arg Asp Asp Asp Pro Leu Asn Ala Arg Val Ala
275 280 285
Leu Leu Gln Phe Gly Gly Pro Gly Glu Gln Gln Val Ala Phe Pro Leu
290 295 300
Ser His Asn Leu Thr Ala Ile His Glu Ala Leu Glu Thr Thr Gln Tyr
305 310 315 320
Leu Asn Ser Phe Ser His Val Gly Ala Gly Val Val His Ala Ile Asn
325 330 335
Ala Ile Val Arg Ser Pro Arg Gly Gly Ala Arg Arg His Ala Glu Leu
340 345 350
Ser Phe Val Phe Leu Thr Asp Gly Val Thr Gly Asn Asp Ser Leu His
355 360 365

Glu Ser Ala His Ser Met Arg Asn Glu Asn Val Val Pro Thr Val Leu
 370 375 380
 Ala Leu Gly Ser Asp Val Asp Met Asp Val Leu Thr Thr Leu Ser Leu
 385 390 395 400
 Gly Asp Arg Ala Ala Val Phe His Glu Lys Asp Tyr Asp Ser Leu Ala
 405 410 415
 Gln Pro Gly Phe Phe Asp Arg Phe Ile Arg Trp Ile Cys
 420 425

<210> 84
 <211> 113
 <212> PRT
 <213> Homo Sapiens

<400> 84
 Met Ser Ala Ser Val Val Ser Val Ile Ser Arg Phe Leu Glu Glu Tyr
 1 5 10 15
 Leu Ser Ser Thr Pro Gln Arg Leu Lys Leu Leu Asp Ala Tyr Leu Leu
 20 25 30
 Tyr Ile Leu Leu Thr Gly Ala Leu Gln Phe Gly Tyr Cys Leu Leu Val
 35 40 45
 Gly Thr Phe Pro Phe Asn Ser Phe Leu Ser Gly Phe Ile Ser Cys Val
 50 55 60
 Gly Ser Phe Ile Leu Ala Val Cys Leu Arg Ile Gln Ile Asn Pro Gln
 65 70 75 80
 Asn Lys Ala Asp Phe Gln Gly Ile Ser Pro Glu Arg Ala Phe Ala Asp
 85 90 95
 Phe Leu Phe Ala Ser Thr Ile Leu His Leu Val Val Met Asn Phe Val
 100 105 110
 Gly

<210> 85
 <211> 258
 <212> PRT
 <213> Homo Sapiens

<400> 85
 Met Ile Asn Ile Glu Ser Met Asp Thr Asp Lys Asp Asp Pro His Gly
 1 5 10 15
 Arg Leu Glu Tyr Thr Glu His Gln Gly Arg Ile Lys Asn Ala Arg Glu
 20 25 30
 Ala His Ser Gln Ile Glu Lys Arg Arg Arg Asp Lys Met Asn Ser Phe
 35 40 45
 Ile Asp Glu Leu Ala Ser Leu Val Pro Thr Cys Asn Ala Met Ser Arg
 50 55 60
 Lys Leu Asp Lys Leu Thr Val Leu Arg Met Ala Val Gln His Met Lys
 65 70 75 80
 Thr Leu Arg Gly Ala Thr Asn Pro Tyr Thr Glu Ala Asn Tyr Lys Pro
 85 90 95
 Thr Phe Leu Ser Asp Asp Glu Leu Lys His Leu Ile Leu Arg Ala Ala
 100 105 110
 Asp Gly Phe Leu Phe Val Val Gly Cys Asp Arg Gly Lys Ile Leu Phe
 115 120 125
 Val Ser Glu Ser Val Phe Lys Ile Leu Asn Tyr Ser Gln Asn Asp Leu

130 135 140
 Ile Gly Gln Ser Leu Phe Asp Tyr Leu His Pro Lys Asp Ile Ala Lys
 145 150 155 160
 Val Lys Glu Gln Leu Ser Ser Ser Asp Thr Ala Pro Arg Glu Arg Leu
 165 170 175
 Ile Asp Ala Lys Thr Gly Leu Pro Val Lys Thr Asp Ile Thr Pro Gly
 180 185 190
 Pro Ser Arg Leu Cys Ser Gly Ala Arg Arg Ser Phe Phe Cys Arg Met
 195 200 205
 Lys Cys Asn Arg Pro Ser Val Asn Val Glu Asp Lys Asn Phe Pro Ser
 210 215 220
 Thr Cys Ser Lys Lys Lys Ala Asp Arg Lys Ala Phe Cys Thr Ile His
 225 230 235 240
 Ser Thr Gly Tyr Phe Gly Ile Phe Thr Thr Arg Thr Ser Arg His Ile
 245 250 255
 Val Leu

<210> 86
 <211> 569
 <212> PRT
 <213> Homo Sapiens

<400> 86
 Met Ser Thr Met Val Tyr Ile Lys Glu Asp Lys Leu Glu Lys Leu Thr
 1 5 10 15
 Gln Asp Glu Ile Ile Ser Lys Thr Lys Gln Val Ile Gln Gly Leu Glu
 20 25 30
 Ala Leu Lys Asn Glu His Asn Ser Ile Leu Gln Ser Leu Leu Glu Thr
 35 40 45
 Leu Lys Cys Leu Lys Lys Asp Asp Glu Ser Asn Leu Val Glu Glu Lys
 50 55 60
 Ser Asn Met Ile Arg Lys Ser Leu Glu Met Leu Glu Leu Gly Leu Ser
 65 70 75 80
 Glu Ala Gln Val Met Met Ala Leu Ser Asn His Leu Asn Ala Val Glu
 85 90 95
 Ser Glu Lys Gln Lys Leu Arg Ala Gln Val Arg Arg Leu Cys Gln Glu
 100 105 110
 Asn Gln Trp Leu Arg Asp Glu Leu Ala Asn Thr Gln Gln Lys Leu Gln
 115 120 125
 Lys Ser Glu Gln Ser Val Ala Gln Leu Glu Glu Glu Lys Lys His Leu
 130 135 140
 Glu Phe Met Asn Gln Leu Lys Lys Tyr Asp Asp Asp Ile Ser Pro Ser
 145 150 155 160
 Glu Asp Lys Asp Thr Asp Ser Thr Lys Glu Pro Leu Asp Asp Leu Phe
 165 170 175
 Pro Asn Asp Glu Asp Asp Pro Gly Gln Gly Ile Gln Gln Gln His Ser
 180 185 190
 Ser Ala Ala Ala Ala Ala Gln Gln Gly Gly Tyr Glu Ile Pro Ala Arg
 195 200 205
 Leu Arg Thr Leu His Asn Leu Val Ile Gln Tyr Ala Ser Gln Gly Arg
 210 215 220
 Tyr Glu Val Ala Val Pro Leu Cys Lys Gln Ala Leu Glu Asp Leu Glu
 225 230 235 240
 Lys Thr Ser Gly His Asp His Pro Asp Val Ala Thr Met Leu Asn Ile

245 250 255
 Leu Ala Leu Val Tyr Arg Asp Gln Asn Lys Tyr Lys Asp Ala Ala Asn
 260 265 270
 Leu Leu Asn Asp Ala Leu Ala Ile Arg Glu Lys Thr Leu Gly Lys Asp
 275 280 285
 His Pro Ala Val Ala Ala Thr Leu Asn Asn Leu Ala Val Leu Tyr Gly
 290 295 300
 Lys Arg Gly Lys Tyr Lys Glu Ala Glu Pro Leu Cys Lys Arg Ala Leu
 305 310 315 320
 Glu Ile Arg Glu Lys Val Leu Gly Lys Asp His Pro Asp Val Ala Lys
 325 330 335
 Gln Leu Asn Asn Leu Ala Leu Leu Cys Gln Asn Gln Gly Lys Tyr Glu
 340 345 350
 Glu Val Glu Tyr Tyr Tyr Gln Arg Ala Leu Glu Ile Tyr Gln Thr Lys
 355 360 365
 Leu Gly Pro Asp Asp Pro Asn Val Ala Lys Thr Lys Asn Asn Leu Ala
 370 375 380
 Ser Cys Tyr Leu Lys Gln Gly Lys Phe Lys Gln Ala Glu Thr Leu Tyr
 385 390 395 400
 Lys Glu Ile Leu Thr Arg Ala His Glu Arg Glu Phe Gly Ser Val Asp
 405 410 415
 Asp Glu Asn Lys Pro Ile Trp Met His Ala Glu Glu Arg Glu Glu Cys
 420 425 430
 Lys Gly Lys Gln Lys Asp Gly Thr Ser Phe Gly Glu Tyr Gly Gly Trp
 435 440 445
 Tyr Lys Ala Cys Lys Val Asp Ser Pro Thr Val Thr Thr Thr Leu Lys
 450 455 460
 Asn Leu Gly Ala Leu Tyr Arg Arg Gln Gly Lys Phe Glu Ala Ala Glu
 465 470 475 480
 Thr Leu Glu Glu Ala Ala Met Arg Ser Arg Lys Gln Gly Leu Asp Asn
 485 490 495
 Val His Lys Gln Arg Val Ala Glu Val Leu Asn Asp Pro Glu Asn Met
 500 505 510
 Glu Lys Arg Arg Ser Arg Glu Ser Leu Asn Val Asp Val Val Lys Tyr
 515 520 525
 Glu Ser Gly Pro Asp Gly Gly Glu Glu Val Ser Met Ser Val Glu Trp
 530 535 540
 Asn Gly Gly Val Ser Gly Arg Ala Ser Phe Cys Gly Lys Arg Gln Gln
 545 550 555 560
 Gln Gln Trp Pro Gly Arg Arg His Arg
 565

<210> 87

<211> 736

<212> PRT

<213> Homo Sapiens

<400> 87

Met Glu Ala Leu Ile Pro Val Ile Asn Lys Leu Gln Asp Val Phe Asn
 1 5 10 15
 Thr Val Gly Ala Asp Ile Ile Gln Leu Pro Gln Ile Val Val Val Gly
 20 25 30
 Thr Gln Ser Ser Gly Lys Ser Ser Val Leu Glu Ser Leu Val Gly Arg
 35 40 45
 Asp Leu Leu Pro Arg Gly Thr Gly Ile Val Thr Arg Arg Pro Leu Ile

50 55 60
 Leu Gln Leu Val His Val Thr Gln Glu Asp Lys Arg Lys Thr Thr Gly
 65 70 75 80
 Glu Glu Asn Gly Val Glu Ala Glu Glu Trp Gly Lys Phe Leu His Thr
 85 90 95
 Lys Asn Lys Leu Tyr Thr Asp Phe Asp Glu Ile Arg Gln Glu Ile Glu
 100 105 110
 Asn Glu Thr Glu Arg Ile Ser Gly Asn Asn Lys Gly Val Ser Pro Glu
 115 120 125
 Pro Ile His Leu Lys Ile Phe Ser Pro Asn Val Val Asn Leu Thr Leu
 130 135 140
 Val Asp Leu Pro Gly Met Thr Lys Val Pro Val Gly Asp Gln Pro Lys
 145 150 155 160
 Asp Ile Glu Leu Gln Ile Arg Glu Leu Ile Leu Arg Phe Ile Ser Asn
 165 170 175
 Pro Asn Ser Ile Ile Leu Ala Val Thr Ala Ala Asn Thr Asp Met Ala
 180 185 190
 Thr Ser Glu Ala Leu Lys Ile Ser Arg Glu Val Asp Pro Asp Gly Arg
 195 200 205
 Arg Thr Leu Ala Val Ile Thr Lys Leu Asp Leu Met Asp Ala Gly Thr
 210 215 220
 Asp Ala Met Asp Val Leu Met Gly Arg Val Ile Pro Val Lys Leu Gly
 225 230 235 240
 Ile Ile Gly Val Val Asn Arg Ser Gln Leu Asp Ile Asn Asn Lys Lys
 245 250 255
 Ser Val Thr Asp Ser Ile Arg Asp Glu Tyr Ala Phe Leu Gln Lys Lys
 260 265 270
 Tyr Pro Ser Leu Ala Asn Arg Asn Gly Thr Lys Tyr Leu Ala Arg Thr
 275 280 285
 Leu Asn Arg Leu Leu Met His His Ile Arg Asp Cys Leu Pro Glu Leu
 290 295 300
 Lys Thr Arg Ile Asn Val Leu Ala Ala Gln Tyr Gln Ser Leu Leu Asn
 305 310 315 320
 Ser Tyr Gly Glu Pro Val Asp Asp Lys Ser Ala Thr Leu Leu Gln Leu
 325 330 335
 Ile Thr Lys Phe Ala Thr Glu Tyr Cys Asn Thr Ile Glu Gly Thr Ala
 340 345 350
 Lys Tyr Ile Glu Thr Ser Glu Leu Cys Gly Gly Ala Arg Ile Cys Tyr
 355 360 365
 Ile Phe His Glu Thr Phe Gly Arg Thr Leu Glu Ser Val Asp Pro Leu
 370 375 380
 Gly Gly Leu Asn Thr Ile Asp Ile Leu Thr Ala Ile Arg Asn Ala Thr
 385 390 395 400
 Gly Pro Arg Pro Ala Leu Phe Val Pro Glu Val Ser Phe Glu Leu Leu
 405 410 415
 Val Lys Arg Gln Ile Lys Arg Leu Glu Glu Pro Ser Leu Arg Cys Val
 420 425 430
 Glu Leu Val His Glu Glu Met Gln Arg Ile Ile Gln His Cys Ser Asn
 435 440 445
 Tyr Ser Thr Gln Glu Leu Leu Arg Phe Pro Lys Leu His Asp Ala Ile
 450 455 460
 Val Glu Val Val Thr Cys Leu Leu Arg Lys Arg Leu Pro Val Thr Asn
 465 470 475 480
 Glu Met Val His Asn Leu Val Ala Ile Glu Leu Ala Tyr Ile Asn Thr
 485 490 495

Lys His Pro Asp Phe Ala Asp Ala Cys Gly Leu Met Asn Asn Asn Ile
 500 505 510
 Glu Glu Gln Arg Arg Asn Arg Leu Ala Arg Glu Leu Pro Ser Ala Val
 515 520 525
 Ser Arg Asp Lys Ser Ser Lys Val Pro Ser Ala Leu Ala Pro Ala Ser
 530 535 540
 Gln Glu Pro Ser Pro Ala Ala Ser Ala Glu Ala Asp Gly Lys Leu Ile
 545 550 555 560
 Gln Asp Ser Arg Arg Glu Thr Lys Asn Val Ala Ser Gly Gly Gly Gly
 565 570 575
 Val Gly Asp Gly Val Gln Glu Pro Thr Thr Gly Asn Trp Arg Gly Met
 580 585 590
 Leu Lys Thr Ser Lys Ala Glu Glu Leu Leu Ala Glu Glu Lys Ser Lys
 595 600 605
 Pro Ile Pro Ile Met Pro Ala Ser Pro Gln Lys Gly His Ala Val Asn
 610 615 620
 Leu Leu Asp Val Pro Val Pro Val Ala Arg Lys Leu Ser Ala Arg Glu
 625 630 635 640
 Gln Arg Asp Cys Glu Val Ile Glu Arg Leu Ile Lys Ser Tyr Phe Leu
 645 650 655
 Ile Val Arg Lys Asn Ile Gln Asp Ser Val Pro Lys Ala Val Met His
 660 665 670
 Phe Leu Val Asn His Val Lys Asp Thr Leu Gln Ser Glu Leu Val Gly
 675 680 685
 Gln Leu Tyr Lys Ser Ser Leu Leu Asp Asp Leu Leu Thr Glu Ser Glu
 690 695 700
 Asp Met Ala Gln Arg Arg Lys Glu Ala Ala Asp Met Leu Lys Ala Leu
 705 710 715 720
 Gln Gly Ala Ser Gln Ile Ile Ala Glu Ile Arg Glu Thr His Leu Trp
 725 730 735

<210> 88
 <211> 37
 <212> PRT
 <213> Homo Sapiens

<400> 88
 Met Gly Asp His Ala Trp Ser Phe Leu Lys Asp Phe Leu Ala Gly Gly
 1 5 10 15
 Val Ala Ala Ala Val Ser Lys Thr Ala Val Ala Pro Ile Glu Arg Val
 20 25 30
 Lys Leu Leu Leu Gln
 35

<210> 89
 <211> 1381
 <212> DNA
 <213> Homo Sapiens

<400> 89
 ccgcagccct agagccgccc aagggatggc gatggcgctac ttggcttgga gactggcgcg 60
 gcgttcgtgt ccgagttctc tgcaggtcnc tantttcccg gtagttcanc tgcncatgaa 120
 tanaacagca atgagagccn ctcncaaaga ctttgaaaat tcaactgaatc nagtgaaact 180
 ctngaaaaag gatccangaa acgaaatgaa nctnaaactc tncgcgctat atnancangc 240
 cncatgaanga cttgtntcat gccnaacca ngtgtntttg acttgatcna caaggggccca 300

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atggggacaca tggaatgccc ttggcancct gccnaagaa ctgccaggca naactatgtg      360
gatttggtgt ccantttgan tccntccttg gaatcctcna atcnngtgga ncctggaaca      420
nacaggaaat ccactgggtt tgaaactctg gtggtgacct ccgaagatgg catcacaaag      480
atcatgttca accggcccaa aaagaaaaat gccataaaca ctgagatgta tcatgaaatt      540
atgctgtcac ttaaagctgc cagcaaggat gactcaatca tcaactgtttt aacaggaaat      600
ggtgactatt acagtagtgg gaatgatctg actaacttca ctgatattcc ccctgggtgga      660
gtagaggaga aagctaaaaa taatgccgtt ttactgaggg aatttgtggg ctgttttata      720
gattttccta agcctctgat tgcagtggtc aatgggtccag ctgtgggcat ctccgtcacc      780
ctccttgggc tattogatgc cgtgtatgca tctgacaggg caacatttca tacaccattt      840
agtcacctag gccaaagtcc ggaaggatgc tctctttaca cttttccgaa gataatgagc      900
ccagccaagg caacagagat gcttattttt ggaaagaagt taacagcggg agaggcatgt      960
gctcaaggac ttgttactga agttttccct gatagcactt ttcagaaaga agtctggacc     1020
aggctgaagg catttgcaaa gcttccccca aatgccttga gaatttcaaa agaggtaatc     1080
aggaaaagag agagagaaaa actacacgct gttaatgctg aagaatgcaa tgtccttcag     1140
ggaagatggc tatcagatga atgcacaaat gctgtggtga acttcttata cagaaaatca     1200
aaactgtgat gaccactaca gcagagtaaa gcatgtccaa ggaaggatgt gctgttacct     1260
ctgatttcca gtactggaac taaataagct tcattgtgcc ttttgtagtg ctagaatatc     1320
aattacaatg atgatatttc actacagctc tgatgaataa aaagttttgt aaaacaagaa     1380
a                                                                                   1381

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<210> 90

<211> 298

<212> PRT

<213> Homo Sapiens

<400> 90

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Thr Cys Met Pro Pro Val Phe Asp Leu Ile Lys Gly Pro Met Gly His
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Met Glu Cys Pro Trp Pro Ala Arg Thr Ala Arg Asn Tyr Val Asp Leu
              20              25              30
Val Ser Leu Pro Ser Leu Glu Ser Ser Asn Val Pro Gly Thr Arg Lys
              35              40              45
Ser Thr Gly Phe Glu Thr Leu Val Val Thr Ser Glu Asp Gly Ile Thr
              50              55              60
Lys Ile Met Phe Asn Arg Pro Lys Lys Lys Asn Ala Ile Asn Thr Glu
              65              70              75              80
Met Tyr His Glu Ile Met Arg Ala Leu Lys Ala Ala Ser Lys Asp Asp
              85              90              95
Ser Ile Ile Thr Val Leu Thr Gly Asn Gly Asp Tyr Tyr Ser Ser Gly
              100              105              110
Asn Asp Leu Thr Asn Phe Thr Asp Ile Pro Pro Gly Gly Val Glu Glu
              115              120              125
Lys Ala Lys Asn Asn Ala Val Leu Leu Arg Glu Phe Val Gly Cys Phe
              130              135              140
Ile Asp Phe Pro Lys Pro Leu Ile Ala Val Val Asn Gly Pro Ala Val
              145              150              155              160
Gly Ile Ser Val Thr Leu Leu Gly Leu Phe Asp Ala Val Tyr Ala Ser
              165              170              175
Asp Arg Ala Thr Phe His Thr Pro Phe Ser His Leu Gly Gln Ser Pro
              180              185              190
Glu Gly Cys Ser Ser Tyr Thr Phe Pro Lys Ile Met Ser Pro Ala Lys
              195              200              205
Ala Thr Glu Met Leu Ile Phe Gly Lys Lys Leu Thr Ala Gly Glu Ala
              210              215              220
Cys Ala Gln Leu Val Thr Glu Val Phe Pro Asp Ser Thr Phe Gln Lys

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Thr Ala Met Ser Asp Ser Tyr Leu Pro Ser Tyr Tyr Ser Pro Ser Ile
 50 55 60
 Gly Phe Ser Tyr Ser Leu Gly Glu Ala Ala Trp Ser Thr Gly Gly Asp
 65 70 75 80
 Thr Ala Met Pro Tyr Leu Thr Ser Tyr Gly Gln Leu Ser Asn Gly Glu
 85 90 95
 Pro His Phe Leu Pro Asp Ala Met Phe Gly Gln Pro Gly Ala Leu Gly
 100 105 110
 Ser Thr Pro Phe Leu Gly Gln His Gly Phe Asn Phe Phe Pro Ser Gly
 115 120 125
 Ile Asp Phe Ser Ala Trp Gly Asn Asn Ser Ser Gln Gly Gln Ser Thr
 130 135 140
 Gln Ser Ser Gly Tyr Ser Ser Asn Tyr Ala Tyr Ala Pro Ser Ser Leu
 145 150 155 160
 Gly Gly Ala Met Ile Asp Gly Gln Ser Ala Phe Ala Asn Glu Thr Leu
 165 170 175
 Asn Lys Ala Pro Gly Met Asn Thr Ile Asp Gln Gly Met Ala Ala Leu
 180 185 190
 Lys Leu Gly Ser Thr Glu Val Ala Ser Asn Val Pro Lys Val Val Gly
 195 200 205
 Ser Ala Val Gly Ser Gly Ser Ile Thr Ser Asn Ile Val Ala Ser Asn
 210 215 220
 Ser Leu Pro Pro Ala Thr Ile Ala Pro Pro Lys Pro Ala Ser Trp Ala
 225 230 235 240
 Asp Ile Ala Ser Lys Pro Ala Lys Gln Gln Pro Lys Leu Lys Thr Lys
 245 250 255
 Asn Gly Ile Ala Gly Ser Ser Leu Pro Pro Pro Pro Ile Lys His Asn
 260 265 270
 Met Asp Ile Gly Thr Trp Asp Asn Lys Gly Pro Val Ala Lys Ala Pro
 275 280 285
 Ser Gln Ala Leu Val Gln Asn Ile Gly Gln Pro Thr Gln Gly Ser Pro
 290 295 300
 Gln Pro Val Gly Gln Gln Ala Asn Asn Ser Pro Pro Val Ala Gln Ala
 305 310 315 320
 Ser Val Gly Gln Gln Thr Gln Pro Leu Pro Pro Pro Pro Gln Pro
 325 330 335
 Ala Gln Leu Ser Val Gln Gln Gln Ala Ala Gln Pro Thr Arg Trp Val
 340 345 350
 Ala Pro Arg Asn Arg Gly Ser Gly Phe Gly His Asn Gly Val Asp Gly
 355 360 365
 Asn Gly Val Gly Gln Ser Gln Ala Gly Ser Gly Ser Thr Pro Ser Glu
 370 375 380
 Pro His Pro Val Leu Glu Lys Leu Arg Ser Ile Asn Asn Tyr Asn Pro
 385 390 395 400
 Lys Asp Phe Asp Trp Glu Ile
 405

<210> 93

<211> 2236

<212> DNA

<213> Homo Sapiens

<400> 93

cctggcccggtgcg gcgtctttcc agctcctggc agccgggcac ccgaaggaa
 gggctcgtgca acgacgcagc tggacctggc ccagccatgg accgaaaagt ggcccagaa

60
120

ttccggcata aggtggattt tctgattgaa aatgatgcag agaaggacta tctctatgat 180
 gtgctgcgaa tgtaccacca gaccatggac gtggccgtgc tctgtgggaga cctgaagctg 240
 gtcatacatg aacccagccg tctgcctctg tttgatgcc a ttcggccgct gatccactg 300
 aagcaccagg tggaaataga tcagctgacc ccccgccgct ccaggaagct gaaggaggtg 360
 cgtctggacc gtctgcaccc cgaaggcctc ggccctgagt tgctgtgtgg cctggagttt 420
 ggctgtgggc tcttcatctc ccacctcatc aaaggcggctc aggcagacag cgtcgggctc 480
 caggtagggg acgagatcgt ccggatcaat ggatattcca tctcctcctg taccatgag 540
 gaggtcatca acctcattcg aaccaagaaa actgtgtcca tcaaagttag acacatcggc 600
 ctgatccccg tgaaaagctc tctgtatgag cccctcactt ggcagtatgt ggatcagttt 660
 gtgtcggaat ctgggggctg gcgaggcagc ctgggctccc ctggaaatcg ggaaaacaag 720
 gagaagaagg tcttcatcag cctggtaggc tcccgaggcc ttggctgcag catttccagc 780
 ggccccatcc agaagcctgg catctttatc agccatgtga aacctggctc cctgtctgct 840
 gaggtgggat tggagatagg ggaccagatt gtggaagtca atggcgctga cttctctaac 900
 ctggatcaca aggaggtgt aaatgtgtg aaaaatagcc gcagcctgac catctccatt 960
 gtagctgcag ctggccggga gctgttcatg acagaccggg agcggtggc agaggcgagg 1020
 cagcgtgagc tgcagcggca ggagcttctc atgcagaagc ggctggcgat ggagtccaac 1080
 aagatcctcc aggagcagca ggagatggag cggcaaagga gaaaagaaat tgcccagaag 1140
 gcagcagagg aaaatgagag ataccggaag gagatggaac agattgtaga ggaggaagag 1200
 aagttaaga agcaatggga agaagactgg ggctcaaagg aacagctact cttgcctaaa 1260
 accatcactg ctgagggtaca cccagtacct cttcgcaagc caaagtatga tcaggagtg 1320
 gaacctgagc tcgagcccgcc agatgacctg gatggaggca cggaggagca gggagagcag 1380
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 gctgctgagc ggcattggtg cattgtgaaa ggggacgaga tcatggcaat caacggcaag 1620
 attgtgacag actacaccct ggctgaggct gacgtgccc tgcagaaggc ctggaatcag 1680
 ggcggggact ggatcgacct tgtggttgcc gtctgcccc caaaggagta tgacgatgag 1740
 ctgaccttct tgctgaagtc caaaagggga aaccaaattc acgcgttagg aaacagttag 1800
 ctccggcccc acctcgtgaa cacaagcctc cggaccagcc ttgagagagg ccacatgaca 1860
 cacaccagat ggcacacctg ggacctgaat ctatcaccca ggaatctcaa actccctttg 1920
 gccctgaacc agggccagat aaggaacagc tcggggccact tttttgaagg ccaatgtgga 1980
 ggaaagggag cagccagccg tttgggagaa gatctcaagg atccagactc tcatctcttt 2040
 cctctggccc agtgaatttg gtctctccca gctttggggg actccttctc tgaaccctaa 2100
 taagacccca ctggagtctc tctctctcca tccctctcct ctgcccctctg ctctaattgc 2160
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 ttccagctta aaaaaa 2236

<210> 94

<211> 652

<212> PRT

<213> Homo Sapiens

<400> 94

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Ile	Glu	Asn	Asp	Ala	Glu	Lys	Asp	Tyr	Leu	Tyr	Asp	Val	Leu	Arg	Met
			20					25					30		
Tyr	His	Gln	Thr	Met	Asp	Val	Ala	Val	Leu	Val	Gly	Asp	Leu	Lys	Leu
			35				40					45			
Val	Ile	Asn	Glu	Pro	Ser	Arg	Leu	Pro	Leu	Phe	Asp	Ala	Ile	Arg	Pro
			50				55				60				
Leu	Ile	Pro	Leu	Lys	His	Gln	Val	Glu	Tyr	Asp	Gln	Leu	Thr	Pro	Arg
65					70					75				80	
Arg	Ser	Arg	Lys	Leu	Lys	Glu	Val	Arg	Leu	Asp	Arg	Leu	His	Pro	Glu
			85					90					95		

Gly Leu Gly Leu Ser Val Arg Gly Gly Leu Glu Phe Gly Cys Gly Leu
 100 105 110
 Phe Ile Ser His Leu Ile Lys Gly Gly Gln Ala Asp Ser Val Gly Leu
 115 120 125
 Gln Val Gly Asp Glu Ile Val Arg Ile Asn Gly Tyr Ser Ile Ser Ser
 130 135 140
 Cys Thr His Glu Glu Val Ile Asn Leu Ile Arg Thr Lys Lys Thr Val
 145 150 155 160
 Ser Ile Lys Val Arg His Ile Gly Leu Ile Pro Val Lys Ser Ser Pro
 165 170 175
 Asp Glu Pro Leu Thr Trp Gln Tyr Val Asp Gln Phe Val Ser Glu Ser
 180 185 190
 Gly Gly Val Arg Gly Ser Leu Gly Ser Pro Gly Asn Arg Glu Asn Lys
 195 200 205
 Glu Lys Lys Val Phe Ile Ser Leu Val Gly Ser Arg Gly Leu Gly Cys
 210 215 220
 Ser Ile Ser Ser Gly Pro Ile Gln Lys Pro Gly Ile Phe Ile Ser His
 225 230 235 240
 Val Lys Pro Gly Ser Leu Ser Ala Glu Val Gly Leu Glu Ile Gly Asp
 245 250 255
 Gln Ile Val Glu Val Asn Gly Val Asp Phe Ser Asn Leu Asp His Lys
 260 265 270
 Glu Ala Val Asn Val Leu Lys Asn Ser Arg Ser Leu Thr Ile Ser Ile
 275 280 285
 Val Ala Ala Ala Gly Arg Glu Leu Phe Met Thr Asp Arg Glu Arg Leu
 290 295 300
 Ala Glu Ala Arg Gln Arg Glu Leu Gln Arg Gln Glu Leu Leu Met Gln
 305 310 315 320
 Lys Arg Leu Ala Met Glu Ser Asn Lys Ile Leu Gln Glu Gln Gln Glu
 325 330 335
 Met Glu Arg Gln Arg Arg Lys Glu Ile Ala Gln Lys Ala Ala Glu Glu
 340 345 350
 Asn Glu Arg Tyr Arg Lys Glu Met Glu Gln Ile Val Glu Glu Glu Glu
 355 360 365
 Lys Phe Lys Lys Gln Trp Glu Glu Asp Trp Gly Ser Lys Glu Gln Leu
 370 375 380
 Leu Leu Pro Lys Thr Ile Thr Ala Glu Val His Pro Val Pro Leu Arg
 385 390 395 400
 Lys Pro Lys Tyr Asp Gln Gly Val Glu Pro Glu Leu Glu Pro Ala Asp
 405 410 415
 Asp Leu Asp Gly Gly Thr Glu Glu Gln Gly Glu Gln Asp Phe Arg Lys
 420 425 430
 Tyr Glu Glu Gly Phe Asp Pro Tyr Ser Met Phe Thr Pro Glu Gln Ile
 435 440 445
 Met Gly Lys Asp Val Arg Leu Leu Arg Ile Lys Lys Glu Gly Ser Leu
 450 455 460
 Asp Leu Ala Leu Glu Gly Gly Val Asp Ser Pro Ile Gly Lys Val Val
 465 470 475 480
 Val Ser Ala Val Tyr Glu Arg Gly Ala Ala Glu Arg His Gly Gly Ile
 485 490 495
 Val Lys Gly Asp Glu Ile Met Ala Ile Asn Gly Lys Ile Val Thr Asp
 500 505 510
 Tyr Thr Leu Ala Glu Ala Asp Ala Ala Leu Gln Lys Ala Trp Asn Gln
 515 520 525
 Gly Gly Asp Trp Ile Asp Leu Val Val Ala Val Cys Pro Pro Lys Glu

530 535 540
 Tyr Asp Asp Glu Leu Thr Phe Leu Leu Lys Ser Lys Arg Gly Asn Gln
 545 550 555 560
 Ile His Ala Leu Gly Asn Ser Glu Leu Arg Pro His Leu Val Asn Thr
 565 570 575
 Lys Pro Arg Thr Ser Leu Glu Arg Gly His Met Thr His Thr Arg Trp
 580 585 590
 His Pro Trp Asp Leu Asn Leu Ser Pro Arg Asn Leu Lys Leu Pro Leu
 595 600 605
 Ala Leu Asn Gln Gly Gln Ile Arg Asn Ser Ser Gly His Phe Phe Glu
 610 615 620
 Gly Gln Cys Gly Gly Lys Gly Ala Ala Ser Arg Leu Gly Glu Asp Leu
 625 630 635 640
 Lys Asp Pro Asp Ser His Ser Phe Pro Leu Ala Gln
 645 650

<210> 95
 <211> 831
 <212> DNA
 <213> Homo Sapiens

<400> 95
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 aaaacnattg cagaaaacat ttagattnta tgaaatatat aatnanancc aaaanccatt 180
 tgaanttaat nganccttac ctgtcntcac taaatcaggg ttntctgcgc caccnaaggg 240
 cngcccancg cctgctgtgt tggcttanta ggcctnagca tangggcagn tgcaatcctt 300
 tcctcctnng gcggcanatg ggcttctgga anaacccttn ccttatcccc ancgcaaggc 360
 ggcccctccc ctgccctnaa aggaaacctc ntggacncag ggaatatang gccaccttga 420
 aggggtggact ggctatcntg gaagatcaga taccaccaag caatttggag acagtctctg 480
 ttgagaataa ccacggtttc catgaaaaga cagcagcgct gaagcttgag gccgagggcg 540
 aggccatgga agatgcagcc gcgccagggg acgaccgagg cggcacacag gagccagccc 600
 cagtgcctgc tgagccgttt gacaacacta cctacaagaa cctgcagcat catgactaca 660
 gcacgtacac cttcttagac ctcaacctcg aactctcaaa attcaggatg cctcagccct 720
 cctcaggccg ggagtcacct cgacactgag ggccctcggt gtgaagatga accttccacc 780
 gtcttcactg catcctggag tgcaaaaata aaatccactc aagagtcaaa a 831

<210> 96
 <211> 184
 <212> PRT
 <213> Homo Sapiens

<400> 96
 Arg Lys Asn Cys Arg Lys His Leu Asp Met Lys Tyr Ile Lys His Leu
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 Leu Pro Tyr Leu Ser Ser Leu Asn Gln Gly Leu Arg His Arg Ala Ala
 20 25 30
 Arg Leu Leu Cys Trp Leu Arg Pro His Gly Cys Asn Pro Phe Leu Leu
 35 40 45
 Arg Met Gly Phe Trp Asn Pro Leu Ile Pro Ala Arg Arg Pro Leu Pro
 50 55 60
 Cys Pro Arg Lys Pro Gly Arg Glu Tyr Ala Thr Leu Lys Gly Gly Leu
 65 70 75 80
 Ala Ile Glu Asp Gln Ile Pro Pro Ser Asn Leu Glu Thr Val Pro Val
 85 90 95

Glu Asn Asn His Gly Phe His Glu Lys Thr Ala Ala Leu Lys Leu Glu
 100 105 110
 Ala Glu Gly Glu Ala Met Glu Asp Ala Ala Ala Pro Gly Asn Asp Arg
 115 120 125
 Gly Gly Thr Gln Glu Pro Ala Pro Val Pro Ala Glu Pro Phe Asp Asn
 130 135 140
 Thr Thr Tyr Lys Asn Leu Gln His His Asp Tyr Ser Thr Tyr Thr Phe
 145 150 155 160
 Leu Asp Leu Asn Leu Glu Leu Ser Lys Phe Arg Met Pro Gln Pro Ser
 165 170 175
 Ser Gly Arg Glu Ser Pro Arg His
 180

<210> 97
 <211> 1008
 <212> DNA
 <213> Homo Sapiens

<400> 97
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 ttcctcatga cccagttgcc cttgaagagc acttcagggg tgatgatgag ggtccagtgt 120
 ccaaccaggg ctacatgcct tatttaaaca gggttcatttt ggaaaagggtc caagacaact 180
 ttgacaagat tgaattcaat aggatgtgtt ggaccctctg tgtcaaaaaa aacctcacia 240
 agaatccccct gctcattaca gaagaanatg cattttaaata atgggttatt ttcaactttt 300
 tatctgagga caagtatcca ttaattattg tgtcagaana gattgaatac ctgcttaaga 360
 agcttacaga agctatggga ggaggttggc agcaagaaca atttgaacat tataaaatca 420
 actttgatga cagtaaaaaat ggcctttctg catgggaact tattgagctt attggaaatg 480
 gacagtttag caaaggcatg gaccggcaga ctgtgtctat ggcaattaat gaagtcttta 540
 atgaacttat attagatgtg ttaaagcagg gttacatgat gaaaaagggc cacagacgga 600
 aaaactggac tgaacgatgg tttgtactaa aaccaacat aatttcttac tatgtgagtg 660
 aggatctgaa ggataagaaa ggagacattc tcttgatga aaattgctgt gtagagtcct 720
 tgcctgacaa agatggaaaag aaatgccttt ttctcgtaaa atgttttgat aagacttttg 780
 aaatcagtg cttcagataag aanaanaaac aggagtggat tcaagccatt cattctacta 840
 ttcattctgtt gaagctgngc agccctccac canacaaaga agccnncag cttctnaaan 900
 aactccggna gaatcatctg gctgaacaag angaactgga gcgacaaatg aangaactcc 960
 aagcccgcga atgaaagcaa ncagcaagag ctggaaggcc ttncggaa 1008

<210> 98
 <211> 312
 <212> PRT
 <213> Homo Sapiens

<400> 98
 Lys Val Ser Lys Ser Gln Leu Lys Val Leu Ser His Asn Leu Cys Thr
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 Val Leu Lys Val Pro His Asp Pro Val Ala Leu Glu Glu His Phe Arg
 20 25 30
 Asp Asp Asp Glu Gly Pro Val Ser Asn Gln Gly Tyr Met Pro Tyr Leu
 35 40 45
 Asn Arg Phe Ile Leu Glu Lys Val Gln Asp Asn Phe Asp Lys Ile Glu
 50 55 60
 Phe Asn Arg Met Cys Trp Thr Leu Cys Val Lys Lys Asn Leu Thr Lys
 65 70 75 80
 Asn Pro Leu Leu Ile Thr Glu Glu Ala Phe Lys Ile Trp Val Ile Phe
 85 90 95

Asn Phe Leu Ser Glu Asp Lys Tyr Pro Leu Ile Ile Val Ser Glu Ile
 100 105 110
 Glu Tyr Leu Leu Lys Lys Leu Thr Glu Ala Met Gly Gly Gly Trp Gln
 115 120 125
 Gln Glu Gln Phe Glu His Tyr Lys Ile Asn Phe Asp Asp Ser Lys Asn
 130 135 140
 Gly Leu Ser Ala Trp Glu Leu Ile Glu Leu Ile Gly Asn Gly Gln Phe
 145 150 155 160
 Ser Lys Gly Met Asp Arg Gln Thr Val Ser Met Ala Ile Asn Glu Val
 165 170 175
 Phe Asn Glu Leu Ile Leu Asp Val Leu Lys Gln Gly Tyr Met Met Lys
 180 185 190
 Lys Gly His Arg Arg Lys Asn Trp Thr Glu Arg Trp Phe Val Leu Lys
 195 200 205
 Pro Asn Ile Ile Ser Tyr Tyr Val Ser Glu Asp Leu Lys Asp Lys Lys
 210 215 220
 Gly Asp Ile Leu Leu Asp Glu Asn Cys Cys Val Glu Ser Leu Pro Asp
 225 230 235 240
 Lys Asp Gly Lys Lys Cys Leu Phe Leu Val Lys Cys Phe Asp Lys Thr
 245 250 255
 Phe Glu Ile Ser Ala Ser Asp Lys Lys Gln Glu Trp Ile Gln Ala Ile
 260 265 270
 His Ser Thr Ile His Leu Leu Lys Leu Ser Pro Pro Pro Lys Glu Ala
 275 280 285
 Gln Leu Leu Lys Leu Arg Asn His Leu Ala Glu Gln Glu Leu Glu Arg
 290 295 300
 Gln Met Glu Leu Gln Ala Arg Gln
 305 310

<210> 99
 <211> 1009
 <212> DNA
 <213> Homo Sapiens

<400> 99
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 aacttttgca gaagatgagg agttacaaaa tatggacaaa gaagatgcat taatttgctt 120
 tgaagaacac attcgggctt tagaaaagga ggaagaagaa gaaaaacaga agagtttgct 180
 gagagaaagg agacgacagc gaaaaaatag ggaatctttc cagatatttt tagatgaatt 240
 acatgaacat ggacaactgc attctatgtc atcttggtatg gaattgtatc caactattag 300
 ttctgatatt agattcacta atatgcttgg tcagcctgga tcaactgcac ttgatctttt 360
 caagttttat gttgaggatc ttaaagcacg ttatcatgac gagaagaaga taataaaaga 420
 cattctaaag gataaaggat ttgtagtga agtaaact acttttgaag attttgtggc 480
 gataatcagt tcaactaaaa gatcaactac attagatgct ggaaatatca aattggcttt 540
 caatagttta ctagaaaagg cagaagcccg tgaacgtgaa agagaaaaag aagaggctcg 600
 gaagatgaaa cgaaaagaat ctgcatttaa gagtatgtta aaacaagctg ctccctccgat 660
 agaattggat gctgtctggg aagatatccg tgagagattt gtaaaagagc cagcatttga 720
 ggacataact ctagaatctg aaagaaaacg aatattttaa gattttatgc atgtgcttga 780
 gcatgaatgt cagcatcatc attcaaagaa caagaaacat tctaagaaat ctaaaaaaca 840
 tcataggaaa cgttcccgtc ctcgatcggg gtcagattca ngatgatgat gatagccatt 900
 caaagaaaaa aagacagcga tgagaagtct cggctcgtntt canaacattc ttccantngc 960
 agagtctgag agaagtntaa aaagtcaaaa nagcatagan aggaaagtt 1009

<210> 100
 <211> 292

<212> PRT

<213> Homo Sapiens

<400> 100

Ala Asn Val Thr Tyr Ser Thr Thr Trp Ser Glu Ala Gln Gln Tyr Leu
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 Met Asp Asn Pro Thr Phe Ala Glu Asp Glu Glu Leu Gln Asn Met Asp
 20 25 30
 Lys Glu Asp Ala Leu Ile Cys Phe Glu Glu His Ile Arg Ala Leu Glu
 35 40 45
 Lys Glu Glu Glu Glu Glu Lys Gln Lys Ser Leu Leu Arg Glu Arg Arg
 50 55 60
 Arg Gln Arg Lys Asn Arg Glu Ser Phe Gln Ile Phe Leu Asp Glu Leu
 65 70 75 80
 His Glu His Gly Gln Leu His Ser Met Ser Ser Trp Met Glu Leu Tyr
 85 90 95
 Pro Thr Ile Ser Ser Asp Ile Arg Phe Thr Asn Met Leu Gly Gln Pro
 100 105 110
 Gly Ser Thr Ala Leu Asp Leu Phe Lys Phe Tyr Val Glu Asp Leu Lys
 115 120 125
 Ala Arg Tyr His Asp Glu Lys Lys Ile Ile Lys Asp Ile Leu Lys Asp
 130 135 140
 Lys Gly Phe Val Val Glu Val Asn Thr Thr Phe Glu Asp Phe Val Ala
 145 150 155 160
 Ile Ile Ser Ser Thr Lys Arg Ser Thr Thr Leu Asp Ala Gly Asn Ile
 165 170 175
 Lys Leu Ala Phe Asn Ser Leu Leu Glu Lys Ala Glu Ala Arg Glu Arg
 180 185 190
 Glu Arg Glu Lys Glu Glu Ala Arg Lys Met Lys Arg Lys Glu Ser Ala
 195 200 205
 Phe Lys Ser Met Leu Lys Gln Ala Ala Pro Pro Ile Glu Leu Asp Ala
 210 215 220
 Val Trp Glu Asp Ile Arg Glu Arg Phe Val Lys Glu Pro Ala Phe Glu
 225 230 235 240
 Asp Ile Thr Leu Glu Ser Glu Arg Lys Arg Ile Phe Lys Asp Phe Met
 245 250 255
 His Val Leu Glu His Glu Cys Gln His His His Ser Lys Asn Lys Lys
 260 265 270
 His Ser Lys Lys Ser Lys Lys His His Arg Lys Arg Ser Arg Ser Arg
 275 280 285
 Ser Gly Ser Asp
 290

<210> 101

<211> 983

<212> DNA

<213> Homo Sapiens

<400> 101

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 ttttatttca gtattaaaat agcaatttta tttattactt ttttatatat agaatttgac 180
 accaaatttt ggaacttaaa aagaagattc ttaaaactta caatccagat tacgatgagg 240
 acctggtgca ggaagcttca tctgaagatg tcctgggcgt tcatatggtg gacaaagaca 300
 cagagagaga cattgagatg aaacggcaac tacggcgact acgggagctc cacctataca 360

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gcacatggaa gaagtaccaa gaggcgatga agacatcctt gggagttcca caacgtgagc 420
gtgacgaagg ctccttgggc aagccattgt gtccaccga gatactctcg gagacgttgc 480
caggctctgt gaagaaaagg gtatgctttc catcagaaga tcatctagag gagtttatag 540
cagaacatct ccctgaagca tccaatcaga gtctcctcac tgttgcccat gcagacgcag 600
gcacccaaac caacggtgac ctggaagacc tggaggagca tggggccaggg cagacagtct 660
ctgaggaagc cacagaagtt cacatgatgg aggggggaccc agacacactg gccgaacttc 720
tgatcagga tgtacttcag gagctgtcca gttacaacgg cgaggaggag gacccanagg 780
aggtgaagac atccttggga gttccacaac gtggtgacct ggaagacctg gaggagcatg 840
tgncagggca gnnnttctct gaggaagcca caggggttca catgatgcag gtggaccag 900
ccacgctggc aaagagtgc ctggaagacc tggaggagca tgtgccagag cagacagtct 960
ctgaggaagc cacaggggtt cac 983

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<210> 102
 <211> 230
 <212> PRT
 <213> Homo Sapiens

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<400> 102
Met Val Asp Lys Asp Thr Glu Arg Asp Ile Glu Met Lys Arg Gln Leu
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Arg Arg Leu Arg Glu Leu His Leu Tyr Ser Thr Trp Lys Lys Tyr Gln
20 25 30
Glu Ala Met Lys Thr Ser Leu Gly Val Pro Gln Arg Glu Arg Asp Glu
35 40 45
Gly Ser Leu Gly Lys Pro Leu Cys Pro Pro Glu Ile Leu Ser Glu Thr
50 55 60
Leu Pro Gly Ser Val Lys Lys Arg Val Cys Phe Pro Ser Glu Asp His
65 70 75 80
Leu Glu Glu Phe Ile Ala Glu His Leu Pro Glu Ala Ser Asn Gln Ser
85 90 95
Leu Leu Thr Val Ala His Ala Asp Ala Gly Thr Gln Thr Asn Gly Asp
100 105 110
Leu Glu Asp Leu Glu Glu His Gly Pro Gly Gln Thr Val Ser Glu Glu
115 120 125
Ala Thr Glu Val His Met Met Glu Gly Asp Pro Asp Thr Leu Ala Glu
130 135 140
Leu Leu Ile Arg Asp Val Leu Gln Glu Leu Ser Ser Tyr Asn Gly Glu
145 150 155 160
Glu Glu Asp Pro Glu Val Lys Thr Ser Leu Gly Val Pro Gln Arg Gly
165 170 175
Asp Leu Glu Asp Leu Glu Glu His Val Gly Gln Phe Ser Glu Glu Ala
180 185 190
Thr Gly Val His Met Met Gln Val Asp Pro Ala Thr Leu Ala Lys Ser
195 200 205
Asp Leu Glu Asp Leu Glu Glu His Val Pro Glu Gln Thr Val Ser Glu
210 215 220
Glu Ala Thr Gly Val His
225 230

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<210> 103
 <211> 843
 <212> DNA
 <213> Homo Sapiens

<400> 103

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cacgcccttt ctaccaagat gatagacagg atcttctcag gagcagtcac acgaggcaga      180
aaagtgcaga aggaagggaa gatcagctat gccgactttg tctggttttt gatctctgag      240
gaagacaaaa aaacaccgac cagcatcgag tactggttcc gctgcatgga cctggacggg      300
gacggcgccc tgtccatgtt cgagctcgag tacttctacg aggagcagtg ccgaaggctg      360
gacagcatgg ccatcgaggc cctgcccttc caggactgcc tctgccagat gctggacctg      420
gtcaagccga ggactgaagg gaagatcacg ctgcaggacc tgaagcgctg caagctggcc      480
aacgtcttct tcgacacctt cttcaacatc gagaagtncc tcgaccacga gcagaaagag      540
cagatctccc tgctcagggg cggtgacagc ggcggggccc agctctcgga ctggggagaag      600
tnccggccga agagtncgac atcctggtgg ccgangaaac cgtggggana nccctgggga      660
agacgggttc naaggcgaa caccacctnt ggancanaaa ctgantgctg tgcgctcccc      720
gctggggcan aggccttctt ccaagcgect cccgctgggg cgccgtggaa ctgttncaaa      780
ttcccctgcg gggacaagaa cttgaaaccg ctgtganncc ccccnana accnccccg      840
gnt                                                                    843

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<210> 104

<211> 197

<212> PRT

<213> Homo Sapiens

<400> 104

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Arg Cys Arg Ser Thr Leu Val Asp Pro Lys Asn Ser Ala Arg Gly Lys
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Phe Trp Glu Leu Asp Thr Asp His Asp Leu Leu Ile Asp Ala Asp Asp
          20          25          30
Leu Ala Arg His Asn Asp His Ala Leu Ser Thr Lys Met Ile Asp Arg
          35          40          45
Ile Phe Ser Gly Ala Val Thr Arg Gly Arg Lys Val Gln Lys Glu Gly
          50          55          60
Lys Ile Ser Tyr Ala Asp Phe Val Trp Phe Leu Ile Ser Glu Glu Asp
65          70          75          80
Lys Lys Thr Pro Thr Ser Ile Glu Tyr Trp Phe Arg Cys Met Asp Leu
          85          90          95
Asp Gly Asp Gly Ala Leu Ser Met Phe Glu Leu Glu Tyr Phe Tyr Glu
          100          105          110
Glu Gln Cys Arg Arg Leu Asp Ser Met Ala Ile Glu Ala Leu Pro Phe
          115          120          125
Gln Asp Cys Leu Cys Gln Met Leu Asp Leu Val Lys Pro Arg Thr Glu
          130          135          140
Gly Lys Ile Thr Leu Gln Asp Leu Lys Arg Cys Lys Leu Ala Asn Val
145          150          155          160
Phe Phe Asp Thr Phe Phe Asn Ile Glu Lys Leu Asp His Glu Gln Lys
          165          170          175
Glu Gln Ile Ser Leu Leu Arg Asp Gly Asp Ser Gly Gly Pro Glu Leu
          180          185          190
Ser Asp Trp Glu Lys
          195

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<210> 105

<211> 2264

<212> DNA

<213> Homo Sapiens

<400> 105

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cgacaacagg gctctattat gaccccaact cgcaatacta ctataattcc ttgacccagc 180
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gcaaaacagc ccagcagatt gccaaagaca tggaacgctg ggctaagagt ttgaataagc 360
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gagaatctgc tgcagcagac gctggctttg ctctctttga gaagaaggga gccttagctg 480
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gccagttccc gaacaaagat gccctagtca ggcaccagca actctcagac cttcacaagc 720
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cgggcgcccga ttcctacaaa gatgctgtcc ggaagccat gtttgcccgg ttcactgaga 1140
tggagtgaga gagagagaga gagagagatg acaaggagca caagaagtgg tccatctccc 1200
gaattcgtctg ttaccgcctg tctcttttaag ggcctgcctt gtgctgttaa tagatcttag 1260
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gacaccaaag ccacctctgt catttgttgt gatgtctttt cttggcaaaa gccttgtgta 1560
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ctggctcctt tacaaaagaa ataccttgag aaaaaaaann aannaaaaaa aannccnann 1680
nnnttttttaa aangggncgg gggccaannn tttccnncc gggnggggna nnaagtaaan 1740
ngtcccaaat nccccaaaaa nggagcccn ntaaaattaa angggccgcn nttttaaan 1800
nttcngaattn gggnaaaccc tnggggttn ccaaatttaa cccctttgaa aaaaaanccc 1860
ctttcncaaa annggntaa tanccaaaaa gggcccccann ccatttttgc ccnttccaaa 1920
aaaatttgnc caancnnaa atgggnaaan ggggaatcca attttttaaa gggnnaaaaan 1980
gggtttaaac nnacgggntt ccaaanttgn ttgggggaat ttttaaattc ccaannnccc 2040
aagggggnca atttagnggn cccnaatcc cccaaaaant gggtcnnggn tnaaanncgc 2100
cnnnccnaa tttntanggg ttacttngn tttaaaaaac ccnccccaaa actccccenn 2160
gaaccnaaaa aanaaaagga ngccattttt ngnnngnaaac ttttttaann nncnnttaa 2220
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<210> 106

<211> 381

<212> PRT

<213> Homo Sapiens

<400> 106

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Gly Thr Lys Tyr Ala Val Pro Asp Thr Ser Thr Tyr Gln Tyr Asp Glu
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Ser Ser Gly Tyr Tyr Tyr Asp Pro Thr Thr Gly Leu Tyr Tyr Asp Pro
35 40 45
Asn Ser Gln Tyr Tyr Tyr Asn Ser Leu Thr Gln Gln Tyr Leu Tyr Trp
50 55 60
Asp Gly Glu Lys Glu Thr Tyr Val Pro Ala Ala Glu Ser Ser Ser His
65 70 75 80

Gln Gln Ser Gly Leu Pro Pro Ala Lys Glu Gly Lys Glu Lys Lys Glu
 85 90 95
 Lys Pro Lys Ser Lys Thr Ala Gln Gln Ile Ala Lys Asp Met Glu Arg
 100 105 110
 Trp Ala Lys Ser Leu Asn Lys Gln Lys Glu Asn Phe Lys Asn Ser Phe
 115 120 125
 Gln Pro Val Asn Ser Leu Arg Glu Glu Glu Arg Arg Glu Ser Ala Ala
 130 135 140
 Ala Asp Ala Gly Phe Ala Leu Phe Glu Lys Lys Gly Ala Leu Ala Glu
 145 150 155 160
 Arg Gln Gln Leu Ile Pro Glu Leu Val Arg Asn Gly Asp Glu Glu Asn
 165 170 175
 Pro Leu Lys Arg Gly Leu Val Ala Ala Tyr Ser Gly Asp Ser Asp Asn
 180 185 190
 Glu Glu Glu Leu Val Glu Arg Leu Glu Ser Glu Glu Glu Lys Leu Ala
 195 200 205
 Asp Trp Lys Lys Met Ala Cys Leu Leu Cys Arg Arg Gln Phe Pro Asn
 210 215 220
 Lys Asp Ala Leu Val Arg His Gln Gln Leu Ser Asp Leu His Lys Gln
 225 230 235 240
 Asn Met Asp Ile Tyr Arg Arg Ser Arg Leu Ser Glu Gln Glu Leu Glu
 245 250 255
 Ala Leu Glu Leu Arg Glu Arg Glu Met Lys Tyr Arg Asp Arg Ala Ala
 260 265 270
 Glu Arg Arg Glu Lys Tyr Gly Ile Pro Glu Pro Pro Glu Pro Lys Arg
 275 280 285
 Lys Lys Gln Phe Asp Ala Gly Thr Val Asn Tyr Glu Gln Pro Thr Lys
 290 295 300
 Asp Gly Ile Asp His Ser Asn Ile Gly Asn Lys Met Leu Gln Ala Met
 305 310 315 320
 Gly Trp Arg Glu Gly Ser Gly Leu Gly Arg Lys Cys Gln Gly Ile Thr
 325 330 335
 Ala Pro Ile Glu Ala Gln Val Arg Leu Lys Gly Ala Gly Leu Gly Ala
 340 345 350
 Lys Gly Ser Ala Tyr Gly Leu Ser Gly Ala Asp Ser Tyr Lys Asp Ala
 355 360 365
 Val Arg Lys Ala Met Phe Ala Arg Phe Thr Glu Met Glu
 370 375 380

<210> 107

<211> 1367

<212> DNA

<213> Homo Sapiens

<400> 107

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 tcgaatgcat attcttcagc gagttccacc ccacgctggg acccaagatc acctatcagg 180
 tccttgaaga cttcatctcc cgagagctgt ttgacacagt ccaagtgtac atcatcacca 240
 agccagagct gcagaacaag cttatcactg tcacagctat ggaaaagaag ctgatcggct 300
 gtctgtgtg catcgaacac aagaagtaca gccgcaatgc tctcctcttc aacctgggct 360
 tcgtgtgtga tgcccaggcc aagacctgcg ccctcgagcc cattgttaaa aagctggctg 420
 gctatctgac cacactagag ctagagagca gcttcgtgtc catggaggag agcaagcaga 480
 agttggtgcc catcatgacc atcttgctgg aggagctaaa tgccctcaggc cgggtgcactc 540
 tgccattga tgagtccaac accatccact tgaaggtgat tgagcagcgg ccagaccctc 600

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cggtggccca ggagtatgat gtacctgtct ttaccaaaga caaggaggat ttcttcaact    660
cacagtggga cctcactaca caacaaatcc tgccctacat tgatgggttc cgccacatcc    720
agaagatttc agcagaggca gatgtggagc tcaacctggt gcgcattgct atccagaacc    780
tgctgtacta cggcggtgtg acactgggtg ccatcctcca gtactccaat gtatactgcc    840
caacgccccaa ggtccaggac ctggtagatg acaagtccct gcaagaggca tgtctatcct    900
acgtgaccaa gcaagggcac aagagggcca gtctccggga tgtgttccag ctatactgca    960
gcctgagccc tggcactacc gtgcgagacc tcattggcgg ccacccccag cagctgcagc   1020
atgttgatga acggaagctg atccagttcg ggcttatgaa gaacctcatc aggcgactac   1080
agaagtatcc tgtgcgggtg actcgggaag agcagagcca ccctgcccgg ctttatacag   1140
gctgccacag ctatgacgag atctgctgca agacaggcat gagctaccat gagctggatg   1200
agcggcttga aaatgacccc aacatcatca tctgctggaa gtgaggctgg tagtgactgg   1260
atggacacat tgctgtgggt agtccctcct actaggaggc ttgtcatact gtctagaggt   1320
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<210> 108

<211> 413

<212> PRT

<213> Homo Sapiens

<400> 108

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      20              25              30
Ala Met Gly Ser Gly Cys Arg Ile Glu Cys Ile Phe Phe Ser Glu Phe
      35              40              45
His Pro Thr Leu Gly Pro Lys Ile Thr Tyr Gln Val Pro Glu Asp Phe
      50              55              60
Ile Ser Arg Glu Leu Phe Asp Thr Val Gln Val Tyr Ile Ile Thr Lys
      65              70              75              80
Pro Glu Leu Gln Asn Lys Leu Ile Thr Val Thr Ala Met Glu Lys Lys
      85              90              95
Leu Ile Gly Cys Pro Val Cys Ile Glu His Lys Lys Tyr Ser Arg Asn
      100             105             110
Ala Leu Leu Phe Asn Leu Gly Phe Val Cys Asp Ala Gln Ala Lys Thr
      115             120             125
Cys Ala Leu Glu Pro Ile Val Lys Lys Leu Ala Gly Tyr Leu Thr Thr
      130             135             140
Leu Glu Leu Glu Ser Ser Phe Val Ser Met Glu Glu Ser Lys Gln Lys
      145             150             155             160
Leu Val Pro Ile Met Thr Ile Leu Leu Glu Glu Leu Asn Ala Ser Gly
      165             170             175
Arg Cys Thr Leu Pro Ile Asp Glu Ser Asn Thr Ile His Leu Lys Val
      180             185             190
Ile Glu Gln Arg Pro Asp Pro Pro Val Ala Gln Glu Tyr Asp Val Pro
      195             200             205
Val Phe Thr Lys Asp Lys Glu Asp Phe Phe Asn Ser Gln Trp Asp Leu
      210             215             220
Thr Thr Gln Gln Ile Leu Pro Tyr Ile Asp Gly Phe Arg His Ile Gln
      225             230             235             240
Lys Ile Ser Ala Glu Ala Asp Val Glu Leu Asn Leu Val Arg Ile Ala
      245             250             255
Ile Gln Asn Leu Leu Tyr Tyr Gly Val Val Thr Leu Val Ser Ile Leu
      260             265             270
Gln Tyr Ser Asn Val Tyr Cys Pro Thr Pro Lys Val Gln Asp Leu Val

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275	280	285
Asp Asp Lys Ser Leu Gln Glu Ala Cys Leu Ser Tyr Val Thr Lys Gln		
290	295	300
Gly His Lys Arg Ala Ser Leu Arg Asp Val Phe Gln Leu Tyr Cys Ser		
305	310	315
Leu Ser Pro Gly Thr Thr Val Arg Asp Leu Ile Gly Arg His Pro Gln		
	325	330
Gln Leu Gln His Val Asp Glu Arg Lys Leu Ile Gln Phe Gly Leu Met		
	340	345
Lys Asn Leu Ile Arg Arg Leu Gln Lys Tyr Pro Val Arg Val Thr Arg		
	355	360
Glu Glu Gln Ser His Pro Ala Arg Leu Tyr Thr Gly Cys His Ser Tyr		
	370	375
Asp Glu Ile Cys Cys Lys Thr Gly Met Ser Tyr His Glu Leu Asp Glu		
385	390	395
Arg Leu Glu Asn Asp Pro Asn Ile Ile Ile Cys Trp Lys		
	405	410

<210> 109

<211> 2113

<212> DNA

<213> Homo Sapiens

<400> 109

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ctatggagca	ggtcaatgag	ctgaaggaga	aaggcaacaa	ggccctgagc	gtgggtaaca	120
tcgatgatgc	cttacagtgc	tactccgaag	ctattaagct	ggatccccac	aaccacgtgc	180
tgtacagcaa	ccgttctgct	gcctatgcca	agaaaggaga	ctaccagaag	gcttatgagg	240
atggctgcaa	gactgtcgac	ctaaagcctg	actggggcaa	gggctattca	cgaaaagcag	300
cagctctaga	gttcttaaac	cgctttgaag	aagccaagcg	aacctatgag	gagggcttaa	360
aacacgaggc	aaataaccct	caactgaaag	agggtttaca	gaatatggag	gccaggttgg	420
cagagagaaa	attcatgaac	cctttcaaca	tgcctaattct	gtatcagaag	ttggagagtg	480
atcccaggac	aaggacacta	ctcagtgatc	ctacctaccg	ggagctgata	gagcagctac	540
gaaacaagcc	ttctgacctg	ggcacgaaac	tacaagatcc	ccggatcatg	accactctca	600
gcgtcctcct	tggggtcgat	ctgggcagta	tggatgagga	ggaagagatt	gcaacacctc	660
caccaccacc	ccctcccaaa	aaggagacca	agccagagcc	aatggaagaa	gatcttccag	720
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actttgacac	agccttgaag	cattacgaca	aagccaagga	gctggacccc	actaacatga	840
cttacattac	caatcaagca	gcggtatact	ttgaaaacgg	cgactacaat	aagtgccggg	900
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ccaaagcata	tgtctgaatt	ggcaactcct	acttcaaaga	agaaaagtac	aaggatgcca	1020
tccatttcta	taacaagtct	ctggcagagc	accgaacccc	agatgtgctc	aagaaatgcc	1080
agcaggcaga	gaaaatcctg	aaggagcaag	agcggtggc	ctacataaac	cccagacctg	1140
ctttggagga	gaagaacaaa	ggcaacgagt	gttttcagaa	aggggactat	cccaggcca	1200
tgaagcatta	tacagaagcc	atcaaaagga	acccgaaaga	tgccaaatta	tacagcaatc	1260
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cgatgaagga	ctacaccaaa	gccatggatg	tgtaccagaa	ggcgctagac	ctggactcca	1440
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gctgggaccg	cggcgagcag	cacggagcgg	aaggagagag	aggggagaga	aggcctcatc	1800
tctctatatt	tatacataac	cccggggaag	acacagagac	tcgtacctgc	gctgtttgtg	1860


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ccgccgctgc ctctggggccc tcccagcaca cgcattggtct cttcaccgct gccctcgagt 1920
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ttttttatatt ggggcagtg gcatgttatg gggaggggag ggggttcttc cagcctcagg 2040
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<210> 110

<211> 543

<212> PRT

<213> Homo Sapiens

<400> 110

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Met Glu Gln Val Asn Glu Leu Lys Glu Lys Gly Asn Lys Ala Leu Ser
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Val Gly Asn Ile Asp Asp Ala Leu Gln Cys Tyr Ser Glu Ala Ile Lys
20      25      30
Leu Asp Pro His Asn His Val Leu Tyr Ser Asn Arg Ser Ala Ala Tyr
35      40      45
Ala Lys Lys Gly Asp Tyr Gln Lys Ala Tyr Glu Asp Gly Cys Lys Thr
50      55      60
Val Asp Leu Lys Pro Asp Trp Gly Lys Gly Tyr Ser Arg Lys Ala Ala
65      70      75      80
Ala Leu Glu Phe Leu Asn Arg Phe Glu Glu Ala Lys Arg Thr Tyr Glu
85      90      95
Glu Gly Leu Lys His Glu Ala Asn Asn Pro Gln Leu Lys Glu Gly Leu
100     105     110
Gln Asn Met Glu Ala Arg Leu Ala Glu Arg Lys Phe Met Asn Pro Phe
115     120     125
Asn Met Pro Asn Leu Tyr Gln Lys Leu Glu Ser Asp Pro Arg Thr Arg
130     135     140
Thr Leu Leu Ser Asp Pro Thr Tyr Arg Glu Leu Ile Glu Gln Leu Arg
145     150     155     160
Asn Lys Pro Ser Asp Leu Gly Thr Lys Leu Gln Asp Pro Arg Ile Met
165     170     175
Thr Thr Leu Ser Val Leu Leu Gly Val Asp Leu Gly Ser Met Asp Glu
180     185     190
Glu Glu Glu Ile Ala Thr Pro Pro Pro Pro Pro Pro Lys Lys Glu
195     200     205
Thr Lys Pro Glu Pro Met Glu Glu Asp Leu Pro Glu Asn Lys Lys Gln
210     215     220
Ala Leu Lys Glu Lys Glu Leu Gly Asn Asp Ala Tyr Lys Lys Lys Asp
225     230     235     240
Phe Asp Thr Ala Leu Lys His Tyr Asp Lys Ala Lys Glu Leu Asp Pro
245     250     255
Thr Asn Met Thr Tyr Ile Thr Asn Gln Ala Ala Val Tyr Phe Glu Lys
260     265     270
Gly Asp Tyr Asn Lys Cys Arg Glu Leu Cys Glu Lys Ala Ile Glu Val
275     280     285
Gly Arg Glu Asn Arg Glu Asp Tyr Arg Gln Ile Ala Lys Ala Tyr Ala
290     295     300
Arg Ile Gly Asn Ser Tyr Phe Lys Glu Glu Lys Tyr Lys Asp Ala Ile
305     310     315     320
His Phe Tyr Asn Lys Ser Leu Ala Glu His Arg Thr Pro Asp Val Leu
325     330     335
Lys Lys Cys Gln Gln Ala Glu Lys Ile Leu Lys Glu Gln Glu Arg Leu

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340 345 350
 Ala Tyr Ile Asn Pro Asp Leu Ala Leu Glu Glu Lys Asn Lys Gly Asn
 355 360 365
 Glu Cys Phe Gln Lys Gly Asp Tyr Pro Gln Ala Met Lys His Tyr Thr
 370 375 380
 Glu Ala Ile Lys Arg Asn Pro Lys Asp Ala Lys Leu Tyr Ser Asn Arg
 385 390 395 400
 Ala Ala Cys Tyr Thr Lys Leu Leu Glu Phe Gln Leu Ala Leu Lys Asp
 405 410 415
 Cys Glu Glu Cys Ile Gln Leu Glu Pro Thr Phe Ile Lys Gly Tyr Thr
 420 425 430
 Arg Lys Ala Ala Ala Leu Glu Ala Met Lys Asp Tyr Thr Lys Ala Met
 435 440 445
 Asp Val Tyr Gln Lys Ala Leu Asp Leu Asp Ser Ser Cys Lys Glu Ala
 450 455 460
 Ala Asp Gly Tyr Gln Arg Cys Met Met Ala Gln Tyr Asn Arg His Asp
 465 470 475 480
 Ser Pro Glu Asp Val Lys Arg Arg Ala Met Ala Asp Pro Glu Val Gln
 485 490 495
 Gln Ile Met Ser Asp Pro Ala Met Arg Leu Ile Leu Glu Gln Met Gln
 500 505 510
 Lys Asp Pro Gln Ala Leu Ser Glu His Leu Lys Asn Pro Val Ile Ala
 515 520 525
 Gln Lys Ile Gln Lys Leu Met Asp Val Gly Leu Ile Ala Ile Arg
 530 535 540

<210> 111

<211> 2765

<212> DNA

<213> Homo Sapiens

<400> 111

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 caaccaccg ctgccgaaat gaagtataag aatccttatg caagggcctt atatgacaat 180
 gtccagagt gtgccgagga actggccttt cgcaaggagg acatcctgac cgtcatagag 240
 cagaacacag ggggactgga aggatgggtg ctgtgctcgt tacacggctg gcaaggcatt 300
 gtcccaggca accgggtgaa gcttctgatt ggtcccatgc aggagactgc ctccagtcac 360
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<210> 112

<211> 834

<212> PRT

<213> Homo Sapiens

<400> 112

Met Lys Tyr Lys Asn Leu Met Ala Arg Ala Leu Tyr Asp Asn Val Pro
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 20 25 30
 Ile Glu Gln Asn Thr Gly Gly Leu Glu Gly Trp Trp Leu Cys Ser Leu
 35 40 45
 His Gly Arg Gln Gly Ile Val Pro Gly Asn Arg Val Lys Leu Leu Ile
 50 55 60
 Gly Pro Met Gln Glu Thr Ala Ser Ser His Glu Gln Pro Ala Ser Gly
 65 70 75 80
 Leu Met Gln Gln Thr Phe Gly Gln Gln Lys Leu Tyr Gln Val Pro Asn
 85 90 95
 Pro Gln Ala Ala Pro Arg Asp Thr Ile Tyr Gln Val Pro Pro Ser Tyr
 100 105 110
 Gln Asn Gln Gly Ile Tyr Gln Val Pro Thr Gly His Gly Thr Gln Glu
 115 120 125
 Gln Glu Val Tyr Gln Val Pro Pro Ser Val Gln Arg Ser Ile Gly Gly
 130 135 140
 Thr Ser Gly Pro His Val Gly Lys Lys Val Ile Thr Pro Val Arg Thr
 145 150 155 160
 Gly His Gly Tyr Val Tyr Glu Tyr Pro Ser Arg Tyr Gln Lys Asp Val
 165 170 175
 Tyr Asp Ile Pro Pro Ser His Thr Thr Gln Gly Val Tyr Asp Ile Pro
 180 185 190

Pro Ser Ser Ala Lys Gly Pro Val Phe Ser Val Pro Val Gly Glu Ile
 195 200 205
 Lys Pro Gln Gly Val Tyr Asp Ile Pro Pro Thr Lys Gly Val Tyr Ala
 210 215 220
 Ile Pro Pro Ser Ala Cys Arg Asp Glu Ala Gly Leu Arg Glu Lys Asp
 225 230 235 240
 Tyr Asp Phe Pro Pro Pro Met Arg Gln Ala Gly Arg Pro Asp Leu Arg
 245 250 255
 Pro Glu Gly Val Tyr Asp Ile Pro Pro Thr Cys Thr Lys Pro Ala Gly
 260 265 270
 Lys Asp Leu His Val Lys Tyr Asn Cys Asp Ile Pro Gly Ala Ala Glu
 275 280 285
 Pro Val Ala Arg Arg His Gln Ser Leu Ser Pro Asn His Pro Pro Pro
 290 295 300
 Gln Leu Gly Gln Ser Val Gly Ser Gln Asn Asp Ala Tyr Asp Val Pro
 305 310 315 320
 Arg Gly Val Gln Phe Leu Glu Pro Pro Ala Glu Thr Ser Glu Lys Ala
 325 330 335
 Asn Pro Gln Glu Arg Asp Gly Val Tyr Asp Val Pro Leu His Asn Pro
 340 345 350
 Pro Asp Ala Lys Gly Ser Arg Asp Leu Val Asp Gly Ile Asn Arg Leu
 355 360 365
 Ser Phe Ser Ser Thr Gly Ser Thr Arg Ser Asn Met Ser Thr Ser Ser
 370 375 380
 Thr Ser Ser Lys Glu Ser Ser Leu Ser Ala Ser Pro Ala Gln Asp Lys
 385 390 395 400
 Arg Leu Phe Leu Asp Pro Asp Thr Ala Ile Glu Arg Leu Gln Arg Leu
 405 410 415
 Gln Gln Ala Leu Glu Met Gly Val Ser Ser Leu Met Ala Leu Val Thr
 420 425 430
 Thr Asp Trp Arg Cys Tyr Gly Tyr Met Glu Arg His Ile Asn Glu Ile
 435 440 445
 Arg Thr Ala Val Asp Lys Val Glu Leu Phe Leu Lys Glu Tyr Leu His
 450 455 460
 Phe Val Lys Gly Ala Val Ala Asn Ala Ala Cys Leu Pro Glu Leu Ile
 465 470 475 480
 Leu His Asn Lys Met Lys Arg Glu Leu Gln Arg Val Glu Asp Ser His
 485 490 495
 Gln Ile Leu Ser Gln Thr Ser His Asp Leu Asn Glu Cys Ser Trp Ser
 500 505 510
 Leu Asn Ile Leu Ala Ile Asn Lys Pro Gln Asn Lys Cys Asp Asp Leu
 515 520 525
 Asp Arg Phe Val Met Val Ala Lys Thr Val Pro Asp Asp Ala Lys Gln
 530 535 540
 Leu Thr Thr Thr Ile Asn Thr Asn Ala Glu Ala Leu Phe Arg Pro Gly
 545 550 555 560
 Pro Gly Ser Leu His Leu Lys Asn Gly Pro Glu Ser Ile Met Asn Ser
 565 570 575
 Thr Glu Tyr Pro His Gly Gly Ser Gln Gly Gln Leu Leu His Pro Gly
 580 585 590
 Asp His Lys Ala Gln Ala His Asn Lys Ala Leu Pro Pro Gly Leu Ser
 595 600 605
 Lys Glu Gln Ala Pro Asp Cys Ser Ser Ser Asp Gly Ser Glu Arg Ser
 610 615 620
 Trp Met Asp Asp Tyr Asp Tyr Val His Leu Gln Gly Lys Glu Glu Phe

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<210> 114

<211> 906

<212> PRT

<213> Homo Sapiens

<400> 114

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Ser Leu Glu Ile Arg Thr Leu Ala Val Glu Arg Leu Leu Glu Pro Leu
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Val Thr Gln Val Thr Thr Leu Val Asn Thr Asn Ser Lys Gly Pro Ser
35 40 45
Asn Lys Lys Arg Gly Arg Ser Lys Lys Ala His Val Leu Ala Ala Ser
50 55 60
Val Glu Gln Ala Thr Glu Asn Phe Leu Glu Lys Gly Asp Lys Ile Ala
65 70 75 80
Lys Glu Ser Gln Phe Leu Lys Glu Glu Leu Val Ala Ala Val Glu Asp

Ala Leu Gln Glu Lys Asp Val Asp Gly Leu Asp Arg Thr Ala Gly Ala
 530 535 540
 Ile Arg Gly Arg Ala Ala Arg Val Ile His Val Val Thr Ser Glu Met
 545 550 555 560
 Asp Asn Tyr Glu Pro Gly Val Tyr Thr Glu Lys Val Leu Glu Ala Thr
 565 570 575
 Lys Leu Leu Ser Asn Thr Val Met Pro Arg Phe Thr Glu Gln Val Glu
 580 585 590
 Ala Ala Val Glu Ala Leu Ser Ser Asp Pro Ala Gln Pro Met Asp Glu
 595 600 605
 Asn Glu Phe Ile Asp Ala Ser Arg Leu Val Tyr Asp Gly Ile Arg Asp
 610 615 620
 Ile Arg Lys Ala Val Leu Met Ile Arg Thr Pro Glu Glu Leu Asp Asp
 625 630 635 640
 Ser Asp Phe Glu Thr Glu Asp Phe Asp Val Arg Ser Arg Thr Ser Val
 645 650 655
 Gln Thr Glu Asp Asp Gln Leu Ile Ala Gly Gln Ser Ala Arg Ala Ile
 660 665 670
 Met Ala Gln Leu Pro Gln Glu Gln Lys Ala Lys Ile Ala Glu Gln Val
 675 680 685
 Ala Ser Phe Gln Glu Glu Lys Ser Lys Leu Asp Ala Glu Val Ser Lys
 690 695 700
 Trp Asp Asp Ser Gly Asn Asp Ile Ile Val Leu Ala Lys Gln Met Cys
 705 710 715 720
 Met Ile Met Met Glu Met Thr Asp Phe Thr Arg Gly Lys Gly Pro Leu
 725 730 735
 Lys Asn Thr Ser Asp Val Ile Ser Ala Ala Lys Lys Ile Ala Glu Ala
 740 745 750
 Gly Ser Arg Met Asp Lys Leu Gly Arg Thr Ile Ala Asp His Cys Pro
 755 760 765
 Asp Ser Ala Cys Lys Gln Asp Leu Leu Ala Tyr Leu Gln Arg Ile Ala
 770 775 780
 Leu Tyr Cys His Gln Leu Asn Ile Cys Ser Lys Val Lys Ala Glu Val
 785 790 795 800
 Gln Asn Leu Gly Gly Glu Leu Val Val Ser Gly Val Asp Ser Ala Met
 805 810 815
 Ser Leu Ile Gln Ala Ala Lys Asn Leu Met Asn Ala Val Val Gln Thr
 820 825 830
 Val Lys Ala Ser Tyr Val Ala Ser Thr Lys Tyr Gln Lys Ser Gln Gly
 835 840 845
 Met Ala Ser Leu Asn Leu Pro Ala Val Ser Trp Lys Met Lys Ala Pro
 850 855 860
 Glu Lys Lys Pro Leu Val Lys Arg Glu Lys Gln Asp Glu Thr Gln Thr
 865 870 875 880
 Lys Ile Lys Arg Ala Ser Gln Lys Lys His Val Asn Pro Val Gln Ala
 885 890 895
 Leu Ser Glu Phe Lys Ala Met Asp Ser Ile
 900 905

<210> 115
 <211> 1701
 <212> DNA
 <213> Homo Sapiens

<400> 115

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 cctgataaga atccccaat gcaggagaca aacttttaaag aaataagttt tgcataatgaa 180
 gtactatcaa atcctgagaa gcgtgagtta tatgacagat acggagagca aggtcttcgg 240
 gaaggcagcg gcggaggtgg gtggcatgga ttgatatttt ctctcaccgt tttttgtggg 300
 ggattgttcg gcttcaggg caatcagagt agaagtcgaa atggcagaag aagaggagag 360
 gacatgatgc atccactcaa agtatcttta gaagatctgt ataatggcaa gacaacaaaa 420
 ctacaactta gcaagaatgt gctctgtagt gcatgcagtg gccaaggcgg aaagtctgga 480
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 gtaattaatg aaaaagaccg ctgtaaaaaa tgtgaaggga agaaggtgat taaagaagtc 660
 aagattcttg aagtccacgt agacaaaggc atgaaacatg gacagagaat tacattcact 720
 ggggaagcag accaggcccc agagtggaa cggagagacat tgttcttttt gctaccagga 780
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 ttttgtgtag atttttatgt ttcatatatt aaattttaa cccacattgt aaagtttgta 1620
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<210> 116

<211> 415

<212> PRT

<213> Homo Sapiens

<400> 116

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 20 25 30
 Lys Glu Tyr His Pro Asp Lys Asn Pro Gln Met Gln Glu Thr Asn Phe
 35 40 45
 Lys Glu Ile Ser Phe Ala Tyr Glu Val Leu Ser Asn Pro Glu Lys Arg
 50 55 60
 Glu Leu Tyr Asp Arg Tyr Gly Glu Gln Gly Leu Arg Glu Gly Ser Gly
 65 70 75 80
 Gly Gly Gly Trp His Gly Leu Ile Phe Ser Leu Thr Val Phe Cys Gly
 85 90 95
 Gly Leu Phe Gly Phe Met Gly Asn Gln Ser Arg Ser Arg Asn Gly Arg
 100 105 110
 Arg Arg Gly Glu Asp Met Met His Pro Leu Lys Val Ser Leu Glu Asp
 115 120 125
 Leu Tyr Asn Gly Lys Thr Thr Lys Leu Gln Leu Ser Lys Asn Val Leu
 130 135 140
 Cys Ser Ala Cys Ser Gly Gln Gly Gly Lys Ser Gly Ala Val Gln Lys

145 150 155 160
 Cys Ser Ala Cys Arg Gly Arg Gly Val Arg Ile Met Ile Arg Gln Leu
 165 170 175
 Ala Pro Gly Met Val Gln Gln Met Gln Ser Val Cys Ser Asp Cys Asn
 180 185 190
 Gly Glu Gly Glu Val Ile Asn Glu Lys Asp Arg Cys Lys Lys Cys Glu
 195 200 205
 Gly Lys Lys Val Ile Lys Glu Val Lys Ile Leu Glu Val His Val Asp
 210 215 220
 Lys Gly Met Lys His Gly Gln Arg Ile Thr Phe Thr Gly Glu Ala Asp
 225 230 235 240
 Gln Ala Pro Glu Trp Asn Pro Glu Thr Leu Phe Phe Leu Leu Pro Gly
 245 250 255
 Glu Lys Asn Met Glu Val Phe Gln Arg Asp Gly Asn Asp Leu His Met
 260 265 270
 Thr Tyr Lys Ile Gly Leu Val Glu Ala Leu Cys Gly Phe Gln Phe Thr
 275 280 285
 Leu Ser His Leu Asp Gly Arg Gln Ile Val Val Lys Tyr Pro Pro Gly
 290 295 300
 Lys Val Ile Glu Pro Gly Cys Val Arg Val Val Arg Gly Glu Gly Met
 305 310 315 320
 Pro Gln Tyr Arg Asn Pro Phe Glu Lys Gly Gly Leu Tyr Ile Lys Phe
 325 330 335
 Asp Val Gln Phe Pro Glu Asn Asn Trp Ile Asn Pro Asp Lys Leu Ser
 340 345 350
 Glu Leu Glu Asp Leu Leu Pro Ser Arg Pro Glu Val Pro Asn Ile Ile
 355 360 365
 Gly Glu Thr Glu Glu Val Glu Leu Gln Glu Phe Asp Ser Thr Arg Gly
 370 375 380
 Ser Gly Gly Gly Gln Arg Arg Glu Ala Tyr Asn Asp Ser Ser Asp Glu
 385 390 395 400
 Glu Ser Ser Ser His His Gly Pro Gly Val Gln Cys Ala His Gln
 405 410 415

<210> 117

<211> 1821

<212> DNA

<213> Homo Sapiens

<400> 117

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 aaacatacaa gcttgcaagg agcttgccca aaccactcgt acagcatatg gacccaaaagg 180
 aatgaacaaa atgggttatca accacttgga gaagttgttt gtgacaaacg atgcagcaac 240
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 tcctgattcc ggccatttca atgttgataa catcagagtt tgtaaaattc tgggctctgg 660
 tatcagttcc tcttcagtat tgcattggcat ggtttttaaag aaggaaaccg aagggtgatgt 720
 aacatctgtc aaagatgcaa aaatagcagt gtactcttgt ccttttgatg gcatgataac 780
 agaaaactaag ggaacagtgt tgataaagac tgctgaagaa ttgatgaatt ttagtaaggg 840
 agaagaaaac ctcatggatg cacaagtcaa agctattgct gatactggtg caaatgtcgt 900

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agtaacaggt ggcaaagtgg cagacatggc tcttcattat gcaaataaat ataatatcat    960
gttagtgagg ctaaactcaa aatgggatct ccgaagactt tgtaaaactg ttggtgctac    1020
agctcttcct agattgacac ctctgtcctt tgaagaaatg ggacactgtg acagtgttta    1080
cctctcagaa gttggagata ctgaggtggt ggtttttaag catgaaaagg aagatggcgc    1140
catttctacc atagtacttc gaggtcttac agacaatctg atggatgaca tagaaagggg    1200
agtagacgat ggtgttaata ctttcaaagt tcttacaagg gataaacgtc ttgtaccggg    1260
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tcaagaagga aataaaaacg ttggattaga tattgaggct gaagtcctg ctgtaaagga    1500
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tactaatgct gcagtcactg tacttagagt ggatcagatc atcatggcaa aaccagctgg    1620
tgggcccaag cctccaagtg ggaagaaaga ctgggatgat gacccaaatg attgaaattg    1680
gcttaatttt tactgtaggt gaaggctgta tttgtagtag tactcaagaa tcacctgatg    1740
ttttcttatt ctctttaaataa taagagttat tttgtgtttg tattcttggc tggatgttat    1800
aataaacata ttgttactgt c                                     1821

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<210> 118

<211> 548

<212> PRT

<213> Homo Sapiens

<400> 118

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Met Ala Leu His Val Pro Lys Ala Pro Gly Phe Ala Gln Met Leu Lys
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          20          25          30
Ile Gln Ala Cys Lys Glu Leu Ala Gln Thr Thr Arg Thr Ala Tyr Gly
          35          40          45
Pro Lys Gly Met Asn Lys Met Val Ile Asn His Leu Glu Lys Leu Phe
          50          55          60
Val Thr Asn Asp Ala Ala Thr Ile Leu Arg Glu Leu Glu Val Gln His
65          70          75          80
Pro Ala Ala Lys Met Ile Val Met Ala Ser His Met Gln Glu Gln Glu
          85          90          95
Val Gly Asp Gly Thr Asn Phe Val Leu Val Phe Ala Gly Ala Leu Leu
          100          105          110
Glu Leu Ala Glu Glu Leu Leu Arg Ile Gly Leu Ser Val Ser Glu Val
          115          120          125
Ile Glu Gly Tyr Glu Ile Ala Cys Arg Lys Ala His Glu Ile Leu Pro
          130          135          140
Asn Leu Val Cys Cys Ser Ala Lys Asn Leu Arg Asp Ile Asp Glu Val
          145          150          155          160
Ser Ser Leu Leu Arg Thr Ser Ile Met Ser Lys Gln Tyr Gly Asn Glu
          165          170          175
Val Phe Leu Ala Lys Leu Ile Ala Gln Ala Cys Val Ser Ile Phe Pro
          180          185          190
Asp Ser Gly His Phe Asn Val Asp Asn Ile Arg Val Cys Lys Ile Leu
          195          200          205
Gly Ser Gly Ile Ser Ser Ser Ser Val Leu His Gly Met Val Phe Lys
          210          215          220
Lys Glu Thr Glu Gly Asp Val Thr Ser Val Lys Asp Ala Lys Ile Ala
          225          230          235          240
Val Tyr Ser Cys Pro Phe Asp Gly Met Ile Thr Glu Thr Lys Gly Thr
          245          250          255

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Val Leu Ile Lys Thr Ala Glu Glu Leu Met Asn Phe Ser Lys Gly Glu
 260 265 270
 Glu Asn Leu Met Asp Ala Gln Val Lys Ala Ile Ala Asp Thr Gly Ala
 275 280 285
 Asn Val Val Val Thr Gly Gly Lys Val Ala Asp Met Ala Leu His Tyr
 290 295 300
 Ala Asn Lys Tyr Asn Ile Met Leu Val Arg Leu Asn Ser Lys Trp Asp
 305 310 315 320
 Leu Arg Arg Leu Cys Lys Thr Val Gly Ala Thr Ala Leu Pro Arg Leu
 325 330 335
 Thr Pro Pro Val Leu Glu Glu Met Gly His Cys Asp Ser Val Tyr Leu
 340 345 350
 Ser Glu Val Gly Asp Thr Gln Val Val Val Phe Lys His Glu Lys Glu
 355 360 365
 Asp Gly Ala Ile Ser Thr Ile Val Leu Arg Gly Ser Thr Asp Asn Leu
 370 375 380
 Met Asp Asp Ile Glu Arg Val Val Asp Asp Gly Val Asn Thr Phe Lys
 385 390 395 400
 Val Leu Thr Arg Asp Lys Arg Leu Val Pro Gly Gly Gly Ala Thr Glu
 405 410 415
 Ile Glu Leu Ala Lys Gln Ile Thr Ser Tyr Gly Glu Thr Cys Pro Gly
 420 425 430
 Leu Glu Gln Tyr Ala Ile Lys Lys Phe Ala Glu Ala Phe Glu Ala Ile
 435 440 445
 Pro Arg Ala Leu Ala Glu Asn Ser Gly Val Lys Ala Asn Glu Val Ile
 450 455 460
 Ser Lys Leu Tyr Ala Val His Gln Glu Gly Asn Lys Asn Val Gly Leu
 465 470 475 480
 Asp Ile Glu Ala Glu Val Pro Ala Val Lys Asp Met Leu Glu Ala Gly
 485 490 495
 Ile Leu Asp Thr Tyr Leu Gly Lys Tyr Trp Ala Ile Lys Leu Ala Thr
 500 505 510
 Asn Ala Ala Val Thr Val Leu Arg Val Asp Gln Ile Ile Met Ala Lys
 515 520 525
 Pro Ala Gly Gly Pro Lys Pro Pro Ser Gly Lys Lys Asp Trp Asp Asp
 530 535 540
 Asp Gln Asn Asp
 545

<210> 119

<211> 1321

<212> DNA

<213> Homo Sapiens

<400> 119

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ctggtagaca	gttactggac	gaagtagaag	tggcgactga	acccgccggt	tcccggatag	120
tccaggagaa	ggtgttcaag	ggcttggacc	tccttgagaa	ggctgccgaa	atgttatcgc	180
agctcgactt	gttcagccga	aatgaagatt	tggaagagat	tgtttccacc	gacctgaagt	240
accttttgg	gccagcgttt	caaggagccc	tcaccatgaa	acaagtcaac	cccagcaagc	300
gtctagatca	tttgcagcgg	gctcgagaac	actttataaa	ctacttaact	cagtgccatt	360
gctatcatgt	ggcagagttt	gagctgcccc	aaaccatgaa	caactctgct	gaaaatcaca	420
ctgccaattc	ctccatggct	tatcctagtc	tcgttgctat	ggcatctcaa	agacaggcta	480
aaatacagag	atacaagcag	aagaaggagt	tggagcatag	gttgtctgca	atgaaatctg	540
ctgtggaaa	tggtcaagca	gatgatgagc	gtgttcgtga	atattatctt	cttcaccttc	600

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agaggtggat tgatatcagc ttagaagaga ttgagagcat tgaccaggaa ataaagatcc      660
tgagagaaaag agactcttca agagagggcat caacttctaa ctcattctgc caggagaggc      720
ctccagtga acccttcatt ctactcggga acatgggtca agccaaagta tttggagctg      780
gttatccaag tctgccaaact atgacgggtga gtgactggta tgagcaacat cggaaatatg      840
gagcattacc ggatcaggga atagccaagg cagcaccaga ggaattcaga aaagcagctc      900
agcaacagga agaacaagaa gaaaaggagg aagaggatga tgaacaaaca ctccacagag      960
cccgaggagt ggatgactgg aaggacaccc atcctagggg ctatgggaac cgacagaaca    1020
tgggctgata tccccacaac accacaggac tgcagggtgc acaactccct gccaaaggaa    1080
accatgcagt cctcccctcc ctggtctcct gcttcagctc tgtacaacga gggcaaagat    1140
gctaaatctt gctttgcatt cagtaaagtg tcaagtgatt aagtgtgtat ttgtacccta    1200
gatgatatga accagcagtc ttgttttggc atcatcctca tcatgttgta ttccagcttc    1260
ttaagtggaa ggaaaagagt gctgagaaat ggctctgtat aatctatggc tatccgaatt    1320
c                                                                 1321

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<210> 120

<211> 339

<212> PRT

<213> Homo Sapiens

<400> 120

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          20          25          30
Ala Gly Ser Arg Ile Val Gln Glu Lys Val Phe Lys Gly Leu Asp Leu
          35          40          45
Leu Glu Lys Ala Ala Glu Met Leu Ser Gln Leu Asp Leu Phe Ser Arg
          50          55          60
Asn Glu Asp Leu Glu Glu Ile Ala Ser Thr Asp Leu Lys Tyr Leu Leu
65          70          75          80
Val Pro Ala Phe Gln Gly Ala Leu Thr Met Lys Gln Val Asn Pro Ser
          85          90          95
Lys Arg Leu Asp His Leu Gln Arg Ala Arg Glu His Phe Ile Asn Tyr
          100          105          110
Leu Thr Gln Cys His Cys Tyr His Val Ala Glu Phe Glu Leu Pro Lys
          115          120          125
Thr Met Asn Asn Ser Ala Glu Asn His Thr Ala Asn Ser Ser Met Ala
          130          135          140
Tyr Pro Ser Leu Val Ala Met Ala Ser Gln Arg Gln Ala Lys Ile Gln
          145          150          155          160
Arg Tyr Lys Gln Lys Lys Glu Leu Glu His Arg Leu Ser Ala Met Lys
          165          170          175
Ser Ala Val Glu Ser Gly Gln Ala Asp Asp Glu Arg Val Arg Glu Tyr
          180          185          190
Tyr Leu Leu His Leu Gln Arg Trp Ile Asp Ile Ser Leu Glu Glu Ile
          195          200          205
Glu Ser Ile Asp Gln Glu Ile Lys Ile Leu Arg Glu Arg Asp Ser Ser
          210          215          220
Arg Glu Ala Ser Thr Ser Asn Ser Ser Arg Gln Glu Arg Pro Pro Val
          225          230          235          240
Lys Pro Phe Ile Leu Thr Arg Asn Met Ala Gln Ala Lys Val Phe Gly
          245          250          255
Ala Gly Tyr Pro Ser Leu Pro Thr Met Thr Val Ser Asp Trp Tyr Glu
          260          265          270
Gln His Arg Lys Tyr Gly Ala Leu Pro Asp Gln Gly Ile Ala Lys Ala

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275	280	285
Ala Pro Glu Glu Phe Arg Lys Ala Ala Gln Gln Gln Glu Glu Gln Glu		
290	295	300
Glu Lys Glu Glu Glu Asp Asp Glu Gln Thr Leu His Arg Ala Arg Glu		
305	310	315
Trp Asp Asp Trp Lys Asp Thr His Pro Arg Gly Tyr Gly Asn Arg Gln		
	325	330
		335
Asn Met Gly		

<210> 121
 <211> 2965
 <212> DNA
 <213> Homo Sapiens

<400> 121

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tgagcccgcg	ggagcccagg	acgcccgttc	cccgccatc	cccgtcccc	gaggccggcc	180
gcctggtcat	ggcgagccg	ggcccggctt	cccagcctga	cgtttctctt	cagcaacggg	240
tagcagaatt	ggaaaaaatt	aatgcagaat	ttttacgtgc	acaacagcag	cttgaacaag	300
aatttaatat	aaagagagca	aaatttaagg	agttatat	ggctaaagag	gaggatctga	360
agaggcaaaa	tgcagtatta	caagctgcac	aagatgattt	gggacacctt	cgaaccagc	420
tgtgggaagc	tcaagcagag	atggagaata	ttaaggcgat	tgccacagtc	tctgagaaca	480
ccaagcaaga	agctatagat	gaagtgaata	gacagtggag	agaagaagtt	gcttcacttc	540
aggctgttat	gaaagaaaca	gttcgtgact	atgagcaaca	gttccacctt	aggetggagc	600
aggagcgaac	acagtgggca	cagtatatag	aatacgcaga	gagggaaata	gctgatttaa	660
gaagaaggct	gtctgaagg	caagaggagg	aaaatttaga	aaatgaaatg	aaaaaggccc	720
aagaggatgc	tgagaaactt	cggctccgtt	tgatgccaat	ggaaaaggaa	attgcagctt	780
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agaactgaa	tcattatctg	gaagctgaga	aatctttag	gactgatcta	gagatgtatg	900
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tgcatgtgtc	attacagcaa	gcagaagact	tcctcctccc	agacactaca	gaggcactgc	2220
gggagttggt	attaaaatac	cgtgaggaca	tcattaatgt	gcggacagca	gcagaccacg	2280
tagaagaaaa	gctgaaggct	gagatacttt	tcctaaaaga	gcagatccaa	gcagaacagt	2340

```

gtttaaaaga aaatcttgaa gaaactctgc aactagaaat agaaaactgc aaggaggaaa 2400
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tggaagtccac attagagag aagtctcaac agcttgagag tcttcaggaa ataaagatca 2520
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cagcaaacag tggggtgatc tgcag 2965

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<210> 122

<211> 862

<212> PRT

<213> Homo Sapiens

<400> 122

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Met Ala Gln Pro Gly Pro Ala Ser Gln Pro Asp Val Ser Leu Gln Gln
 1          5          10          15
Arg Val Ala Glu Leu Glu Lys Ile Asn Ala Glu Phe Leu Arg Ala Gln
          20          25          30
Gln Gln Leu Glu Gln Glu Phe Asn Gln Lys Arg Ala Lys Phe Lys Glu
          35          40          45
Leu Tyr Leu Ala Lys Glu Glu Asp Leu Lys Arg Gln Asn Ala Val Leu
          50          55          60
Gln Ala Ala Gln Asp Asp Leu Gly His Leu Arg Thr Gln Leu Trp Glu
65          70          75          80
Ala Gln Ala Glu Met Glu Asn Ile Lys Ala Ile Ala Thr Val Ser Glu
          85          90          95
Asn Thr Lys Gln Glu Ala Ile Asp Glu Val Lys Arg Gln Trp Arg Glu
          100          105          110
Glu Val Ala Ser Leu Gln Ala Val Met Lys Glu Thr Val Arg Asp Tyr
          115          120          125
Glu His Gln Phe His Leu Arg Leu Glu Gln Glu Arg Thr Gln Trp Ala
          130          135          140
Gln Tyr Arg Glu Tyr Ala Glu Arg Glu Ile Ala Asp Leu Arg Arg Arg
          145          150          155          160
Leu Ser Glu Gly Gln Glu Glu Glu Asn Leu Glu Asn Glu Met Lys Lys
          165          170          175
Ala Gln Glu Asp Ala Glu Lys Leu Arg Ser Val Val Met Pro Met Glu
          180          185          190
Lys Glu Ile Ala Ala Leu Lys Asp Lys Leu Thr Glu Ala Glu Asp Lys
          195          200          205
Ile Lys Glu Leu Glu Ala Ser Lys Val Lys Glu Leu Asn His Tyr Leu
          210          215          220
Glu Ala Glu Lys Ser Cys Arg Thr Asp Leu Glu Met Tyr Val Ala Val
          225          230          235          240
Leu Asn Thr Gln Lys Ser Val Leu Gln Glu Asp Ala Glu Lys Leu Arg
          245          250          255
Lys Glu Leu His Glu Val Cys His Leu Leu Glu Gln Glu Arg Gln Gln
          260          265          270
His Asn Gln Leu Lys His Thr Trp Gln Lys Ala Asn Asp Gln Phe Leu
          275          280          285
Glu Ser Gln Arg Leu Leu Met Arg Asp Met Gln Arg Met Glu Ile Val

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290 295 300
 Leu Thr Ser Glu Gln Leu Arg Gln Val Glu Glu Leu Lys Lys Lys Asp
 305 310 315 320
 Gln Glu Asp Asp Glu Gln Gln Arg Leu Asn Lys Arg Lys Asp His Lys
 325 330 335
 Lys Ala Asp Val Glu Glu Glu Ile Lys Ile Pro Val Val Cys Ala Leu
 340 345 350
 Thr Gln Glu Glu Ser Ser Ala Gln Leu Ser Asn Glu Glu Glu His Leu
 355 360 365
 Asp Ser Thr Arg Gly Ser Val His Ser Leu Asp Ala Gly Leu Leu Leu
 370 375 380
 Pro Ser Gly Asp Pro Phe Ser Lys Ser Asp Asn Asp Met Phe Lys Asp
 385 390 395 400
 Gly Leu Arg Arg Ala Gln Ser Thr Asp Ser Leu Gly Thr Ser Gly Ser
 405 410 415
 Leu Gln Ser Lys Ala Leu Gly Tyr Asn Tyr Lys Ala Lys Ser Ala Gly
 420 425 430
 Asn Leu Asp Glu Ser Asp Phe Gly Pro Leu Val Gly Ala Asp Ser Val
 435 440 445
 Ser Glu Asn Phe Asp Thr Ala Ser Leu Gly Ser Leu Gln Met Pro Ser
 450 455 460
 Gly Phe Met Leu Thr Lys Asp Gln Glu Arg Ala Ile Lys Ala Met Thr
 465 470 475 480
 Pro Glu Gln Glu Glu Thr Ala Ser Leu Leu Ser Ser Val Thr Gln Gly
 485 490 495
 Met Glu Ser Ala Tyr Val Ser Pro Ser Gly Tyr Arg Leu Val Ser Glu
 500 505 510
 Thr Glu Trp Asn Leu Leu Gln Lys Glu Val His Asn Ala Gly Asn Lys
 515 520 525
 Leu Gly Arg Arg Cys Asp Met Cys Ser Asn Tyr Glu Lys Gln Leu Gln
 530 535 540
 Gly Ile Gln Ile Gln Glu Ala Glu Thr Arg Asp Gln Val Lys Lys Leu
 545 550 555 560
 Gln Leu Met Leu Arg Gln Ala Asn Asp Gln Leu Glu Lys Thr Met Lys
 565 570 575
 Asp Lys Gln Glu Leu Glu Asp Phe Ile Lys Gln Ser Ser Glu Asp Ser
 580 585 590
 Ser His Gln Ile Ser Ala Leu Val Leu Arg Ala Gln Ala Ser Glu Ile
 595 600 605
 Leu Leu Glu Glu Leu Gln Gln Gly Leu Ser Gln Ala Lys Arg Asp Val
 610 615 620
 Gln Glu Gln Met Ala Val Leu Met Gln Ser Arg Glu Gln Val Ser Glu
 625 630 635 640
 Glu Leu Val Arg Leu Gln Lys Asp Asn Asp Ser Leu Gln Gly Lys His
 645 650 655
 Ser Leu His Val Ser Leu Gln Gln Ala Glu Asp Phe Ile Leu Pro Asp
 660 665 670
 Thr Thr Glu Ala Leu Arg Glu Leu Val Leu Lys Tyr Arg Glu Asp Ile
 675 680 685
 Ile Asn Val Arg Thr Ala Ala Asp His Val Glu Glu Lys Leu Lys Ala
 690 695 700
 Glu Ile Leu Phe Leu Lys Glu Gln Ile Gln Ala Glu Gln Cys Leu Lys
 705 710 715 720
 Glu Asn Leu Glu Glu Thr Leu Gln Leu Glu Ile Glu Asn Cys Lys Glu
 725 730 735

Glu Ile Ala Ser Ile Ser Ser Leu Lys Ala Glu Leu Glu Arg Ile Lys
740 745 750
Val Glu Lys Gly Gln Leu Glu Ser Thr Leu Arg Glu Lys Ser Gln Gln
755 760 765
Leu Glu Ser Leu Gln Glu Ile Lys Ile Ser Leu Glu Glu Gln Leu Lys
770 775 780
Lys Glu Thr Ala Ala Lys Ala Thr Val Glu Gln Leu Met Phe Glu Glu
785 790 795 800
Lys Asn Lys Ala Gln Arg Leu Gln Thr Glu Leu Asp Val Ser Glu Gln
805 810 815
Val Gln Arg Asp Phe Val Lys Leu Ser Gln Thr Leu Gln Val Gln Leu
820 825 830
Glu Arg Ile Arg Gln Ala Asp Ser Leu Glu Arg Ile Arg Ala Ile Leu
835 840 845
Asn Asp Thr Lys Leu Thr Asp Ile Asn Gln Leu Pro Glu Thr
850 855 860

<210> 123
<211> 544
<212> DNA
<213> Homo Sapiens

<400> 123
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ttttaagggg agacaggatt caacttttga aacctccata tacagatgaa aataaaaaag 120
ttggttttggc attaaaggac cttgctaagc agtactctga cagactagaa tgctgtgaaa 180
atgaagtaga aaaggtaata gaagaaatac gttgcaaggc aattgagcgt ggaacaggaa 240
atgacaatta tagaacaacg ggaattgcta caatcgaggt gtttttacca ccaagactaa 300
aaaaagatag gaaaaacttg ttggagaccc gattgcacat cactggcaga gaactgaggt 360
ccaaaatagc tgaaaccttt ggacttcaag aanattatat caaaattgtc ataaataaga 420
agcaactacn actagggaaa acccttgaag ancaaggcgt ggctcacaat gtgaaagcga 480
tggtgcttga actaaaacaa tctgaagagg acgcgaggaa aaacttccag ttagaggaag 540
agga 544

<210> 124
<211> 178
<212> PRT
<213> Homo Sapiens

<400> 124
Glu Trp Arg Gly Ala Gly Met Ala Gln Lys Lys Tyr Leu Gln Ala Lys
1 5 10 15
Leu Thr Gln Phe Leu Arg Glu Asp Arg Ile Gln Leu Trp Lys Pro Pro
20 25 30
Tyr Thr Asp Glu Asn Lys Lys Val Gly Leu Ala Leu Lys Asp Leu Ala
35 40 45
Lys Gln Tyr Ser Asp Arg Leu Glu Cys Cys Glu Asn Glu Val Glu Lys
50 55 60
Val Ile Glu Glu Ile Arg Cys Lys Ala Ile Glu Arg Gly Thr Gly Asn
65 70 75 80
Asp Asn Tyr Arg Thr Thr Gly Ile Ala Thr Ile Glu Val Phe Leu Pro
85 90 95
Pro Arg Leu Lys Lys Asp Arg Lys Asn Leu Leu Glu Thr Arg Leu His
100 105 110
Ile Thr Gly Arg Glu Leu Arg Ser Lys Ile Ala Glu Thr Phe Gly Leu

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      115      120      125
Gln Glu Tyr Ile Lys Ile Val Ile Asn Lys Lys Gln Leu Leu Gly Lys
      130      135      140
Thr Leu Glu Gln Gly Val Ala His Asn Val Lys Ala Met Val Leu Glu
145      150      155      160
Leu Lys Gln Ser Glu Glu Asp Ala Arg Lys Asn Phe Gln Leu Glu Glu
      165      170      175
Glu Glu

```

<210> 125
 <211> 1302
 <212> DNA
 <213> Homo Sapiens

```

<400> 125
atggagggtgg tggaccccgca gcagctgggc atgttcacgg agggcgagct gatgtcgggtg      60
ggtatggaca cgttcaccca ccgcacgcac tccaccgagg tcacttacca gccgcgccgc      120
aagcggggcca agctcatcgg caagtacctg atggggggacc tgctggggga aggtctcttac      180
ggcaagggtga aggagggtgct ggactcggag acgctgtgca ggaggggccgt caagatcctc      240
aagaagaaga agttgcgaag gatccccaac ggggaggcca acgtgaagaa ggaaattcaa      300
ctactgagga ggttacggca caaaaatgtc atccagctgg tggatgtgtt atacaacgaa      360
gagaagcaga aaatgtatat ggtgatggag tactgcgtgt gtggcatgca ggaaatgctg      420
gacacgctgc cggagaagcg tttcccagtg tgccaggccc acgggtactt ctgtcagctg      480
attgacggcc tggagtacct gcatagccag ggcattgtgc acaaggacat caagccgggg      540
aacctgctgc tcaccaccgg tggcacccctc aaaatctccg acctggggcgt ggccgaggca      600
ctgcaccogt tcgcggcgga cgacacctgc cggaccagcc agggctcccc ggctttccag      660
ccgcccgaga ttgccaacgg cctggacacc ttctccggct tcaagggtgga catctggtcg      720
gctgggggtca ccctctacaa catcaccacg ggtctgtacc ccttcgaagg ggacaacatc      780
tacaagttgt ttgagaacat cgggaagggg agctacgcca tcccgggcca ctgtggcccc      840
ccgctctctg acctgctgaa agggatgctt gagtacgaac cggccaagag gttctccatc      900
cggcagatcc ggcagcacag ctggttccgg aagaaacatc ctccggctga agcaccagtg      960
cccatcccac cgagcccaga caccaaggac cgggtggcgca gcatgactgt ggtgccgtac      1020
ttggaggacc tgcacggcgc ggacgaggac gaggacctct tcgacatcga ggatgacatc      1080
atctacactc aggacttcac ggtgcccgga cagggtccag aagaggaggc cagtcacaat      1140
ggacagcgcc ggggcctccc caaggccgtg tgtatgaacg gcacagaggc ggcgagctg      1200
agcaccaaat ccagggcgga gggccgggccc cccaacctg cccgcaaggc ctgctccgcc      1260
agcagcaaga tccgcgggct gtcggcctgc aagcagcagt ga      1302

```

<210> 126
 <211> 433
 <212> PRT
 <213> Homo Sapiens

```

<400> 126
Met Glu Val Val Asp Pro Gln Gln Leu Gly Met Phe Thr Glu Gly Glu
  1      5      10      15
Leu Met Ser Val Gly Met Asp Thr Phe Ile His Arg Ile Asp Ser Thr
      20      25      30
Glu Val Ile Tyr Gln Pro Arg Arg Lys Arg Ala Lys Leu Ile Gly Lys
      35      40      45
Tyr Leu Met Gly Asp Leu Leu Gly Glu Gly Ser Tyr Gly Lys Val Lys
      50      55      60
Glu Val Leu Asp Ser Glu Thr Leu Cys Arg Arg Ala Val Lys Ile Leu
      65      70      75      80

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gaacttgctc gactgagaga ctcaggactc tcacagaagg aggaagagga ggacactttt 180
attgaagaac aacaactaga agaagagaag ctattggaaa gagagaggca aagattacat 240
gaggagtggg tgctaagaga gcagaaggca caagaagaat tcagaataaaa gaagggaaaag 300
gaagaggcgg ctaaaaaacg gcaagaagaa caagagagaa agttaaaagga acaatgggaa 360
gaacagcaga ggaaagagag agaagaggag gacagaaaac gacaggagaa gaaagaaaaa 420
gaggaagctt tgcagaagat gctggatcag gctgaaaatg agttggaaaa tggtaggaca 480
tggaacaaac cagaaccacc cgtggatttc agagtaatgg agaaggatcg agctaattgt 540
cccttctaca gtaaaacagg agcttgacga tttggagata gatgttcacg taaacataat 600
ttcccaacat ccagtctac ccttcttatt aagagcatgt ttacgacgtt tggaaatggag 660
cagtgcagga gggatgacta tgaccctgac gcaagcctgg agtacagcga ggaagaaacc 720
taccaacagt tcttagactt ctatgaggat gtgttgcccc agttcaagaa cgtggggaaa 780
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gcaggacgac agctgcagtg tgaattctgc cccgtgaccc ggtggaaaat ggcgatttgt 960
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cgcagccggg gccggggcag ccggagccgg agccggagcc ggagccgcag gagccgccg 1380
agccggagcc aaagtctctc taggtccgca agtcgtggca ggaggaggtc gggtaataga 1440
gacagaactg ttcagagtcc caaatccaaa taaactagtt ttgttctt 1488

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<210> 128

<211> 482

<212> PRT

<213> Homo Sapiens

<400> 128

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Met Ala Ala Pro Glu Lys Met Thr Phe Pro Glu Lys Pro Ser His Lys
1      5      10      15
Lys Tyr Arg Ala Ala Leu Lys Lys Glu Lys Arg Lys Lys Arg Arg Gln
20      25      30
Glu Leu Ala Arg Leu Arg Asp Ser Gly Leu Ser Gln Lys Glu Glu Glu
35      40      45
Glu Asp Thr Phe Ile Glu Glu Gln Gln Leu Glu Glu Lys Leu Leu
50      55      60
Glu Arg Glu Arg Gln Arg Leu His Glu Glu Trp Leu Leu Arg Glu Gln
65      70      75      80
Lys Ala Gln Glu Glu Phe Arg Ile Lys Lys Glu Lys Glu Glu Ala Ala
85      90      95
Lys Lys Arg Gln Glu Glu Gln Glu Arg Lys Leu Lys Glu Gln Trp Glu
100     105     110
Glu Gln Gln Arg Lys Glu Arg Glu Glu Glu Glu Gln Lys Arg Gln Glu
115     120     125
Lys Lys Glu Lys Glu Glu Ala Leu Gln Lys Met Leu Asp Gln Ala Glu
130     135     140
Asn Glu Leu Glu Asn Gly Thr Thr Trp Gln Asn Pro Glu Pro Pro Val
145     150     155     160
Asp Phe Arg Val Met Glu Lys Asp Arg Ala Asn Cys Pro Phe Tyr Ser
165     170     175
Lys Thr Gly Ala Cys Arg Phe Gly Asp Arg Cys Ser Arg Lys His Asn
180     185     190
Phe Pro Thr Ser Ser Pro Thr Leu Leu Ile Lys Ser Met Phe Thr Thr

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195 200 205
 Phe Gly Met Glu Gln Cys Arg Arg Asp Asp Tyr Asp Pro Asp Ala Ser
 210 215 220
 Leu Glu Tyr Ser Glu Glu Glu Thr Tyr Gln Gln Phe Leu Asp Phe Tyr
 225 230 235 240
 Glu Asp Val Leu Pro Glu Phe Lys Asn Val Gly Lys Val Ile Gln Phe
 245 250 255
 Lys Val Ser Cys Asn Leu Glu Pro His Leu Arg Gly Asn Val Tyr Val
 260 265 270
 Gln Tyr Gln Ser Glu Glu Glu Cys Gln Ala Ala Leu Ser Leu Phe Asn
 275 280 285
 Gly Arg Trp Tyr Ala Gly Arg Gln Leu Gln Cys Glu Phe Cys Pro Val
 290 295 300
 Thr Arg Trp Lys Met Ala Ile Cys Gly Leu Phe Glu Ile Gln Gln Cys
 305 310 315 320
 Pro Arg Gly Lys His Cys Asn Phe Leu His Val Phe Arg Asn Pro Asn
 325 330 335
 Asn Glu Phe Trp Glu Ala Asn Arg Asp Ile Tyr Leu Ser Pro Asp Arg
 340 345 350
 Thr Gly Ser Ser Phe Gly Lys Asn Ser Glu Arg Arg Glu Arg Met Gly
 355 360 365
 His His Asp Asp Tyr Tyr Ser Arg Leu Arg Gly Arg Arg Asn Pro Ser
 370 375 380
 Pro Asp His Ser Tyr Lys Arg Asn Gly Glu Ser Glu Arg Lys Ser Ser
 385 390 395 400
 Arg His Arg Gly Lys Lys Ser His Lys Arg Thr Ser Lys Ser Arg Glu
 405 410 415
 Arg His Asn Ser Arg Ser Arg Gly Arg Asn Arg Asp Arg Ser Arg Asp
 420 425 430
 Arg Ser Arg Gly Arg Gly Ser Arg Ser Arg Ser Arg Ser Arg Ser Arg
 435 440 445
 Arg Ser Arg Arg Ser Arg Ser Gln Ser Ser Ser Arg Ser Arg Ser Arg
 450 455 460
 Gly Arg Arg Arg Ser Gly Asn Arg Asp Arg Thr Val Gln Ser Pro Lys
 465 470 475 480
 Ser Lys

<210> 129

<211> 1663

<212> DNA

<213> Homo Sapiens

<400> 129

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aggccctgag ccaactccgg gtgctctgct gtgagtggct gaggcccgag atccacacca      60
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tccaggcctg ggtgcaggag cattgcccg agagcgctga agaggctgtc actctcctcg      180
aagatctgga gcgggaactg gatgagccag gacaccaggt ctcaactcct ccaaacgaac      240
agaaaccggt gtgggagaag atatcctoct caggaactgc aaaggaatcc ccgagcagca      300
tgcagccaca gcccttggag accagtcaca aatacgagtc ttggggggccc ctgtacatcc      360
aagagtcttg tgaggagcag gagttcgctc aagatccaag aaaggtccga gattgcagat      420
tgagtaccca gcacgaggaa tcagcagatg agcagaaagg ttctgaagca gaggggctca      480
aaggggatat aatttctgtg attatcgcca ataaacctga ggccagctta gagaggcagt      540
gcgtaaacct tgaaaatgaa aaaggaacaa aacccccctt tcaagaggca ggctccaaga      600
aaggtagaga atcagttcct actaaacctt cccaggagga gagacgttat atatgtgctg      660

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aatgtggcaa agccttttagt aatagctcaa atctcaccaa acacaggaga acacacactg      720
gggagaaacc ttacgtgtgc accaagtgtg ggaaagcttt cagccacagc tcaaacctca      780
ccctccacta cagaacacac ttggtggacc ggccctatga ctgtaagtgt ggaaaagctt      840
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agtgcaaaga ttgtggcaag gctttcagcg ggaaaggcag cctcattcgt cactatcgga      960
tccacactgg ggagaagcct tatcagtgtg acgaatgtgg gaagagcttc agtcagcatg     1020
cgggcctcag ctcccaccag agactccaca ccggagagaa gccatataag tgtaaggagt     1080
gtgggaaagc cttcaaccac agctccaact tcaataaaca ccacagaatc cacaccgggg      1140
aaaagcccta ctggtgtcat cactgtggaa agaccttctg tagcaagtcc aatctttcca      1200
aacatcagcg agtccacact ggagagggag aagcaccgta actttcaagc gtcctgttg      1260
ttgtcgttgt tttaaacttt agaattctgaa aaccagaaag aagtcttgtc attgcagcag      1320
catcgattcc ggtgatagag tttgtatcac tcaacatcag gggatgcctg aggagtgcga      1380
gtccacagc aacatggcag gcaggaggtc ctcagaaggt gtcaggaggt tccacactcg      1440
ccagttcact ggagcagagt cccttcgcca cacttagggg cccagtaagc catgccagca      1500
ttaccttttg cgtagttaaa cagacgtgta tccagtctag ttaaggaaga aacattaaga      1560
ttgtttaatt tttaacatat attcaagaat tttattttgt aaagaattga gccacattga      1620
acacaattga atgagattca gaataaactt ataacatctt aaa                        1663

```

<210> 130

<211> 412

<212> PRT

<213> Homo Sapiens

<400> 130

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Ala Leu Ser Gln Leu Arg Val Leu Cys Cys Glu Trp Leu Arg Pro Glu
 1          5          10          15
Ile His Thr Lys Glu Gln Ile Leu Glu Leu Leu Val Leu Glu Gln Phe
          20          25          30
Leu Thr Ile Leu Pro Gln Glu Leu Gln Ala Trp Val Gln Glu His Cys
          35          40          45
Pro Glu Ser Ala Glu Glu Ala Val Thr Leu Leu Glu Asp Leu Glu Arg
          50          55          60
Glu Leu Asp Glu Pro Gly His Gln Val Ser Thr Pro Pro Asn Glu Gln
          65          70          75          80
Lys Pro Val Trp Glu Lys Ile Ser Ser Ser Gly Thr Ala Lys Glu Ser
          85          90          95
Pro Ser Ser Met Gln Pro Gln Pro Leu Glu Thr Ser His Lys Tyr Glu
          100          105          110
Ser Trp Gly Pro Leu Tyr Ile Gln Glu Ser Gly Glu Glu Gln Glu Phe
          115          120          125
Ala Gln Asp Pro Arg Lys Val Arg Asp Cys Arg Leu Ser Thr Gln His
          130          135          140
Glu Glu Ser Ala Asp Glu Gln Lys Gly Ser Glu Ala Glu Gly Leu Lys
          145          150          155          160
Gly Asp Ile Ile Ser Val Ile Ile Ala Asn Lys Pro Glu Ala Ser Leu
          165          170          175
Glu Arg Gln Cys Val Asn Leu Glu Asn Glu Lys Gly Thr Lys Pro Pro
          180          185          190
Leu Gln Glu Ala Gly Ser Lys Lys Gly Arg Glu Ser Val Pro Thr Lys
          195          200          205
Pro Thr Pro Gly Glu Arg Arg Tyr Ile Cys Ala Glu Cys Gly Lys Ala
          210          215          220
Phe Ser Asn Ser Ser Asn Leu Thr Lys His Arg Arg Thr His Thr Gly
          225          230          235          240
Glu Lys Pro Tyr Val Cys Thr Lys Cys Gly Lys Ala Phe Ser His Ser

```

245 250 255
 Ser Asn Leu Thr Leu His Tyr Arg Thr His Leu Val Asp Arg Pro Tyr
 260 265 270
 Asp Cys Lys Cys Gly Lys Ala Phe Gly Gln Ser Ser Asp Leu Leu Lys
 275 280 285
 His Gln Arg Met His Thr Glu Glu Ala Pro Tyr Gln Cys Lys Asp Cys
 290 295 300
 Gly Lys Ala Phe Ser Gly Lys Gly Ser Leu Ile Arg His Tyr Arg Ile
 305 310 315 320
 His Thr Gly Glu Lys Pro Tyr Gln Cys Asn Glu Cys Gly Lys Ser Phe
 325 330 335
 Ser Gln His Ala Gly Leu Ser Ser His Gln Arg Leu His Thr Gly Glu
 340 345 350
 Lys Pro Tyr Lys Cys Lys Glu Cys Gly Lys Ala Phe Asn His Ser Ser
 355 360 365
 Asn Phe Asn Lys His His Arg Ile His Thr Gly Glu Lys Pro Tyr Trp
 370 375 380
 Cys His His Cys Gly Lys Thr Phe Cys Ser Lys Ser Asn Leu Ser Lys
 385 390 395 400
 His Gln Arg Val His Thr Gly Glu Gly Glu Ala Pro
 405 410

<210> 131
 <211> 724
 <212> DNA
 <213> Homo Sapiens

<400> 131
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 tgatattcag gacctcctgg agagtgtcag gctggacaaa gaaaaagcag agactttggc 120
 tagtagcttg caggaagatc tgggtcatcac ccgaaatgat gccaatcgat tacaggatgc 180
 cattgctaag gtagaggatg aataccgagc cttccaagaa gaagctaaga aacaaattga 240
 agatttgaat atgacgttag aaaaattaag atcagacctg gatgaaaaag aaacagaaag 300
 gagtgcacatg aaagaaacca tctttgaact tgaagatgaa gtagaacaac atcgtgctgt 360
 gaaacttcat gacaacctca ttatttctga tctagagaat acagttaaaa aactccagga 420
 ccaaaagcac gacatggaaa gagaaataaa gacactccac agaagacttc gggaagaatc 480
 tgcggaatgg cggcagtttc aggtgatctt ccagactgca gtagtcattg caaatgacat 540
 taaatctgaa gcccaagagg agattggtga tctaaagcgc cgggtacatg aggtcaaga 600
 aaaaaatgag aaactcacia aagaattgga ggaaataagt ccgccaagcc agaangac 660
 gangccggtg ttccantaca tgnatgcccg tgagagagaa tttggcaggc cttaaggcag 720
 ggaa 724

<210> 132
 <211> 218
 <212> PRT
 <213> Homo Sapiens

<400> 132
 Glu Asn Glu Lys Gln Lys Val Ala Glu Leu Tyr Ser Ile His Asn Ser
 1 5 10 15
 Gly Asp Lys Ser Asp Ile Gln Asp Leu Leu Glu Ser Val Arg Leu Asp
 20 25 30
 Lys Glu Lys Ala Glu Thr Leu Ala Ser Ser Leu Gln Glu Asp Leu Ala
 35 40 45
 His Thr Arg Asn Asp Ala Asn Arg Leu Gln Asp Ala Ile Ala Lys Val

50 55 60
 Glu Asp Glu Tyr Arg Ala Phe Gln Glu Glu Ala Lys Lys Gln Ile Glu
 65 70 75 80
 Asp Leu Asn Met Thr Leu Glu Lys Leu Arg Ser Asp Leu Asp Glu Lys
 85 90 95
 Glu Thr Glu Arg Ser Asp Met Lys Glu Thr Ile Phe Glu Leu Glu Asp
 100 105 110
 Glu Val Glu Gln His Arg Ala Val Lys Leu His Asp Asn Leu Ile Ile
 115 120 125
 Ser Asp Leu Glu Asn Thr Val Lys Lys Leu Gln Asp Gln Lys His Asp
 130 135 140
 Met Glu Arg Glu Ile Lys Thr Leu His Arg Arg Leu Arg Glu Glu Ser
 145 150 155 160
 Ala Glu Trp Arg Gln Phe Gln Ala Asp Leu Gln Thr Ala Val Val Ile
 165 170 175
 Ala Asn Asp Ile Lys Ser Glu Ala Gln Glu Glu Ile Gly Asp Leu Lys
 180 185 190
 Arg Arg Val His Glu Ala Gln Glu Lys Asn Glu Lys Leu Thr Lys Glu
 195 200 205
 Leu Glu Glu Ile Ser Pro Pro Ser Gln Lys
 210 215

<210> 133
 <211> 719
 <212> DNA
 <213> Homo Sapiens

<400> 133
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 tgggtggaggg tttgcagaaa caaccagga gaccaaggcg gtgactgtcc atgttcacgg 120
 ccaggaagtc ctgtcagagg agacggtgca tttaggagcg gagcctgagt cacctaata 180
 gctgcaggat cctgtgcaaa gctcgacccc cgagcagtc cctgaggaaa ccacacagag 240
 cccagatctg ggggcaccgg cagagcagcg tccacaccag gaagaggagc tccagaccct 300
 gcaggagagc gaggtccag tgcccagga cccagacctt cctgcagaga ggagctctgg 360
 agactcagag atggttgctc ttcttactgc tctgtcacag ggactggtaa cgttcaagga 420
 tgtggccgta tgcttttccc aggaccagtg gactgatctg gacccaacac agaaagagtt 480
 ctatggagaa tatgtcttgg aagaagactg tggaattggt gtctctctgt catttccaat 540
 cccagacct gatgagatct cccagggttag agaggaagag cccttgggtc ccagatatcc 600
 aagagcctna ggagactcaa gagccagaaa tcctgagttt tacctacaca ggagatagga 660
 gtnaagatga aggaaaatgt ctggagccag gaagaatctg agtttggagg atataccca 719

<210> 134
 <211> 217
 <212> PRT
 <213> Homo Sapiens

<400> 134
 Arg Thr Thr Glu Leu Gly Ala Gly Pro Thr Ala Arg Lys Trp Arg Gly
 1 5 10 15
 Gly Ser Asp Ala Gly Gly Gly Phe Ala Glu Thr Thr Gln Glu Thr Lys
 20 25 30
 Ala Val Thr Val His Val His Gly Gln Glu Val Leu Ser Glu Glu Thr
 35 40 45
 Val His Leu Gly Ala Glu Pro Glu Ser Pro Asn Glu Leu Gln Asp Pro
 50 55 60

Val Gln Ser Ser Thr Pro Glu Gln Ser Pro Glu Glu Thr Thr Gln Ser
65 70 75 80
Pro Asp Leu Gly Ala Pro Ala Glu Gln Arg Pro His Gln Glu Glu Glu
85 90 95
Leu Gln Thr Leu Gln Glu Ser Glu Val Pro Val Pro Glu Asp Pro Asp
100 105 110
Leu Pro Ala Glu Arg Ser Ser Gly Asp Ser Glu Met Val Ala Leu Leu
115 120 125
Thr Ala Leu Ser Gln Gly Leu Val Thr Phe Lys Asp Val Ala Val Cys
130 135 140
Phe Ser Gln Asp Gln Trp Ser Asp Leu Asp Pro Thr Gln Lys Glu Phe
145 150 155 160
Tyr Gly Glu Tyr Val Leu Glu Glu Asp Cys Gly Ile Val Val Ser Leu
165 170 175
Ser Phe Pro Ile Pro Arg Pro Asp Glu Ile Ser Gln Val Arg Glu Glu
180 185 190
Glu Pro Leu Gly Pro Arg Tyr Pro Arg Ala Gly Asp Ser Arg Ala Arg
195 200 205
Asn Pro Glu Phe Tyr Leu His Arg Arg
210 215

<210> 135
<211> 1027
<212> DNA
<213> Homo Sapiens

<400> 135
gcgagggcgga gggcgaggcg gtgctcatgg aggaggacct gatccagcag agcctggacg 60
actacgacgc cggcaggtac agcccgcggc tgctcacggc gcacgagctg cactggacg 120
cgcacgtgct ggaaccggat gaggacctgc agcgctgcga gctctcgcg cagcagctcc 180
agggtcacggg agacgccagc gagagcgccg aggacatctt cttccggcgg gccaaaggagg 240
gcatgggcca ggacgaggcg cagttcagcg tggagatgcc actcaccggc aaggcctacc 300
tgtggggcca caagtaccgg ccacgcaagc cgcgcttctt caaccgcgtg cacacgggct 360
tcgagtggaa caagtacaac cagacgcact acgactttga caaccaccg cccaagatcg 420
tgcagggata caagttcaac atcttctacc cgcacctcat cgacaagcgc tccacgcccg 480
agtacttctt ggaggcctgc gccgacaaca aggatttcgc catcctgcgc ttcacgcggg 540
gccgcctacg aggacatcgc tttcaagatc gtcaaccgcg agtgggaata ctngcaccgc 600
cacggcttcc gctgccagtt tgccaacggc attttccanc tngctttca cttcaagcgc 660
tnccgctatc ggcggtgacg gccctgggga acggcaggcc aggagggccg agggccacac 720
gggtgccaca gccaggtcg gagtggcca gccggcaggc ttgtttttca gcatccgacg 780
ggaacatctc caacagaagc aaaacggaaa gtgcctcccg gacccccaga gggccaccca 840
acctcaccag tcaccagccc cagaccaccc acagcccctc ccagacaccc cgcctcatct 900
ggaaatagtt ccgtttgttt ctctaaaaag acttgtaggt gggaaaaaaa atcttttggg 960
ctcatggaat tggcctattg gcaagatcgc atgttttttt aataaacgtt gtatttttaga 1020
ataaaaa 1027

<210> 136
<211> 299
<212> PRT
<213> Homo Sapiens

<400> 136
Glu Gly Glu Gly Glu Ala Val Leu Met Glu Glu Asp Leu Ile Gln Gln
1 5 10 15
Ser Leu Asp Asp Tyr Asp Ala Gly Arg Tyr Ser Pro Arg Leu Leu Thr

20 25 30
 Ala His Glu Leu Pro Leu Asp Ala His Val Leu Glu Pro Asp Glu Asp
 35 40 45
 Leu Gln Arg Leu Gln Leu Ser Arg Gln Gln Leu Gln Val Thr Gly Asp
 50 55 60
 Ala Ser Glu Ser Ala Glu Asp Ile Phe Phe Arg Arg Ala Lys Glu Gly
 65 70 75 80
 Met Gly Gln Asp Glu Ala Gln Phe Ser Val Glu Met Pro Leu Thr Gly
 85 90 95
 Lys Ala Tyr Leu Trp Ala Asp Lys Tyr Arg Pro Arg Lys Pro Arg Phe
 100 105 110
 Phe Asn Arg Val His Thr Gly Phe Glu Trp Asn Lys Tyr Asn Gln Thr
 115 120 125
 His Tyr Asp Phe Asp Asn Pro Pro Lys Ile Val Gln Gly Tyr Lys
 130 135 140
 Phe Asn Ile Phe Tyr Pro Asp Leu Ile Asp Lys Arg Ser Thr Pro Glu
 145 150 155 160
 Tyr Phe Leu Glu Ala Cys Ala Asp Asn Lys Asp Phe Ala Ile Leu Arg
 165 170 175
 Phe Thr Arg Gly Arg Leu Arg Gly His Arg Phe Gln Asp Arg Gln Pro
 180 185 190
 Arg Val Gly Ile Leu Ala Pro Pro Arg Leu Pro Leu Pro Val Cys Gln
 195 200 205
 Arg His Phe Pro Leu Ser Leu Gln Ala Leu Pro Leu Ser Ala Val Thr
 210 215 220
 Ala Leu Gly Asn Gly Arg Pro Gly Gly Pro Arg Ala Thr Arg Val Pro
 225 230 235 240
 Gln Pro Arg Ser Glu Trp Pro Ser Arg Gln Ala Cys Phe Ser Ala Ser
 245 250 255
 Asp Gly Asn Ile Ser Asn Arg Ser Lys Thr Glu Ser Ala Ser Arg Thr
 260 265 270
 Pro Arg Gly Pro Pro Asn Leu Thr Ser His Gln Pro Gln Thr Thr His
 275 280 285
 Ser Pro Ser Gln Thr Pro Arg Leu Ile Trp Lys
 290 295

<210> 137
 <211> 766
 <212> DNA
 <213> Homo Sapiens

<400> 137
 caaagggttta cacagtaa ac aatgtgaatg tgatcaccaa aatacgcaca gaacatctga 60
 ccgaggagga aaaaaagaga tataaagaca ggaacccgct ggaatctttg ctgggaactg 120
 tggaacacca atttggtgca caaggggacc tcaccacgga atgtgctact gcaacaacc 180
 ccacagccat cagcctgat gagtacttca atgaagagtt tgatctgaaa gacagggaca 240
 ttggaaggcc gaaagagctg acgattagaa cacagaagtt taaagcaatg ttgtggatgt 300
 gtgaagagtt tcccctctct ctggtggagc aggtcattcc catcattgac ctaatggctc 360
 gaacgagtgc tcatTTTTGCA agactgagag atttcatcaa attggaattc ccacctggat 420
 ttccctgtcaa aatagcttcc cacatcaca actttgaggt tgatcaatct gtgtttgaaa 480
 ttcccgaatc ttactatgtt caagacaatg gcagaaatgt gcatttgcaa gatgaagatt 540
 acgagataat gcagtttgcc atccagcaaa gtctgctgga gtccagcagg agccaggaac 600
 tttcaggacc agcttcgaat ggagggatca gccagacaaa cacctatgac gccagtatg 660
 agagggccat ncaggagagc cttctaccag cacagaaagc ctgtgcccc agcgccccctg 720
 agcgagacna gccgttttga taatggactt gcagctaagc catgga 766

<210> 138
 <211> 243
 <212> PRT
 <213> Homo Sapiens

<400> 138
 Lys Val Tyr Thr Val Asn Asn Val Asn Val Ile Thr Lys Ile Arg Thr
 1 5 10 15
 Glu His Leu Thr Glu Glu Glu Lys Lys Arg Tyr Lys Asp Arg Asn Pro
 20 25 30
 Leu Glu Ser Leu Leu Gly Thr Val Glu His Gln Phe Gly Ala Gln Gly
 35 40 45
 Asp Leu Thr Thr Glu Cys Ala Thr Ala Asn Asn Pro Thr Ala Ile Thr
 50 55 60
 Pro Asp Glu Tyr Phe Asn Glu Glu Phe Asp Leu Lys Asp Arg Asp Ile
 65 70 75 80
 Gly Arg Pro Lys Glu Leu Thr Ile Arg Thr Gln Lys Phe Lys Ala Met
 85 90 95
 Leu Trp Met Cys Glu Glu Phe Pro Leu Ser Leu Val Glu Gln Val Ile
 100 105 110
 Pro Ile Ile Asp Leu Met Ala Arg Thr Ser Ala His Phe Ala Arg Leu
 115 120 125
 Arg Asp Phe Ile Lys Leu Glu Phe Pro Pro Gly Phe Pro Val Lys Ile
 130 135 140
 Ala Ser His Ile Thr Asn Phe Glu Val Asp Gln Ser Val Phe Glu Ile
 145 150 155 160
 Pro Glu Ser Tyr Tyr Val Gln Asp Asn Gly Arg Asn Val His Leu Gln
 165 170 175
 Asp Glu Asp Tyr Glu Ile Met Gln Phe Ala Ile Gln Gln Ser Leu Leu
 180 185 190
 Glu Ser Ser Arg Ser Gln Glu Leu Ser Gly Pro Ala Ser Asn Gly Gly
 195 200 205
 Ile Ser Gln Thr Asn Thr Tyr Asp Ala Gln Tyr Glu Arg Ala Gln Glu
 210 215 220
 Ser Leu Leu Pro Ala Gln Lys Ala Cys Ala Pro Ser Ala Pro Glu Arg
 225 230 235 240
 Asp Pro Phe

<210> 139
 <211> 3060
 <212> DNA
 <213> Homo Sapiens

<400> 139
 ccggggcggga gtgcggcgag agccggctgg ctgagcttag cgtccgagga ggccggcgcg 60
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 cgcgcggggc gtggccagag tctggcggcg gcctggcgga gcgagagaca gcgcccgcgc 180
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 ggcgcaggta aggcgggcgc cgccatggtg gaccgggtg gcttcgcgga ggcgtggaag 480
 ggcagttcc cggactcaga gccccgcgc atggagctgc gctcagtggg cgacatcgag 540
 caggagctgg agcgtgcaa ggcctccatt cggcgctgg agcaggaggt gaaccaggag 600

cgcttccgca tgatctacct gcagacgttg ctggccaagg aaaagaagag ctatgaccgg 660
cagcgatggg gcttccggcg cgcggcgag gccccgacg gcgcctccga gccccgagcg 720
tccgcgtcgc gccccgagcc agcgcccgcc gacggagccg acccgccgcc cgccgaggag 780
cccgaggccc ggcccgcagg cgagggttct ccgggtaagg ccaggcccg gaccgcccgc 840
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aggctgaaga agaagctgtc ggagcaggag tcaactgctg tgcctatgtc tcccagcatg 2940
gccttcaggg tgcacagccg caacggcaag agttacacgt tcctgatctc ctctgactat 3000
gagcgtgcag agtggagggg gaacatccgg gagcagcaga agaagtgtt cagaagcttc 3060

<210> 140

<211> 872

<212> PRT

<213> Homo Sapiens

<400> 140

Met Val Asp Pro Val Gly Phe Ala Glu Ala Trp Lys Ala Gln Phe Pro
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Asp Ser Glu Pro Pro Arg Met Glu Leu Arg Ser Val Gly Asp Ile Glu
20 25 30
Gln Glu Leu Glu Arg Cys Lys Ala Ser Ile Arg Arg Leu Glu Gln Glu
35 40 45
Val Asn Gln Glu Arg Phe Arg Met Ile Tyr Leu Gln Thr Leu Leu Ala

50		55		60															
Lys	Glu	Lys	Lys	Ser	Tyr	Asp	Arg	Gln	Arg	Trp	Gly	Phe	Arg	Arg	Ala				
65					70					75					80				
Ala	Gln	Ala	Pro	Asp	Gly	Ala	Ser	Glu	Pro	Arg	Ala	Ser	Ala	Ser	Arg				
				85					90					95					
Pro	Gln	Pro	Ala	Pro	Ala	Asp	Gly	Ala	Asp	Pro	Pro	Pro	Ala	Glu	Glu				
			100					105					110						
Pro	Glu	Ala	Arg	Pro	Asp	Gly	Glu	Gly	Ser	Pro	Gly	Lys	Ala	Arg	Pro				
		115					120					125							
Gly	Thr	Ala	Arg	Arg	Pro	Gly	Ala	Ala	Ala	Ser	Gly	Glu	Arg	Asp	Asp				
130						135					140								
Arg	Gly	Pro	Pro	Ala	Ser	Val	Ala	Ala	Leu	Arg	Ser	Asn	Phe	Glu	Arg				
145				150						155					160				
Ile	Arg	Lys	Gly	His	Gly	Gln	Pro	Gly	Ala	Asp	Ala	Glu	Lys	Pro	Phe				
				165					170					175					
Tyr	Val	Asn	Val	Glu	Phe	His	His	Glu	Arg	Gly	Leu	Val	Lys	Val	Asn				
			180					185					190						
Asp	Lys	Glu	Val	Ser	Asp	Arg	Ile	Ser	Ser	Leu	Gly	Ser	Gln	Ala	Met				
		195					200					205							
Gln	Met	Glu	Arg	Lys	Lys	Ser	Gln	His	Gly	Ala	Gly	Ser	Ser	Val	Gly				
210						215					220								
Asp	Ala	Ser	Arg	Pro	Pro	Tyr	Arg	Gly	Arg	Ser	Ser	Glu	Ser	Ser	Cys				
225				230						235					240				
Gly	Val	Asp	Gly	Asp	Tyr	Glu	Asp	Ala	Glu	Leu	Asn	Pro	Arg	Phe	Leu				
			245						250					255					
Lys	Asp	Asn	Leu	Ile	Asp	Ala	Asn	Gly	Gly	Ser	Arg	Pro	Pro	Trp	Pro				
			260					265					270						
Pro	Leu	Glu	Tyr	Gln	Pro	Tyr	Gln	Ser	Ile	Tyr	Val	Gly	Gly	Met	Met				
		275					280					285							
Glu	Gly	Glu	Gly	Lys	Gly	Pro	Leu	Leu	Arg	Ser	Gln	Ser	Thr	Ser	Glu				
290						295					300								
Gln	Glu	Lys	Arg	Leu	Thr	Trp	Pro	Arg	Arg	Ser	Tyr	Ser	Pro	Arg	Ser				
305				310						315					320				
Phe	Glu	Asp	Cys	Gly	Gly	Gly	Tyr	Thr	Pro	Asp	Cys	Ser	Ser	Asn	Glu				
			325						330					335					
Asn	Leu	Thr	Ser	Ser	Glu	Glu	Asp	Phe	Ser	Ser	Gly	Gln	Ser	Ser	Arg				
			340					345					350						
Val	Ser	Pro	Ser	Pro	Thr	Thr	Tyr	Arg	Met	Phe	Arg	Asp	Lys	Ser	Arg				
		355					360					365							
Ser	Pro	Ser	Gln	Asn	Ser	Gln	Gln	Ser	Phe	Asp	Ser	Ser	Ser	Pro	Pro				
370						375					380								
Thr	Pro	Gln	Cys	His	Lys	Arg	His	Arg	His	Cys	Pro	Val	Val	Val	Ser				
385				390						395					400				
Glu	Ala	Thr	Ile	Val	Gly	Val	Arg	Lys	Thr	Gly	Gln	Ile	Trp	Pro	Asn				
			405						410					415					
Asp	Gly	Glu	Gly	Ala	Phe	His	Gly	Asp	Ala	Asp	Gly	Ser	Phe	Gly	Thr				
			420					425					430						
Pro	Pro	Gly	Tyr	Gly	Cys	Ala	Ala	Asp	Arg	Ala	Glu	Glu	Gln	Arg	Arg				
		435					440					445							
His	Gln	Asp	Gly	Leu	Pro	Tyr	Ile	Asp	Asp	Ser	Pro	Ser	Ser	Ser	Pro				
450						455					460								
His	Leu	Ser	Ser	Lys	Gly	Arg	Gly	Ser	Arg	Asp	Ala	Leu	Val	Ser	Gly				
465				470						475					480				
Ala	Leu	Glu	Ser	Thr	Lys	Ala	Ser	Glu	Leu	Asp	Leu	Glu	Lys	Gly	Leu				
			485						490					495					

Glu Met Arg Lys Trp Val Leu Ser Gly Ile Leu Ala Ser Glu Glu Thr
 500 505 510
 Tyr Leu Ser His Leu Glu Ala Leu Leu Leu Pro Met Lys Pro Leu Lys
 515 520 525
 Ala Ala Ala Thr Thr Ser Gln Pro Val Leu Thr Ser Gln Gln Ile Glu
 530 535 540
 Thr Ile Phe Phe Lys Val Pro Glu Leu Tyr Glu Ile His Lys Glu Phe
 545 550 555 560
 Tyr Asp Gly Leu Phe Pro Arg Val Gln Gln Trp Ser His Gln Gln Arg
 565 570 575
 Val Gly Asp Leu Phe Gln Lys Leu Ala Ser Gln Leu Gly Val Tyr Arg
 580 585 590
 Ala Phe Val Asp Asn Tyr Gly Val Ala Met Glu Met Ala Glu Lys Cys
 595 600 605
 Cys Gln Ala Asn Ala Gln Phe Ala Glu Ile Ser Glu Asn Leu Arg Ala
 610 615 620
 Arg Ser Asn Lys Asp Ala Lys Asp Pro Thr Thr Lys Asn Ser Leu Glu
 625 630 635 640
 Thr Leu Leu Tyr Lys Pro Val Asp Arg Val Thr Arg Ser Thr Leu Val
 645 650 655
 Leu His Asp Leu Leu Lys His Thr Pro Ala Ser His Pro Asp His Pro
 660 665 670
 Leu Leu Gln Asp Ala Leu Arg Ile Ser Gln Asn Phe Leu Ser Ser Ile
 675 680 685
 Asn Glu Glu Ile Thr Pro Arg Arg Gln Ser Met Thr Val Lys Lys Gly
 690 695 700
 Glu His Arg Gln Leu Leu Lys Asp Ser Phe Met Val Glu Leu Val Glu
 705 710 715 720
 Gly Ala Arg Lys Leu Arg His Val Phe Leu Phe Thr Glu Leu Leu Leu
 725 730 735
 Cys Thr Lys Leu Lys Lys Gln Ser Gly Gly Lys Thr Gln Gln Tyr Asp
 740 745 750
 Cys Lys Trp Tyr Ile Pro Leu Thr Asp Leu Ser Phe Gln Met Val Asp
 755 760 765
 Glu Leu Glu Ala Val Pro Asn Ile Pro Leu Val Pro Asp Glu Glu Leu
 770 775 780
 Asp Ala Leu Lys Ile Lys Ile Ser Gln Ile Lys Ser Asp Ile Gln Arg
 785 790 795 800
 Glu Lys Arg Ala Asn Lys Gly Ser Lys Ala Thr Glu Arg Leu Lys Lys
 805 810 815
 Lys Leu Ser Glu Gln Glu Ser Leu Leu Leu Leu Met Ser Pro Ser Met
 820 825 830
 Ala Phe Arg Val His Ser Arg Asn Gly Lys Ser Tyr Thr Phe Leu Ile
 835 840 845
 Ser Ser Asp Tyr Glu Arg Ala Glu Trp Arg Glu Asn Ile Arg Glu Gln
 850 855 860
 Gln Lys Lys Cys Phe Arg Ser Phe
 865 870

<210> 141

<211> 691

<212> DNA

<213> Homo Sapiens

<400> 141

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gaccctcac actcacctag ccaccatgga catcgccatc caccacccct ggatccgcgcg      60
ccccctcttt cctttccact cccccagccg cctctttgac cagttcttcg gagagcacct      120
gttgaggtct gatcttttcc cgacgtctac ttccctgagt cccttctacc ttcgccacc      180
ctccttctctg cgggcaccca gctggtttga cactggactc tcagagatgc gcctggagaa      240
ggacagggttc tctgtcaacc tggatgtgaa gcacttctcc ccagaggaac tcaaagttaa      300
gggtgttgga gatgtgattg aggtgcatgg aaaacatgaa gagcgccagg atgaacatgg      360
tttcatctcc agggagtctc acaggaaata ccgcatccca gctgatgtag accctctcac      420
cattacttca tccctgtcat ctgatggggt cctcactgtg aatggacca ggaaacaggt      480
ctctggccct gagcgacca ttcccatcac ccgtgaagag aagcctgctg tcaccgcgc      540
ccccaagaaa tagatgccct ttcttgaatt gcatttttta aaacaagaaa gtttccccac      600
cagtgaatga aagtcttggt actagtgtg aagcttatta atgctaaggg caggcccaaa      660
ttatcaagct aataaaatat cattcagcaa c                                     691

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<210> 142

<211> 175

<212> PRT

<213> Homo Sapiens

<400> 142

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Met Asp Ile Ala Ile His His Pro Trp Ile Arg Arg Pro Phe Phe Pro
 1           5           10           15
Phe His Ser Pro Ser Arg Leu Phe Asp Gln Phe Phe Gly Glu His Leu
          20           25           30
Leu Glu Ser Asp Leu Phe Pro Thr Ser Thr Ser Leu Ser Pro Phe Tyr
          35           40           45
Leu Arg Pro Pro Ser Phe Leu Arg Ala Pro Ser Trp Phe Asp Thr Gly
          50           55           60
Leu Ser Glu Met Arg Leu Glu Lys Asp Arg Phe Ser Val Asn Leu Asp
65           70           75           80
Val Lys His Phe Ser Pro Glu Glu Leu Lys Val Lys Val Leu Gly Asp
          85           90           95
Val Ile Glu Val His Gly Lys His Glu Glu Arg Gln Asp Glu His Gly
          100          105          110
Phe Ile Ser Arg Glu Phe His Arg Lys Tyr Arg Ile Pro Ala Asp Val
          115          120          125
Asp Pro Leu Thr Ile Thr Ser Ser Leu Ser Ser Asp Gly Val Leu Thr
130          135          140
Val Asn Gly Pro Arg Lys Gln Val Ser Gly Pro Glu Arg Thr Ile Pro
145          150          155          160
Ile Thr Arg Glu Glu Lys Pro Ala Val Thr Ala Ala Pro Lys Lys
          165          170          175

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<210> 143

<211> 1300

<212> DNA

<213> Homo Sapiens

<400> 143

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atctgctggg aatttcttgg gttgacagct cttggatccc tattttgaac agtggtagt      60
tcctggatta cttttcagaa agaagtaatc ctttttatga cagaacatgt aataatgaag      120
tggtcaaaat gcagaggcta acattagaac acttgaatca gatggttgga atcgagtaca      180
tccttttgca tgetcaagag ccattctttt tcatcattcg gaagcaacag cggcagtccc      240
ctgcccaggt tatcccaacta gctgattact atatcattgc tggagtgate tatcaggcac      300
cagacttggg atcagttata aactctagag tgcttactgc agtgcattgg attcagtcag      360
cttttgatga agctatgtca tactgtogat atcatccttc caaagggtat tgggtggcact      420

```

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tcaaagatca tgaagagcaa gataaagtca gacctaaagc caaaaggaaa gaagaaccaa      480
gctctatttt tcagagacaa cgtgtggatg ctttactttt agacctcaga caaaaatttc      540
cacccaaatt tgtgcagcta aagcctggag aaaagcctgt tcaagtggat caaaciaaaga      600
aagaggcaga acctatacca gaaactgtaa aacctgagga gaaggagacc ccnnagaat      660
gtacaaccag accgggagtg ctaaaggccc ccctgaaaaa cggatgagac ttcagtgagt      720
actggacaaa agagaagcct ggaagactcc tcatgctagt tatcacacct cagtactgtg      780
gctcttgagc tttgaagtac tttattgtaa ctttcttatt tgtatggaat gcgcttattt      840
tttgaaagga tattaggccg gatgtggtgg ctcacgcctg taatcccagc actttgggag      900
gccatggcgg gtggatcact tgaggtcaga agttcaagac cagcctgacc aatatggtga      960
aaccctgtct ctactaaaaa tacaaaaatt agccgggcgt ggtggcgggc gcccgtagtc     1020
ccagctactc gggaggctga gacaggagac ttgcttgaac ccgggaggtg gaggttgccc     1080
tgagctgatt atcatgctgt tgcactccag cttgggcgac agagcgagac tttgtctcaa     1140
aaaagaagaa aagatattac tcccatcatg atttcttgtg aatatttggt atatgtcttc     1200
tgtaaccttt cctctcccg acttgagcaa cctacacact cacatgttta ctggtagata     1260
tgtttaaaag caaaataaag gtatttgtat atattgaaaa     1300

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<210> 144

<211> 233

<212> PRT

<213> Homo Sapiens

<400> 144

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Leu Leu Gly Ile Ser Trp Val Asp Ser Ser Trp Ile Pro Ile Leu Asn
 1           5           10           15
Ser Gly Ser Val Leu Asp Tyr Phe Ser Glu Arg Ser Asn Pro Phe Tyr
          20           25           30
Asp Arg Thr Cys Asn Asn Glu Val Val Lys Met Gln Arg Leu Thr Leu
          35           40           45
Glu His Leu Asn Gln Met Val Gly Ile Glu Tyr Ile Leu Leu His Ala
          50           55           60
Gln Glu Pro Ile Leu Phe Ile Ile Arg Lys Gln Gln Arg Gln Ser Pro
65           70           75           80
Ala Gln Val Ile Pro Leu Ala Asp Tyr Tyr Ile Ile Ala Gly Val Ile
          85           90           95
Tyr Gln Ala Pro Asp Leu Gly Ser Val Ile Asn Ser Arg Val Leu Thr
          100          105          110
Ala Val His Gly Ile Gln Ser Ala Phe Asp Glu Ala Met Ser Tyr Cys
          115          120          125
Arg Tyr His Pro Ser Lys Gly Tyr Trp Trp His Phe Lys Asp His Glu
          130          135          140
Glu Gln Asp Lys Val Arg Pro Lys Ala Lys Arg Lys Glu Glu Pro Ser
145          150          155          160
Ser Ile Phe Gln Arg Gln Arg Val Asp Ala Leu Leu Leu Asp Leu Arg
          165          170          175
Gln Lys Phe Pro Pro Lys Phe Val Gln Leu Lys Pro Gly Glu Lys Pro
          180          185          190
Val Gln Val Asp Gln Thr Lys Lys Glu Ala Glu Pro Ile Pro Glu Thr
          195          200          205
Val Lys Pro Glu Glu Lys Glu Thr Pro Glu Cys Thr Thr Arg Pro Gly
210          215          220
Val Leu Lys Ala Pro Leu Lys Asn Gly
225          230

```

<210> 145

<211> 1528

<212> DNA

<213> Homo Sapiens

<400> 145

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ccccctttt tttttaaaact aaaatggagg ctggtttctt gccttaagga gcccattgcc      60
tttcccgtctg aagtctagat gttgacatgt aataaagcgg gcagcaggat ggtgggtggat      120
gcgggccaact ccaatgggccc tttccagccc gtggtccttc tccatattcg agatgttccct      180
cctgctgatac aagagaagct ttttatccag aagttacgtc agtggtgcgt cctctttgac      240
tttgtttctg atccactaag tgacctaaag tggaaggaag taaaacgagc tgctttaagt      300
gaaatggtag aatatatcac ccataatcgg aatgtgatca cagagcctat ttaccagaa      360
gtagtccata tgtttgacgt taacatgttt cgaacattac caccttcctc caatcctacg      420
ggagcgggaat ttgaccggga ggaagatgaa ccaacgttag aagcagcctg gcctcatcta      480
cagcttgttt atgaattttt ctttaagattt ttagagtctc cagatttcca acctaataata      540
gcgaagaaat atattgatca gaagtttgta ttgcagcttt tagagctctt tgacagttaa      600
gatcctcggg agagagattt tcttaaaacc acccttcaca gaatctatgg gaaattccta      660
ggcttgagag cttacatcag aaaacagata aataatatat tttatagggt tattttatgaa      720
acagagctac ataattggcat agcagagtta ctggaaatat tgggaagtat aattaatgga      780
tttgccttac cactaaaaga agagcacaag attttcttat tgaagggtgt actacctttg      840
cacaaagtga aatctctgag tgtctaccat cccagctgg catactgtgt agtgcagttt      900
ttagaaaagg acagcacctt cacggaacca gtggtgatgg cacttctcaa atactggcca      960
aagactcaca gtccaaaaga agtaatgttc ttaaacgaat tagaagagat tttagatgtc     1020
attgaacatc cagaatttgt gaagatcatg gaaccctctt tccggcagtt ggccaaatgt     1080
gtctccagcc cacacttcca ggtggcagag cgagctctct attactggaa taatgaatac     1140
atcatgagtt taatcagtga caacgcagcg aagattctgc ccatcatgtt tccttctctg     1200
taccgcaact caaagaccca ttggaacaag acaatacatg gcttgatata caacgccttg     1260
aagctcttca tggagatgaa ccaaaagcta tttgatgact gtacacaaca gttcaaagca     1320
gagaaactaa aagagaagct aaaaatgaaa gaacgggaag aagcatgggt taaaatagaa     1380
aatctagcca aagccaatcc ccaggtacta aaaaagagaa taacatgaaa aggccagggt     1440
ttacttgaat gtttttataa gataggaata tatgtcttca ccatgggggg ggtctcgatt     1500
tcactaacgt tgtatatgaa aatgtctg                                     1528

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<210> 146

<211> 449

<212> PRT

<213> Homo Sapiens

<400> 146

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Met Leu Thr Cys Asn Lys Ala Gly Ser Arg Met Val Val Asp Ala Ala
 1              5              10              15
Asn Ser Asn Gly Pro Phe Gln Pro Val Val Leu Leu His Ile Arg Asp
      20              25              30
Val Pro Pro Ala Asp Gln Glu Lys Leu Phe Ile Gln Lys Leu Arg Gln
      35              40              45
Cys Cys Val Leu Phe Asp Phe Val Ser Asp Pro Leu Ser Asp Leu Lys
      50              55              60
Trp Lys Glu Val Lys Arg Ala Ala Leu Ser Glu Met Val Glu Tyr Ile
65              70              75              80
Thr His Asn Arg Asn Val Ile Thr Glu Pro Ile Tyr Pro Glu Val Val
      85              90              95
His Met Phe Ala Val Asn Met Phe Arg Thr Leu Pro Pro Ser Ser Asn
      100             105             110
Pro Thr Gly Ala Glu Phe Asp Pro Glu Glu Asp Glu Pro Thr Leu Glu
      115             120             125
Ala Ala Trp Pro His Leu Gln Leu Val Tyr Glu Phe Phe Leu Arg Phe
      130             135             140

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Leu Glu Ser Pro Asp Phe Gln Pro Asn Ile Ala Lys Lys Tyr Ile Asp
 145 150 155 160
 Gln Lys Phe Val Leu Gln Leu Leu Glu Leu Phe Asp Ser Glu Asp Pro
 165 170 175
 Arg Glu Arg Asp Phe Leu Lys Thr Thr Leu His Arg Ile Tyr Gly Lys
 180 185 190
 Phe Leu Gly Leu Arg Ala Tyr Ile Arg Lys Gln Ile Asn Asn Ile Phe
 195 200 205
 Tyr Arg Phe Ile Tyr Glu Thr Glu His His Asn Gly Ile Ala Glu Leu
 210 215 220
 Leu Glu Ile Leu Gly Ser Ile Ile Asn Gly Phe Ala Leu Pro Leu Lys
 225 230 235 240
 Glu Glu His Lys Ile Phe Leu Leu Lys Val Leu Leu Pro Leu His Lys
 245 250 255
 Val Lys Ser Leu Ser Val Tyr His Pro Gln Leu Ala Tyr Cys Val Val
 260 265 270
 Gln Phe Leu Glu Lys Asp Ser Thr Leu Thr Glu Pro Val Val Met Ala
 275 280 285
 Leu Leu Lys Tyr Trp Pro Lys Thr His Ser Pro Lys Glu Val Met Phe
 290 295 300
 Leu Asn Glu Leu Glu Glu Ile Leu Asp Val Ile Glu Pro Ser Glu Phe
 305 310 315 320
 Val Lys Ile Met Glu Pro Leu Phe Arg Gln Leu Ala Lys Cys Val Ser
 325 330 335
 Ser Pro His Phe Gln Val Ala Glu Arg Ala Leu Tyr Tyr Trp Asn Asn
 340 345 350
 Glu Tyr Ile Met Ser Leu Ile Ser Asp Asn Ala Ala Lys Ile Leu Pro
 355 360 365
 Ile Met Phe Pro Ser Leu Tyr Arg Asn Ser Lys Thr His Trp Asn Lys
 370 375 380
 Thr Ile His Gly Leu Ile Tyr Asn Ala Leu Lys Leu Phe Met Glu Met
 385 390 395 400
 Asn Gln Lys Leu Phe Asp Asp Cys Thr Gln Gln Phe Lys Ala Glu Lys
 405 410 415
 Leu Lys Glu Lys Leu Lys Met Lys Glu Arg Glu Glu Ala Trp Val Lys
 420 425 430
 Ile Glu Asn Leu Ala Lys Ala Asn Pro Gln Val Leu Lys Lys Arg Ile
 435 440 445
 Thr

<210> 147

<211> 1580

<212> DNA

<213> Homo Sapiens

<400> 147

atccccctccg gttttcctca gtctccacgt acgtccctca aagcgcgtcc taaaaccg	60
ataaccggag cgctcccat ggaccacacg gagggcttgc ccgcggagga gccgcctgcg	120
catgctccat cgctgggaa atttggtgag cggcctccac cttaaagact tactagggaa	180
gctatgcgaa attattttaa agagcgaggg gatcaaacag tacttattct tcatgcaaaa	240
gttgacaga agtcatatgg aaatgaaaaa aggttttttt gccacactcc ttgtgtatat	300
cttatgggca gcggatggaa gaaaaaaaaa gaacaaatgg aacgcgatgg ttgttctgaa	360
caagagtctc aaccgtgtgc atttattggg ataggaaata gtgaccaaga aatgcagcag	420
ctaaacttgg aaggaaagaa ctattgcaca gccaaaacat tgtatatatc tgactcagac	480

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aagcgaaagc acttcatttt ttctgtaaag atgttctatg gcaacagtga tgacattggt      540
gtgttcctca gcaagcggat aaaagtcatc tccaaacctt ccaaaaagaa gcagtcattg      600
aaaaatgctg acttatgcat tgcctcagga acaaagggtg ctctgttttaa tcgactacga      660
tcccagacag ttagtaccag atacttgcat gtagaaggag gtaattttca tgccagttca      720
cagcagtggg gagccttttt tattcatctc ttggatgatg atgaatcaga aggagaagaa      780
ttcacagtcc gagatgtcta catccattat ggacaaacat gcaaacttgt gtgctcagtt      840
actggcatgg cactcccaag attgataatt atgaaagttg ataagcatac cgcattattg      900
gatgcagatg atcctgtgtc acaactccat aaatgtgcat ttaccttaa ggatacagaa      960
agaatgtatt tgtgcctttc tcaagaaaga ataattcaat ttcaggccac tccatgtcca     1020
aaagaacca aataagagat gataaatgat ggcgcttcct ggacaatcat tagcacagat     1080
aaggcagagt atacatttta tgagggaatg ggccctgtcc ttgccccagt cactcctgtg     1140
cctgtggtag agagccttca gttgaatggc ggtggggacg tagcaatgct tgaacttaca     1200
ggacagaatt tcaactccaa tttacgagtg tggtttgggg atgtagaagc tgaaactatg     1260
tacaggtgtg gagagagtat gctctgtgtc gtcccagaca tttctgcatt ccgagaaggt     1320
tgagatggg tccggcaacc agtccaggtt ccagtaactt tggtcgaaa tgatggaatc     1380
atttattcca ccagccttac ctttacctac acaccagaac cagggccacg gccacattgc     1440
agtgtagcag gagcaatcct tccagccaat tcaagccagg tgccccctaa cgaatcaaac     1500
acaaacagcg agggaagtta cacaacgcc agcacaaatt caaccagtgt cacatcatct     1560
acagccacag tggatccta                                     1580

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<210> 148

<211> 500

<212> PRT

<213> Homo Sapiens

<400> 148

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Met Asp His Thr Glu Gly Leu Pro Ala Glu Glu Pro Pro Ala His Ala
 1          5          10          15
Pro Ser Pro Gly Lys Phe Gly Glu Arg Pro Pro Pro Lys Arg Leu Thr
 20          25          30
Arg Glu Ala Met Arg Asn Tyr Leu Lys Glu Arg Gly Asp Gln Thr Val
 35          40          45
Leu Ile Leu His Ala Lys Val Ala Gln Lys Ser Tyr Gly Asn Glu Lys
 50          55          60
Arg Phe Phe Cys Pro Pro Cys Val Tyr Leu Met Gly Ser Gly Trp
 65          70          75          80
Lys Lys Lys Lys Glu Gln Met Glu Arg Asp Gly Cys Ser Glu Gln Glu
 85          90          95
Ser Gln Pro Cys Ala Phe Ile Gly Ile Gly Asn Ser Asp Gln Glu Met
 100         105         110
Gln Gln Leu Asn Leu Glu Gly Lys Asn Tyr Cys Thr Ala Lys Thr Leu
 115         120         125
Tyr Ile Ser Asp Ser Asp Lys Arg Lys His Phe Ile Phe Ser Val Lys
 130         135         140
Met Phe Tyr Gly Asn Ser Asp Asp Ile Gly Val Phe Leu Ser Lys Arg
 145         150         155         160
Ile Lys Val Ile Ser Lys Pro Ser Lys Lys Lys Gln Ser Leu Lys Asn
 165         170         175
Ala Asp Leu Cys Ile Ala Ser Gly Thr Lys Val Ala Leu Phe Asn Arg
 180         185         190
Leu Arg Ser Gln Thr Val Ser Thr Arg Tyr Leu His Val Glu Gly Gly
 195         200         205
Asn Phe His Ala Ser Ser Gln Trp Gly Ala Phe Phe Ile His Leu
 210         215         220
Leu Asp Asp Asp Glu Ser Glu Gly Glu Glu Phe Thr Val Arg Asp Val

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225 230 235 240
 Tyr Ile His Tyr Gly Gln Thr Cys Lys Leu Val Cys Ser Val Thr Gly
 245 250 255
 Met Ala Leu Pro Arg Leu Ile Ile Met Lys Val Asp Lys His Thr Ala
 260 265 270
 Leu Leu Asp Ala Asp Asp Pro Val Ser Gln Leu His Lys Cys Ala Phe
 275 280 285
 Tyr Leu Lys Asp Thr Glu Arg Met Tyr Leu Cys Leu Ser Gln Glu Arg
 290 295 300
 Ile Ile Gln Phe Gln Ala Thr Pro Cys Pro Lys Glu Pro Asn Lys Glu
 305 310 315 320
 Met Ile Asn Asp Gly Ala Ser Trp Thr Ile Ile Ser Thr Asp Lys Ala
 325 330 335
 Glu Tyr Thr Phe Tyr Glu Gly Met Gly Pro Val Leu Ala Pro Val Thr
 340 345 350
 Pro Val Pro Val Val Glu Ser Leu Gln Leu Asn Gly Gly Gly Asp Val
 355 360 365
 Ala Met Leu Glu Leu Thr Gly Gln Asn Phe Thr Pro Asn Leu Arg Val
 370 375 380
 Trp Phe Gly Asp Val Glu Ala Glu Thr Met Tyr Arg Cys Gly Glu Ser
 385 390 395 400
 Met Leu Cys Val Val Pro Asp Ile Ser Ala Phe Arg Glu Gly Trp Arg
 405 410 415
 Trp Val Arg Gln Pro Val Gln Val Pro Val Thr Leu Val Arg Asn Asp
 420 425 430
 Gly Ile Ile Tyr Ser Thr Ser Leu Thr Phe Thr Tyr Thr Pro Glu Pro
 435 440 445
 Gly Pro Arg Pro His Cys Ser Val Ala Gly Ala Ile Leu Pro Ala Asn
 450 455 460
 Ser Ser Gln Val Pro Pro Asn Glu Ser Asn Thr Asn Ser Glu Gly Ser
 465 470 475 480
 Tyr Thr Asn Ala Ser Thr Asn Ser Thr Ser Val Thr Ser Ser Thr Ala
 485 490 495
 Thr Val Val Ser
 500

<210> 149

<211> 1248

<212> DNA

<213> Homo Sapiens

<400> 149

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caagatatcg aattccaaat ttgagggcct ccgggctctg ggcgccggagg gagagctcag      60
gccgccatgc ggcacaggac ccacgagctg agacaggggg atgacagctc ggacgaagag      120
gacaaggagc gggtcgcgct ggtgggtgcac ccgggcacgg cacggctggg gagcccgagc      180
gaggagtctt tccacaaggt ccggacaatt cgtcagacta ttgtcaaact ggggaataaa      240
gtccaggagt tggagaaaca gcaggtcacc atcctggcca cggcccttcc cgaggagagc      300
atgaagcagg agctgcagaa cctgcgcgat gagatcaaac agctggggag ggagatccgc      360
ctgcagctga aggccataga gccccagaag gaggaagctg atgagaacta taactccgtc      420
aacacaagaa tgagaaaaaac ccagcatggg gtccctgtccc agcaattcgt ggagctcatc      480
aacaagtgca attcaatgca gtccgaatac cgggagaaga acgtggagcg gattcggagg      540
cagctgaaga tcaccaatgc tggcatggtg tctgatgagg agttggatca gatgctggac      600
agtgggcaaa gcgaggtggt tgtgtccaat atccttaagg acacgcaggt gactcgacag      660
gccttaaatg agatctcggc ccggcacagt gagatccagc agcttgaacg cagtattcgt      720
gagctgcacg acatattcac ttttctggct accgaagtgg agatgcaggg ggagatgatc      780

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```

aatcggattg agaagaacat cctgagctca gcggactacg tggaacgtgg gcaggagcac      840
gtcaagacgg ccctggagaa ccagaagaag gtgaggaaga agaaagtctt gattgccatc      900
tgtgtgtcca tcaccgtcgt cctcctagca gtcatcattg gcgtcacagt ggttggataa      960
tgtgcacat tgttggcact aggagcacca ggaacccagg gcctggcctt ctctcccagc     1020
agcctggggg gcaggcagag cctccagtcg gaccccttcc tcacacactg gcccctatgc     1080
agaagggcag acagtctctc tggggttggc agctgctcat tcatgatggc ctctccttc      1140
aggcctcaat gcctggggga ggctgcact gtcttgattg gccgggacac acgggttttgt     1200
aaaaaattaa aaaacaaaaa aagagcatag aaaaaaaaaa aaccgagt      1248

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<210> 150

<211> 297

<212> PRT

<213> Homo Sapiens

<400> 150

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Met Arg Asp Arg Thr His Glu Leu Arg Gln Gly Asp Asp Ser Ser Asp
 1          5          10          15
Glu Glu Asp Lys Glu Arg Val Ala Leu Val Val His Pro Gly Thr Ala
 20          25          30
Arg Leu Gly Ser Pro Asp Glu Glu Phe Phe His Lys Val Arg Thr Ile
 35          40          45
Arg Gln Thr Ile Val Lys Leu Gly Asn Lys Val Gln Glu Leu Glu Lys
 50          55          60
Gln Gln Val Thr Ile Leu Ala Thr Pro Leu Pro Glu Glu Ser Met Lys
 65          70          75          80
Gln Glu Leu Gln Asn Leu Arg Asp Glu Ile Lys Gln Leu Gly Arg Glu
 85          90          95
Ile Arg Leu Gln Leu Lys Ala Ile Glu Pro Gln Lys Glu Glu Ala Asp
100          105          110
Glu Asn Tyr Asn Ser Val Asn Thr Arg Met Arg Lys Thr Gln His Gly
115          120          125
Val Leu Ser Gln Gln Phe Val Glu Leu Ile Asn Lys Cys Asn Ser Met
130          135          140
Gln Ser Glu Tyr Arg Glu Lys Asn Val Glu Arg Ile Arg Arg Gln Leu
145          150          155          160
Lys Ile Thr Asn Ala Gly Met Val Ser Asp Glu Glu Leu Asp Gln Met
165          170          175
Leu Asp Ser Gly Gln Ser Glu Val Phe Val Ser Asn Ile Leu Lys Asp
180          185          190
Thr Gln Val Thr Arg Gln Ala Leu Asn Glu Ile Ser Ala Arg His Ser
195          200          205
Glu Ile Gln Gln Leu Glu Arg Ser Ile Arg Glu Leu His Asp Ile Phe
210          215          220
Thr Phe Leu Ala Thr Glu Val Glu Met Gln Gly Glu Met Ile Asn Arg
225          230          235          240
Ile Glu Lys Asn Ile Leu Ser Ser Ala Asp Tyr Val Glu Arg Gly Gln
245          250          255
Glu His Val Lys Thr Ala Leu Glu Asn Gln Lys Lys Val Arg Lys Lys
260          265          270
Lys Val Leu Ile Ala Ile Cys Val Ser Ile Thr Val Val Leu Leu Ala
275          280          285
Val Ile Ile Gly Val Thr Val Val Gly
290          295

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<210> 151

<211> 1953
 <212> DNA
 <213> Homo Sapiens

<400> 151

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acgcctgcca ggagcaagcc gaagagccag ccggccggcg cactccgact ccgagcagtc      60
tctgtccttc gacccgagcc ccgcgccctt tccgggaccc ctgcccccgcg ggcagcgctg      120
ccaacctgcc ggccatggag accccgtccc agcggcgcgcg caccgcagc ggggcgcagg      180
ccagctccac tccgctgtcg cccacccgca tcacccggct gcaggagaag gaggacctgc      240
aggagctcaa tgatcgcttg gcggtctaca tcgaccgtgt gcgctcgctg gaaacggaga      300
acgcagggct gcgccttcgc atcaccgagt ctgaagaggt ggtcagccgc gaggtgtccg      360
gcatcaaggc cgcctacgag gccgagctcg gggatgcccg caagaccctt gactcagtag      420
ccaaggagcg cgcccgcctg cagctggagc tgagcaaagt gcgtgaggag ttaaggagc      480
tgaaagcgcg caataccaag aaggaggggtg acctgatagc tgctcaggct cggctgaagg      540
acctggaggc tctgctgaac tccaaggagg ccgcactgag cactgctctc agtgagaagc      600
gcacgctgga gggcgagctg catgatctgc ggggccagggt ggccaagctt gaggcagccc      660
taggtgaggc caagaagcaa cttcaggatg agatgctgcg gcgggtggat gctgagaaca      720
ggctgcagac catgaaggag gaactggact tccagaagaa catctacagt gaggagctgc      780
gtgagaccaa gcgcgctcat gagaccgcag tgggtggagat tgacaatggg aagcagcgtg      840
agtttgagag ccggctggcg gatgcgctgc aggaactgcg ggcccagcat gaggaccagg      900
tggagcagta taagaaggag ctggagaaga cttattctgc caagctggac aatgccaggc      960
agtctgctga gaggaacagc aacctggtgg gggctgcccc cgaggagctg cagcagtcgc     1020
gcatccgcat cgacagcctc tctgcccgag tcagccagct ccagaagcag ctggcagcca     1080
aggaggcgaa gcttcgagac ctggaggact cactggcccc tgagcgggac accagccggc     1140
ggctgctggc ggaaaaggag cgggagatgg ccgagatgcg ggcaaggatg cagcagcagc     1200
tggaacgagta ccaggagctt ctggacatca agctggccct ggacatggag atccacgcct     1260
accgcaagct cttggagggc gaggaggaga ggctacgcct gtcccccagc cctacctgcg     1320
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ctagcgggcg cgtggccgtg gaggaggtgg atgaggaggg caagtttgct cggctgcgca     1500
acaagtccaa tgaggaccag tccatgggca attggcagat caagcgccag aatggagatg     1560
atcccttgct gacttacgag tccccaccaa agttcacctt gaaggctggg caggtggtga     1620
cgatctgggc tgcaggagct ggggccaccc acagccccc taccgacctg gtgtggaagg     1680
cacagaacac ctggggctgc gggaaacagc tgcgtagcgc tctcatcaac tccactgggg     1740
aagaagtggc catgcgcaag ctggtgcgct cagtgaactgt ggttgaggac gacgaggatg     1800
aggatggaga tgacctgtc catcaccacc acgtgagtgg tagccgccgc tgaggccgag     1860
cctgcactgg ggcaccagc caggcctggg ggcagcctct cccagcctc cccgtgccaa     1920
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<210> 152
 <211> 572
 <212> PRT
 <213> Homo Sapiens

<400> 152

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Met Glu Thr Pro Ser Gln Arg Arg Ala Thr Arg Ser Gly Ala Gln Ala
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Ser Ser Thr Pro Leu Ser Pro Thr Arg Ile Thr Arg Leu Gln Glu Lys
          20          25          30
Glu Asp Leu Gln Glu Leu Asn Asp Arg Leu Ala Val Tyr Ile Asp Arg
      35          40          45
Val Arg Ser Leu Glu Thr Glu Asn Ala Gly Leu Arg Leu Arg Ile Thr
      50          55          60
Glu Ser Glu Glu Val Val Ser Arg Glu Val Ser Gly Ile Lys Ala Ala
65          70          75          80

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515 520 525
 Ala Leu Ile Asn Ser Thr Gly Glu Glu Val Ala Met Arg Lys Leu Val
 530 535 540
 Arg Ser Val Thr Val Val Glu Asp Asp Glu Asp Glu Asp Gly Asp Asp
 545 550 555 560
 Leu Leu His His His His Val Ser Gly Ser Arg Arg
 565 570

<210> 153
 <211> 1610
 <212> DNA
 <213> Homo Sapiens

<400> 153
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 cgggcctttg tgaaaatgtg taagcaggat ccgagcgctt tgtacaccga ggaaatgcgc 180
 ttcctgaggg agtgggtgga gagcataggt ggtaaagtac cacctgctac tcagaaagct 240
 atatcagaag aaaataccaa ggaagaaaaa cctgatagta agaaggtgga ggaagactta 300
 aaggcagacg aaccatcaag tgaggaaagt gatctagaaa ttgataaaga aggtgtgatt 360
 gaaccagaca ctgatgctcc tcaagaaatg ggagatgaaa atgcggagat aacggaggag 420
 atgatggatc aggcaaatga taaaaaagtg gctgctattg aagccctaaa tcatgggtgaa 480
 ctccagaaag ccattgactt attcacagat gccatcaagc tgaatcctcg cttggccatt 540
 ttgtatgcca agagggccag tgtcttcgtc aaattacaga agccaaatgc tgccatccga 600
 gactgtgaca gagccattga aataaaatcct gattcagctc agccttacia gtggcggggg 660
 aaagcacaca gacttctagg ccactgggaa gaagcagccc atgatcttgc ccttgctgt 720
 aaattggatt atgatgaaga tgctagtga atgctgaaag aagttcaacc tagggcacag 780
 aaaattgcag aacatcggag aaagtatgag cgaaaacgtg aagagcgaga gatcaaagaa 840
 agaatagaac gagttaagaa ggctcgagaa gagcatgaga gagcccagag ggaggaagaa 900
 gccagacgac agtcaggagc tcagtatggc tcttttccag gtggccttcc tgggggaatg 960
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 agcaacccaa aggttatgaa tctcatcagt aaattgtcag ccaaatttgg aggtcaagcg 1200
 taatgtcctt ctgataaata aagcccttgc tgaaggaaaa gcaacctaga tcaccttatg 1260
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 ccattagggg attcattcag ataattgttt cctactagga attacaaact ttaaacactt 1440
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 ttactaatca ttttggattt ttttctttga attattggca gggaatatac ttatgtatgg 1560
 aagattactg ctctgagtga aataaaaagtt attagtgcga ggcaaacata 1610

<210> 154
 <211> 369
 <212> PRT
 <213> Homo Sapiens

<400> 154
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 20 25 30
 Glu Trp Val Glu Ser Ile Gly Gly Lys Val Pro Pro Ala Thr Gln Lys
 35 40 45
 Ala Ile Ser Glu Glu Asn Thr Lys Glu Glu Lys Pro Asp Ser Lys Lys

50 55 60
Val Glu Glu Asp Leu Lys Ala Asp Glu Pro Ser Ser Glu Glu Ser Asp
65 70 75 80
Leu Glu Ile Asp Lys Glu Gly Val Ile Glu Pro Asp Thr Asp Ala Pro
85 90 95
Gln Glu Met Gly Asp Glu Asn Ala Glu Ile Thr Glu Glu Met Met Asp
100 105 110
Gln Ala Asn Asp Lys Lys Val Ala Ala Ile Glu Ala Leu Asn Asp Gly
115 120 125
Glu Leu Gln Lys Ala Ile Asp Leu Phe Thr Asp Ala Ile Lys Leu Asn
130 135 140
Pro Arg Leu Ala Ile Leu Tyr Ala Lys Arg Ala Ser Val Phe Val Lys
145 150 155 160
Leu Gln Lys Pro Asn Ala Ala Ile Arg Asp Cys Asp Arg Ala Ile Glu
165 170 175
Ile Asn Pro Asp Ser Ala Gln Pro Tyr Lys Trp Arg Gly Lys Ala His
180 185 190
Arg Leu Leu Gly His Trp Glu Glu Ala Ala His Asp Leu Ala Leu Ala
195 200 205
Cys Lys Leu Asp Tyr Asp Glu Asp Ala Ser Ala Met Leu Lys Glu Val
210 215 220
Gln Pro Arg Ala Gln Lys Ile Ala Glu His Arg Arg Lys Tyr Glu Arg
225 230 235 240
Lys Arg Glu Glu Arg Glu Ile Lys Glu Arg Ile Glu Arg Val Lys Lys
245 250 255
Ala Arg Glu Glu His Glu Arg Ala Gln Arg Glu Glu Glu Ala Arg Arg
260 265 270
Gln Ser Gly Ala Gln Tyr Gly Ser Phe Pro Gly Gly Phe Pro Gly Gly
275 280 285
Met Pro Gly Asn Phe Pro Gly Gly Met Pro Gly Met Gly Gly Gly Met
290 295 300
Pro Gly Met Ala Gly Met Pro Gly Leu Asn Glu Ile Leu Ser Asp Pro
305 310 315 320
Glu Val Leu Ala Ala Met Gln Asp Pro Glu Val Met Val Ala Phe Gln
325 330 335
Asp Val Ala Gln Asn Pro Ala Asn Met Ser Lys Tyr Gln Ser Asn Pro
340 345 350
Lys Val Met Asn Leu Ile Ser Lys Leu Ser Ala Lys Phe Gly Gly Gln
355 360 365
Ala

<210> 155

<211> 1323

<212> DNA

<213> Homo Sapiens

<400> 155

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cagaaaagat	ggaaaaaagg	acatgtgcac	tctgccccaa	agatgtcgaa	tataatgtcc	180
tgtactttgc	acaatcagag	aatatagctg	ctcatgagaa	ttgtttgctg	tattcttcag	240
gacttgtgga	atgtgaggat	caggatccac	ttaatcctga	tagaagtttt	gatgtggaat	300
cagtaaagaa	agaaatccag	agaggaagga	agttgaaatg	caaattttgt	cataaaagag	360
gagccaccgt	gggatgtgat	ttaaaaaact	gtaacaagaa	ttaccacttt	ttctgtgcc	420

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agaaggacga cgcagttcca cagtctgatg gagttcgagg aatttataaa ctgctttgcc 480
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aaagaggaag gaagaaaccc ctctcaggca atcatgtaca gccacccgaa acaatgaaat 600
gtaatacatt cataagacaa gtgaaagaag agcatggcag acacacagat gcaactgtga 660
aagttccttt tcttaagaaa tgcaaggga gaggacttc ttaattactt acttgaagaa 720
atattagnca aagttcattc aattccagaa aaactcatgg atgagactta cttcagaatc 780
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aatccacaca tctttagaac tagtcgtctc ctcttggcct cagcagctct tccctgttct 1140
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tcccagcacc tagtatgctc agtaaagtgt tgtggaataa gtgcataaaa tgttcttaac 1260
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<210> 156

<211> 191

<212> PRT

<213> Homo Sapiens

<400> 156

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 1          5          10          15
Val Leu Tyr Phe Ala Gln Ser Glu Asn Ile Ala Ala His Glu Asn Cys
          20          25          30
Leu Leu Tyr Ser Ser Gly Leu Val Glu Cys Glu Asp Gln Asp Pro Leu
          35          40          45
Asn Pro Asp Arg Ser Phe Asp Val Glu Ser Val Lys Lys Glu Ile Gln
          50          55          60
Arg Gly Arg Lys Leu Lys Cys Lys Phe Cys His Lys Arg Gly Ala Thr
65          70          75          80
Val Gly Cys Asp Leu Lys Asn Cys Asn Lys Asn Tyr His Phe Phe Cys
          85          90          95
Ala Lys Lys Asp Asp Ala Val Pro Gln Ser Asp Gly Val Arg Gly Ile
          100          105          110
Tyr Lys Leu Leu Cys Gln Gln His Ala Gln Phe Pro Ile Ile Ala Gln
          115          120          125
Ser Ala Lys Phe Ser Gly Val Lys Arg Lys Arg Gly Arg Lys Lys Pro
          130          135          140
Leu Ser Gly Asn His Val Gln Pro Pro Glu Thr Met Lys Cys Asn Thr
          145          150          155          160
Phe Ile Arg Gln Val Lys Glu Glu His Gly Arg His Thr Asp Ala Thr
          165          170          175
Val Lys Val Pro Phe Leu Lys Lys Cys Lys Gly Ser Arg Thr Ser
          180          185          190

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<210> 157

<211> 4065

<212> DNA

<213> Homo Sapiens

<400> 157

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gacacaataa	ataaaatcag	agattttacga	atgaaagctg	aagattatga	agtagtgaag	240
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gtatatgcta	tgaagcttct	cagcaaattt	gaaatgataa	agagatctga	ttctgctttt	360
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tatgcattcc	aagatgatcg	ttatctctac	atgggtgatgg	aatacatgcc	tgggtggagat	480
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gaagtagttc	ttgcattgga	tgcaatccat	tccatgggtt	ttattcacag	agatgtgaag	600
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ctcaaccaag	aaagagagaa	attcaaccag	atggtagtga	aacatcagaa	ggaactgaat	3180
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gccagcaaag	agagtgtat	tgagcaattg	cgtgctaaac	ttttggacct	ctcggattct	3300
acaagtgttg	ctagttttcc	tagtgctgat	gaaactgatg	gtaacctccc	agagtcaaga	3360

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attgaagggtt ggcttttcagt accaaataga ggaaatatca aacgatatgg ctggaagaaa 3420
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caatccaatc catctatggt attggacata gataaaactgt ttcacgttag acctgtaacc 3540
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<210> 158
 <211> 1354
 <212> PRT
 <213> Homo Sapiens

<400> 158

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Leu Leu Arg Asp Pro Lys Ser Glu Val Asn Ser Asp Cys Leu Leu Asp
          20          25          30
Gly Leu Asp Ala Leu Val Tyr Asp Leu Asp Phe Pro Ala Leu Arg Lys
          35          40          45
Asn Lys Asn Ile Asp Asn Phe Leu Ser Arg Tyr Lys Asp Thr Ile Asn
          50          55          60
Lys Ile Arg Asp Leu Arg Met Lys Ala Glu Asp Tyr Glu Val Val Lys
65          70          75          80
Val Ile Gly Arg Gly Ala Phe Gly Glu Val Gln Leu Val Arg His Lys
          85          90          95
Ser Thr Arg Lys Val Tyr Ala Met Lys Leu Leu Ser Lys Phe Glu Met
          100          105          110
Ile Lys Arg Ser Asp Ser Ala Phe Phe Trp Glu Glu Arg Asp Ile Met
          115          120          125
Ala Phe Ala Asn Ser Pro Trp Val Val Gln Leu Phe Tyr Ala Phe Gln
          130          135          140
Asp Asp Arg Tyr Leu Tyr Met Val Met Glu Tyr Met Pro Gly Gly Asp
145          150          155          160
Leu Val Asn Leu Met Ser Asn Tyr Asp Val Pro Glu Lys Trp Ala Arg
          165          170          175
Phe Tyr Thr Ala Glu Val Val Leu Ala Leu Asp Ala Ile His Ser Met
          180          185          190
Gly Phe Ile His Arg Asp Val Lys Pro Asp Asn Met Leu Leu Asp Lys
          195          200          205
Ser Gly His Leu Lys Leu Ala Asp Phe Gly Thr Cys Met Lys Met Asn
          210          215          220
Lys Glu Gly Met Val Arg Cys Asp Thr Ala Val Gly Thr Pro Asp Tyr
225          230          235          240
Ile Ser Pro Glu Val Leu Lys Ser Gln Gly Gly Asp Gly Tyr Tyr Gly
          245          250          255
Arg Glu Cys Asp Trp Trp Ser Val Gly Val Phe Leu Tyr Glu Met Leu
          260          265          270
Val Gly Asp Thr Pro Phe Tyr Ala Asp Ser Leu Val Gly Thr Tyr Ser
          275          280          285

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Lys Ile Met Asn His Lys Asn Ser Leu Thr Phe Pro Asp Asp Asn Asp
 290 295 300
 Ile Ser Lys Glu Ala Lys Asn Leu Ile Cys Ala Phe Leu Thr Asp Arg
 305 310 315 320
 Glu Val Arg Leu Gly Arg Asn Gly Val Glu Glu Ile Lys Arg His Leu
 325 330 335
 Phe Phe Lys Asn Asp Gln Trp Ala Trp Glu Thr Leu Arg Asp Thr Val
 340 345 350
 Ala Pro Val Val Pro Asp Leu Ser Ser Asp Ile Asp Thr Ser Asn Phe
 355 360 365
 Asp Asp Leu Glu Glu Asp Lys Gly Glu Glu Glu Thr Phe Pro Ile Pro
 370 375 380
 Lys Ala Phe Val Gly Asn Gln Leu Pro Phe Val Gly Phe Thr Tyr Tyr
 385 390 395 400
 Ser Asn Arg Arg Tyr Leu Ser Ser Ala Asn Pro Asn Asp Asn Arg Thr
 405 410 415
 Ser Ser Asn Ala Asp Lys Ser Leu Gln Glu Ser Leu Gln Lys Thr Ile
 420 425 430
 Tyr Lys Leu Glu Glu Gln Leu His Asn Glu Met Gln Leu Lys Asp Glu
 435 440 445
 Met Glu Gln Lys Cys Arg Thr Ser Asn Ile Lys Leu Asp Lys Ile Met
 450 455 460
 Lys Glu Leu Asp Glu Glu Gly Asn Gln Arg Arg Asn Leu Glu Ser Thr
 465 470 475 480
 Val Ser Gln Ile Glu Lys Glu Lys Met Leu Leu Gln His Arg Ile Asn
 485 490 495
 Glu Tyr Gln Arg Lys Ala Glu Gln Glu Asn Glu Lys Arg Arg Asn Val
 500 505 510
 Glu Asn Glu Val Ser Thr Leu Lys Asp Gln Leu Glu Asp Leu Lys Lys
 515 520 525
 Val Ser Gln Asn Ser Gln Leu Ala Asn Glu Lys Leu Ser Gln Leu Gln
 530 535 540
 Lys Gln Leu Glu Glu Ala Asn Asp Leu Leu Arg Thr Glu Ser Asp Thr
 545 550 555 560
 Ala Val Arg Leu Arg Lys Ser His Thr Glu Met Ser Lys Ser Ile Ser
 565 570 575
 Gln Leu Glu Ser Leu Asn Arg Glu Leu Gln Glu Arg Asn Arg Ile Leu
 580 585 590
 Glu Asn Ser Lys Ser Gln Thr Asp Lys Asp Tyr Tyr Gln Leu Gln Ala
 595 600 605
 Ile Leu Glu Ala Glu Arg Arg Asp Arg Gly His Asp Ser Glu Met Ile
 610 615 620
 Gly Asp Leu Gln Ala Arg Ile Thr Ser Leu Gln Glu Glu Val Lys His
 625 630 635 640
 Leu Lys His Asn Leu Glu Lys Val Glu Gly Glu Arg Lys Glu Ala Gln
 645 650 655
 Asp Met Leu Asn His Ser Glu Lys Glu Lys Asn Asn Leu Glu Ile Asp
 660 665 670
 Leu Asn Tyr Lys Leu Lys Ser Leu Gln Gln Arg Leu Glu Gln Glu Val
 675 680 685
 Asn Glu His Lys Val Thr Lys Ala Arg Leu Thr Asp Lys His Gln Ser
 690 695 700
 Ile Glu Glu Ala Lys Ser Val Ala Met Cys Glu Met Glu Lys Lys Leu
 705 710 715 720
 Lys Glu Glu Arg Glu Ala Arg Glu Lys Ala Glu Asn Arg Val Val Gln

•

Asp Ile Asp Lys Leu Phe His Val Arg Pro Val Thr Gln Gly Asp Val
 1170 1175 1180
 Tyr Arg Ala Glu Thr Glu Glu Ile Pro Lys Ile Phe Gln Ile Leu Tyr
 1185 1190 1195 120
 Ala Asn Glu Gly Glu Cys Arg Lys Asp Val Glu Met Glu Pro Val Gln
 1205 1210 1215
 Gln Ala Glu Lys Thr Asn Phe Gln Asn His Lys Gly His Glu Phe Ile
 1220 1225 1230
 Pro Thr Leu Tyr His Phe Pro Ala Asn Cys Asp Ala Cys Ala Lys Pro
 1235 1240 1245
 Leu Trp His Val Phe Lys Pro Pro Pro Ala Leu Glu Cys Arg Arg Cys
 1250 1255 1260
 His Val Lys Cys His Arg Asp His Leu Asp Lys Lys Glu Asp Leu Ile
 1265 1270 1275 128
 Cys Pro Cys Lys Val Ser Tyr Asp Val Thr Ser Ala Arg Asp Met Leu
 1285 1290 1295
 Leu Leu Ala Cys Ser Gln Asp Glu Gln Lys Lys Trp Val Thr His Leu
 1300 1305 1310
 Val Lys Lys Ile Pro Lys Asn Pro Pro Ser Gly Phe Val Arg Ala Ser
 1315 1320 1325
 Pro Arg Thr Leu Ser Thr Arg Ser Thr Ala Asn Gln Ser Phe Arg Lys
 1330 1335 1340
 Val Val Lys Asn Thr Ser Gly Lys Thr Ser
 1345 1350

<210> 159
 <211> 683
 <212> DNA
 <213> Homo Sapiens

<400> 159
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 gtaatgtggc acttgaatgc agtgagccaa gcacaagtgt atctgcttat gaccagttga 120
 aggcaccggc atcccctggt gctggaaacc cacctgggac cccaaagggg aagagagagc 180
 tgatgagcaa tggcccagggt tccattattg gtgctaaagc tgggaagaat tctggcaaaa 240
 agaagggcct taacaatgaa ctgaacaacc ttccagtaat ctccaacatg acggctgcgt 300
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 cagctctggt gtcactcaaa gac 683

<210> 160
 <211> 227
 <212> PRT
 <213> Homo Sapiens

<400> 160
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 20 25 30
 Val Ser Ala Tyr Asp Gln Leu Lys Ala Pro Ala Ser Pro Gly Ala Gly

35 40 45
 Asn Pro Pro Gly Thr Pro Lys Gly Lys Arg Glu Leu Met Ser Asn Gly
 50 55 60
 Pro Gly Ser Ile Ile Gly Ala Lys Ala Gly Lys Asn Ser Gly Lys Lys
 65 70 75 80
 Lys Gly Leu Asn Asn Glu Leu Asn Asn Leu Pro Val Ile Ser Asn Met
 85 90 95
 Thr Ala Ala Leu Asp Ser Cys Ser Ala Ala Asp Gly Ser Leu Ala Ala
 100 105 110
 Glu Met Pro Lys Leu Glu Ala Glu Gly Leu Ile Asp Lys Lys Asn Leu
 115 120 125
 Gly Asp Lys Glu Lys Gly Lys Lys Ala Asn Asn Cys Lys Thr Asp Lys
 130 135 140
 Asn Leu Ser Lys Leu Lys Ser Ala Arg Pro Ile Ala Pro Ala Pro Ala
 145 150 155 160
 Pro Thr Pro Pro Gln Leu Ile Ala Ile Pro Thr Ala Thr Phe Thr Thr
 165 170 175
 Thr Thr Thr Gly Thr Ile Pro Gly Leu Pro Ser Leu Thr Thr Thr Val
 180 185 190
 Val Gln Ala Thr Pro Lys Ser Pro Pro Leu Lys Pro Ile Gln Pro Lys
 195 200 205
 Pro Thr Ile Met Gly Glu Pro Ile Thr Val Asn Pro Ala Leu Val Ser
 210 215 220
 Leu Lys Asp
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<210> 161
 <211> 662
 <212> DNA
 <213> Homo Sapiens

<400> 161
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 gcaaagcctt cccaattgt aaatttgctg aaaaatgttt gtttgttcac ccaaattgta 240
 aatatgatgc aaagtgtact aaaccagatt gtcccttcac tcatgtgagt agaagaattc 300
 cagtactgtc tccaaaacca gttgcaccac cagcaccacc ttccagtagt cagctctgcc 360
 gttacttccc tgcttgtaag aagatggaat gtcccttcta tcatccaaaa cattgtaggt 420
 ttaacactca atgtacaaga ccggactgca cattctacca tcccaccatt aatgtcccac 480
 cagcagatgc cttgaaatgg attcgacctc aaaccagcga atagcaccca gtctgcctg 540
 gcagaagatc atgcagtttg gaagttttca tgtctgatga aagatctcta cagaacttgt 600
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 aa 662

<210> 162
 <211> 173
 <212> PRT
 <213> Homo Sapiens

<400> 162
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 Ser Phe Ser Asn Ala Glu Met Ser Glu Leu Ser Val Ala Gln Lys Pro
 20 25 30

Glu Lys Leu Leu Glu Arg Cys Lys Tyr Trp Pro Ala Cys Lys Asn Gly
 35 40 45
 Asp Glu Cys Ala Tyr His His Pro Ile Ser Pro Cys Lys Ala Phe Pro
 50 55 60
 Asn Cys Lys Phe Ala Glu Lys Cys Leu Phe Val His Pro Asn Cys Lys
 65 70 75 80
 Tyr Asp Ala Lys Cys Thr Lys Pro Asp Cys Pro Phe Thr His Val Ser
 85 90 95
 Arg Arg Ile Pro Val Leu Ser Pro Lys Pro Val Ala Pro Pro Ala Pro
 100 105 110
 Pro Ser Ser Ser Gln Leu Cys Arg Tyr Phe Pro Ala Cys Lys Lys Met
 115 120 125
 Glu Cys Pro Phe Tyr His Pro Lys His Cys Arg Phe Asn Thr Gln Cys
 130 135 140
 Thr Arg Pro Asp Cys Thr Phe Tyr His Pro Thr Ile Asn Val Pro Pro
 145 150 155 160
 Arg His Ala Leu Lys Trp Ile Arg Pro Gln Thr Ser Glu
 165 170

<210> 163
 <211> 2912
 <212> DNA
 <213> Homo Sapiens

<400> 163

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gcctttcagg	cagaaattgc	ccagttgatg	tcattgatca	tcaatacttt	ctactcgaac	180
aaagagatct	ttctgagaga	gctcatttca	aattcatcag	atgcattgga	caaaatccgg	240
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cgaagaataa	aggagattgt	gaagaaacat	tctcagttta	ttggatatcc	cattactctt	720
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aaggaaaagt	acatcgatca	agaagagctc	aacaaaacaa	agcccatctg	gaccagaaat	960
cccgcgata	ttactaatga	ggagtacgga	gaattctata	agagcttgac	caatgactgg	1020
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tatctgaact	tcattagagg	ggtggtagac	tggaggatc	tcctctaaa	catatcccgt	1260
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225 230 235 240
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 245 250 255
 Glu Ile Glu Asp Val Gly Ser Asp Glu Glu Glu Glu Lys Lys Asp Gly
 260 265 270
 Asp Lys Lys Lys Lys Lys Lys Ile Lys Glu Lys Tyr Ile Asp Gln Glu
 275 280 285
 Glu Leu Asn Lys Thr Lys Pro Ile Trp Thr Arg Asn Pro Asp Asp Ile
 290 295 300
 Thr Asn Glu Glu Tyr Gly Glu Phe Tyr Lys Ser Leu Thr Asn Asp Trp
 305 310 315 320
 Glu Asp His Leu Ala Val Lys His Phe Ser Val Glu Gly Gln Leu Glu
 325 330 335
 Phe Arg Ala Leu Leu Phe Val Pro Arg Arg Ala Pro Phe Asp Leu Phe
 340 345 350
 Glu Asn Arg Lys Lys Lys Asn Asn Ile Lys Leu Tyr Val Arg Arg Val
 355 360 365
 Phe Ile Met Asp Asn Cys Glu Glu Leu Ile Pro Glu Tyr Leu Asn Phe
 370 375 380
 Ile Arg Gly Val Val Asp Ser Glu Asp Leu Pro Leu Asn Ile Ser Arg
 385 390 395 400
 Glu Met Leu Gln Gln Ser Lys Ile Leu Lys Val Ile Arg Lys Asn Leu
 405 410 415
 Val Lys Lys Cys Leu Glu Leu Phe Thr Glu Leu Ala Glu Asp Lys Glu
 420 425 430
 Asn Tyr Lys Lys Phe Tyr Glu Gln Phe Ser Lys Asn Ile Lys Leu Gly
 435 440 445
 Ile His Glu Asp Ser Gln Asn Arg Lys Lys Leu Ser Glu Leu Leu Arg
 450 455 460
 Tyr Tyr Thr Ser Ala Ser Gly Asp Glu Met Val Ser Leu Lys Asp Tyr
 465 470 475 480
 Cys Thr Arg Met Lys Glu Asn Gln Lys His Ile Tyr Tyr Ile Thr Gly
 485 490 495
 Glu Thr Lys Asp Gln Val Ala Asn Ser Ala Phe Val Glu Arg Leu Arg
 500 505 510
 Lys His Gly Leu Glu Val Ile Tyr Met Ile Glu Pro Ile Asp Glu Tyr
 515 520 525
 Cys Val Gln Gln Leu Lys Glu Phe Glu Gly Lys Thr Leu Val Ser Val
 530 535 540
 Thr Lys Glu Gly Leu Glu Leu Pro Glu Asp Glu Glu Glu Lys Lys Lys
 545 550 555 560
 Gln Glu Glu Lys Lys Thr Lys Phe Glu Asn Leu Cys Lys Ile Met Lys
 565 570 575
 Asp Ile Leu Glu Lys Lys Val Glu Lys Val Val Val Ser Asn Arg Leu
 580 585 590
 Val Thr Ser Pro Cys Cys Ile Val Thr Ser Thr Tyr Gly Trp Thr Ala
 595 600 605
 Asn Met Glu Arg Ile Met Lys Ala Gln Ala Leu Arg Asp Asn Ser Thr
 610 615 620
 Met Gly Tyr Met Ala Ala Lys Lys His Leu Glu Ile Asn Pro Asp His
 625 630 635 640
 Ser Ile Ile Glu Thr Leu Arg Gln Lys Ala Glu Ala Asp Lys Asn Asp
 645 650 655
 Lys Ser Val Lys Asp Leu Val Ile Leu Leu Tyr Glu Thr Ala Leu Leu
 660 665 670

Ser Ser Gly Phe Ser Leu Glu Asp Pro Gln Thr His Ala Asn Arg Ile
 675 680 685
 Tyr Arg Met Ile Lys Leu Gly Leu Gly Ile Asp Glu Asp Asp Pro Thr
 690 695 700
 Ala Asp Asp Thr Ser Ala Ala Val Thr Glu Glu Met Pro Pro Leu Glu
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 Gly Asp Asp Asp Thr Ser Arg Met Glu Glu Val Asp
 725 730

<210> 165
 <211> 790
 <212> DNA
 <213> Homo Sapiens

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 aatacatgag tatggaatta ttgcaagaag ctggtgtctc cgttcccaaa ggatatgtgg 240
 caaagtcacc agatgaagct tatgcaattg ccaaaaaatt aggttcaaaa gatgtcgtga 300
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 gaggagtga gatagttttc tctccagaag aagcaaaagc tgtttcttca caaatgattg 420
 ggaaaaaatt gtttaccaag caaacgggag aaaagggcag aatatgcaat caagtattgg 480
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 ttcaagggtcc tgtattaata ggaagttcac atggtggtgt caacattgaa gatgttgctg 600
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 aacaagctct tcagcttgca cagaagaatg ggatttcccc taatattgng ggaatcagca 720
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<210> 166
 <211> 259
 <212> PRT
 <213> Homo Sapiens

<400> 166
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 Gln Val Leu Gly Ser Ser Gly Leu Phe Asn Asn His Gly Leu Gln Val
 35 40 45
 Gln Gln Gln Gln Gln Arg Asn Leu Ser Leu His Glu Tyr Met Ser Met
 50 55 60
 Glu Leu Leu Gln Glu Ala Gly Val Ser Val Pro Lys Gly Tyr Val Ala
 65 70 75 80
 Lys Ser Pro Asp Glu Ala Tyr Ala Ile Ala Lys Lys Leu Gly Ser Lys
 85 90 95
 Asp Val Val Ile Lys Ala Gln Val Leu Ala Gly Gly Arg Gly Lys Gly
 100 105 110
 Thr Phe Glu Ser Gly Leu Lys Gly Gly Val Lys Ile Val Phe Ser Pro
 115 120 125
 Glu Glu Ala Lys Ala Val Ser Gln Met Ile Gly Lys Lys Leu Phe
 130 135 140
 Thr Lys Gln Thr Gly Glu Lys Gly Arg Ile Cys Asn Gln Val Leu Val

145		150		155		160
Cys Glu Arg Lys Tyr Pro Arg Arg Glu Tyr Tyr Phe Ala Ile Thr Met						
	165		170		175	
Glu Arg Ser Phe Gln Gly Pro Val Leu Ile Gly Ser Ser His Gly Gly						
	180		185		190	
Val Asn Ile Glu Asp Val Ala Ala Glu Ser Pro Glu Ala Ile Ile Lys						
	195		200		205	
Glu Pro Ile Asp Ile Glu Glu Gly Ile Lys Lys Glu Gln Ala Leu Gln						
	210		215		220	
Leu Ala Gln Lys Asn Gly Ile Ser Pro Asn Ile Gly Ile Ser Ser Arg						
225		230		235		240
Lys Thr Trp Ser Ser Phe Thr Phe Leu Lys Tyr Asp Ala Thr Leu Asp						
	245		250		255	
Arg Lys Leu						

<210> 167

<211> 5307

<212> DNA

<213> Homo Sapiens

<400> 167

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5307

<210> 168
 <211> 1148
 <212> PRT
 <213> Homo Sapiens

<400> 168
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 20 25 30
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 35 40 45
 Ser Glu Lys Gln Thr Arg Gln Ala Pro Lys Arg Lys Ser Val Arg Arg
 50 55 60
 Gly Arg Lys Pro Pro Leu Lys Lys Lys Leu Arg Ser Ser Val Ala
 65 70 75 80
 Ala Pro Glu Lys Ser Ser Ser Asn Asp Ser Val Asp Glu Glu Thr Ala
 85 90 95
 Glu Ser Asp Thr Ser Pro Val Leu Glu Lys Glu His Gln Pro Asp Val
 100 105 110
 Asp Ser Ser Asn Ile Cys Thr Val Gln Thr His Val Glu Asn Gln Ser
 115 120 125
 Ala Asn Cys Leu Lys Ser Cys Asn Glu Gln Ile Glu Glu Ser Glu Lys
 130 135 140
 His Thr Ala Asn Tyr Asp Thr Glu Glu Arg Val Gly Ser Ser Ser Ser
 145 150 155 160
 Glu Ser Cys Ala Gln Asp Leu Pro Val Leu Val Gly Glu Glu Gly Glu
 165 170 175
 Val Lys Lys Leu Glu Asn Thr Gly Ile Glu Ala Asn Val Leu Cys Leu
 180 185 190
 Glu Ser Glu Ile Ser Glu Asn Ile Leu Glu Lys Gly Gly Asp Pro Leu
 195 200 205
 Glu Lys Gln Asp Gln Ile Ser Gly Leu Ser Gln Ser Glu Val Lys Thr
 210 215 220
 Asp Val Cys Thr Val His Leu Pro Asn Asp Phe Pro Thr Cys Leu Thr
 225 230 235 240
 Ser Glu Ser Lys Val Tyr Gln Pro Val Ser Cys Pro Leu Ser Asp Leu
 245 250 255
 Ser Glu Asn Val Glu Ser Val Val Asn Glu Glu Lys Ile Thr Glu Ser
 260 265 270
 Ser Leu Val Glu Ile Thr Glu His Lys Asp Phe Thr Leu Lys Thr Glu
 275 280 285
 Glu Leu Ile Glu Ser Pro Lys Leu Glu Ser Ser Glu Gly Glu Ile Ile
 290 295 300
 Gln Thr Val Asp Arg Gln Ser Val Lys Ser Pro Glu Val Gln Leu Leu
 305 310 315 320
 Gly His Val Glu Thr Glu Asp Val Glu Ile Ile Ala Thr Cys Asp Thr
 325 330 335
 Phe Gly Asn Glu Asp Phe Asn Asn Ile Gln Asp Ser Glu Asn Asn Leu
 340 345 350
 Leu Lys Asn Asn Leu Leu Asn Thr Lys Leu Glu Lys Ser Leu Glu Glu

355 360 365
 Lys Asn Glu Ser Leu Thr Glu His Pro Arg Ser Thr Glu Leu Pro Lys
 370 375 380
 Thr His Ile Glu Gln Ile Gln Lys His Phe Ser Glu Asp Asn Asn Glu
 385 390 395 400
 Met Ile Pro Met Glu Cys Asp Ser Phe Cys Ser Asp Gln Asn Glu Ser
 405 410 415
 Glu Val Glu Pro Ser Val Asn Ala Asp Leu Lys Gln Met Asn Glu Asn
 420 425 430
 Ser Val Thr His Cys Ser Glu Asn Asn Met Pro Ser Ser Asp Leu Ala
 435 440 445
 Asp Glu Lys Val Glu Thr Val Ser Gln Pro Ser Glu Ser Pro Lys Asp
 450 455 460
 Thr Ile Asp Lys Thr Lys Lys Pro Arg Thr Arg Arg Ser Arg Phe His
 465 470 475 480
 Ser Pro Ser Thr Thr Trp Ser Pro Asn Lys Asp Thr Pro Gln Glu Lys
 485 490 495
 Lys Arg Pro Gln Ser Pro Ser Pro Arg Arg Glu Thr Gly Lys Glu Ser
 500 505 510
 Arg Lys Ser Gln Ser Pro Ser Pro Lys Asn Glu Ser Ala Arg Gly Arg
 515 520 525
 Lys Lys Ser Arg Ser Gln Ser Pro Lys Lys Asp Ile Ala Arg Glu Arg
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 Arg Gln Ser Gln Ser Arg Ser Pro Lys Arg Asp Thr Thr Arg Glu Ser
 545 550 555 560
 Arg Arg Ser Glu Ser Leu Ser Pro Arg Arg Glu Thr Ser Arg Glu Asn
 565 570 575
 Lys Arg Ser Gln Pro Arg Val Lys Asp Ser Ser Pro Gly Glu Lys Ser
 580 585 590
 Arg Ser Gln Ser Arg Glu Arg Glu Ser Asp Arg Asp Gly Gln Arg Arg
 595 600 605
 Glu Arg Glu Arg Arg Thr Arg Lys Trp Ser Arg Ser Arg Ser His Ser
 610 615 620
 Arg Ser Pro Ser Arg Cys Arg Thr Lys Ser Lys Ser Ser Ser Phe Gly
 625 630 635 640
 Arg Ile Asp Arg Asp Ser Tyr Ser Pro Arg Trp Lys Gly Arg Trp Ala
 645 650 655
 Asn Asp Gly Trp Arg Cys Pro Arg Gly Asn Asp Arg Tyr Arg Lys Asn
 660 665 670
 Asp Pro Glu Lys Gln Asn Glu Asn Thr Arg Lys Glu Lys Asn Asp Ile
 675 680 685
 His Leu Asp Ala Asp Asp Pro Asn Ser Ala Asp Lys His Arg Asn Asp
 690 695 700
 Cys Pro Asn Trp Ile Thr Glu Lys Ile Asn Ser Gly Pro Asp Pro Arg
 705 710 715 720
 Thr Arg Asn Pro Glu Lys Leu Lys Glu Ser His Trp Glu Glu Asn Arg
 725 730 735
 Asn Glu Asn Ser Gly Asn Ser Trp Asn Lys Asn Phe Gly Ser Gly Trp
 740 745 750
 Val Ser Asn Arg Gly Arg Gly Arg Gly Asn Arg Gly Arg Gly Thr Tyr
 755 760 765
 Arg Ser Ser Phe Ala Tyr Lys Asp Gln Asn Glu Asn Arg Trp Gln Asn
 770 775 780
 Arg Lys Pro Leu Ser Gly Asn Ser Asn Ser Ser Gly Ser Glu Ser Phe
 785 790 795 800

Lys Phe Val Glu Gln Gln Ser Tyr Lys Arg Lys Ser Glu Gln Glu Phe
 805 810 815
 Ser Phe Asp Thr Pro Ala Asp Arg Ser Gly Trp Thr Ser Ala Ser Ser
 820 825 830
 Trp Ala Val Arg Lys Thr Leu Pro Ala Asp Val Gln Asn Tyr Tyr Ser
 835 840 845
 Arg Arg Gly Arg Asn Ser Ser Gly Pro Gln Ser Gly Trp Met Lys Gln
 850 855 860
 Glu Glu Glu Thr Ser Gly Gln Asp Ser Ser Leu Lys Asp Gln Thr Asn
 865 870 875 880
 Gln Gln Val Asp Gly Ser Gln Leu Pro Ile Asn Met Met Gln Pro Gln
 885 890 895
 Met Asn Val Met Gln Gln Gln Met Asn Ala Gln His Gln Pro Met Asn
 900 905 910
 Ile Phe Pro Tyr Pro Val Gly Val His Ala Pro Leu Met Asn Ile Gln
 915 920 925
 Arg Asn Pro Phe Asn Ile His Pro Gln Leu Pro Leu His Leu His Thr
 930 935 940
 Gly Val Pro Leu Met Gln Val Ala Thr Pro Thr Ser Val Ser Gln Gly
 945 950 955 960
 Leu Pro Pro Pro Pro Pro Pro Pro Pro Pro Ser Gln Gln Val Asn Tyr
 965 970 975
 Ile Ala Ser Gln Pro Asp Gly Lys Gln Leu Gln Gly Ile Pro Ser Ser
 980 985 990
 Ser His Val Ser Asn Asn Met Ser Thr Pro Val Leu Pro Ala Pro Thr
 995 1000 1005
 Ala Ala Pro Gly Asn Thr Gly Met Val Gln Gly Pro Ser Ser Gly Asn
 1010 1015 1020
 Thr Ser Ser Ser Ser His Ser Lys Ala Ser Asn Ala Ala Val Lys Leu
 1025 1030 1035 104
 Ala Glu Ser Lys Val Ser Val Ala Val Glu Ala Ser Ala Asp Ser Ser
 1045 1050 1055
 Lys Thr Asp Lys Lys Leu Gln Ile Gln Glu Lys Ala Ala Gln Glu Val
 1060 1065 1070
 Lys Leu Ala Ile Lys Pro Phe Tyr Gln Asn Lys Asp Ile Thr Lys Glu
 1075 1080 1085
 Glu Tyr Lys Glu Ile Val Arg Lys Ala Val Asp Lys Val Cys His Ser
 1090 1095 1100
 Lys Ser Gly Glu Val Asn Ser Thr Lys Val Ala Asn Leu Val Lys Ala
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 Tyr Val Asp Lys Tyr Lys Tyr Ser Arg Lys Gly Ser Gln Lys Lys Thr
 1125 1130 1135
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 1140 1145

<210> 169
 <211> 597
 <212> DNA
 <213> Homo Sapiens

<400> 169
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 gaagtgtctac caaaacacgc aatgactgtc ctaaaagtgc gttctgggat acacctgtaa 180
 acttggtatca agttccctcc cctctcctca aaatatatcg acttgtgctg aaagaaatca 240

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ctttccctga	ttcagtggca	ggtaacatat	ttcatgtaca	aaatgaactg	caacaccacg	360
gcaaacaagg	gacaggccct	caaagttgtc	ggtagggagc	caggaccccg	ccagtggcgt	420
ggggagacac	cgtactaaac	aagcttgcaa	acagcaggca	ccttcctgcc	actgaggagg	480
aagggtctgc	taaggagggc	cggggcggag	gaagccaagc	tctgcaggcc	ctgacaaagt	540
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<210> 170

<211> 3344

<212> DNA

<213> Homo Sapiens

<400> 170

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ctctaacagc	aagtgaatc	cggcagcgat	ttatagattt	cttcaagagg	aacgagcata	180
cgtatgttca	ctcgtctgcc	accatcccat	tggatgaccc	cactttgtct	tttgccaatg	240
caggcatgaa	ccagtttaaa	ccatttttcc	tgaacacaa	tgacccatct	caccccatgg	300
caaaagctgag	cagagctgcc	aataccocaga	agtgcattccg	ggctgggggg	aaacaaaatg	360
acctggacga	tgtgggcaag	gatgtctatc	atcacacctt	cttcgagatg	ctgggctctt	420
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aagagtttgg	cattcccatt	gaaagacttt	atgttactta	ctttggcggg	gatgaagcag	540
ctggcttaga	agcagatctg	gaatgcaaac	agatctggca	aaatttgggg	ctggatgaca	600
ccaaaatcct	cccaggcaac	atgaaggata	acttctggga	gatgggtgac	acgggcccct	660
gtggtccttg	cagttagatc	cactacgacc	ggattggtgg	tcgggacgcc	gcacatcttg	720
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tcaggaaagc	agagagcttg	aagaaatgtc	tctctgtcat	ggaagccaaa	gtgaaggctc	2460
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ctgccctgag ccctccacgt cagtgccatc ggtctagaac cactaaccoc gcattgctgt 3240
tgatcgtcac gctcgcatct atagataacg gctctccaga cctgagcttt ccgcgtcagc 3300
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<210> 171

<211> 1004

<212> PRT

<213> Homo Sapiens

<400> 171

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Val Thr Phe Lys Met Asp Ser Thr Leu Thr Ala Ser Glu Ile Arg Gln
35          40          45
Arg Phe Ile Asp Phe Phe Lys Arg Asn Glu His Thr Tyr Val His Ser
50          55          60
Ser Ala Thr Ile Pro Leu Asp Asp Pro Thr Leu Leu Phe Ala Asn Ala
65          70          75          80
Gly Met Asn Gln Phe Lys Pro Ile Phe Leu Asn Thr Ile Asp Pro Ser
85          90          95
His Pro Met Ala Lys Leu Ser Arg Ala Ala Asn Thr Gln Lys Cys Ile
100         105         110
Arg Ala Gly Lys Lys Gln Asn Asp Leu Asp Asp Val Gly Lys Asp Val
115         120         125
Tyr His His Thr Phe Phe Glu Met Leu Gly Ser Trp Ser Phe Gly Asp
130         135         140
Tyr Phe Lys Glu Leu Ala Cys Lys Met Ala Leu Glu Leu Leu Thr Gln
145         150         155         160
Glu Phe Gly Ile Pro Ile Glu Arg Leu Tyr Val Thr Tyr Phe Gly Gly
165         170         175
Asp Glu Ala Ala Gly Leu Glu Ala Asp Leu Glu Cys Lys Gln Ile Trp
180         185         190
Gln Asn Leu Gly Leu Asp Asp Thr Lys Ile Leu Pro Gly Asn Met Lys
195         200         205
Asp Asn Phe Trp Glu Met Gly Asp Thr Gly Pro Cys Gly Pro Cys Ser
210         215         220
Glu Ile His Tyr Asp Arg Ile Gly Gly Arg Asp Ala Ala His Leu Val
225         230         235         240
Asn Gln Asp Asp Pro Asn Val Leu Glu Ile Trp Asn Leu Val Phe Ile
245         250         255
Gln Tyr Asn Arg Glu Ala Asp Gly Ile Leu Lys Pro Leu Pro Lys Lys
260         265         270

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Ser Ile Asp Thr Gly Met Gly Leu Glu Arg Leu Val Ser Val Leu Gln
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 Asn Lys Met Ser Asn Tyr Asp Thr Asp Leu Phe Val Pro Tyr Phe Glu
 290 295 300
 Ala Ile Gln Lys Gly Thr Gly Ala Arg Pro Tyr Thr Gly Lys Val Gly
 305 310 315 320
 Ala Glu Asp Ala Asp Gly Ile Asp Met Ala Tyr Arg Val Leu Ala Asp
 325 330 335
 His Ala Arg Thr Ile Thr Val Ala Leu Ala Asp Gly Gly Arg Pro Asp
 340 345 350
 Asn Thr Gly Arg Gly Tyr Val Leu Arg Arg Ile Leu Arg Arg Ala Val
 355 360 365
 Arg Tyr Ala His Glu Lys Leu Asn Ala Ser Arg Gly Phe Phe Ala Thr
 370 375 380
 Leu Val Asp Val Val Val Gln Ser Leu Gly Asp Ala Phe Pro Glu Leu
 385 390 395 400
 Lys Lys Asp Pro Asp Met Val Lys Asp Ile Ile Asn Glu Glu Glu Val
 405 410 415
 Gln Phe Leu Lys Thr Leu Ser Arg Gly Arg Arg Ile Leu Asp Arg Lys
 420 425 430
 Ile Gln Ser Leu Gly Asp Ser Lys Thr Ile Pro Gly Asp Thr Ala Trp
 435 440 445
 Leu Leu Tyr Asp Thr Tyr Gly Phe Pro Val Asp Leu Thr Gly Leu Ile
 450 455 460
 Ala Glu Glu Lys Gly Leu Val Val Asp Met Asp Gly Phe Glu Glu Glu
 465 470 475 480
 Arg Lys Leu Ala Gln Leu Lys Ser Gln Gly Lys Gly Ala Gly Gly Glu
 485 490 495
 Asp Leu Ile Met Leu Asp Ile Tyr Ala Ile Glu Glu Leu Arg Ala Arg
 500 505 510
 Gly Leu Glu Val Thr Asp Asp Ser Pro Lys Tyr Asn Tyr His Leu Asp
 515 520 525
 Ser Ser Gly Ser Tyr Val Phe Glu Asn Thr Val Ala Thr Val Met Ala
 530 535 540
 Leu Arg Arg Glu Lys Met Phe Val Glu Glu Val Ser Thr Gly Gln Glu
 545 550 555 560
 Cys Gly Val Val Leu Asp Lys Thr Cys Phe Tyr Ala Glu Gln Gly Gly
 565 570 575
 Gln Ile Tyr Asp Glu Gly Tyr Leu Val Lys Val Asp Asp Ser Ser Glu
 580 585 590
 Asp Lys Thr Glu Phe Thr Val Lys Asn Ala Gln Val Arg Gly Gly Tyr
 595 600 605
 Val Leu His Ile Gly Thr Ile Tyr Gly Asp Leu Lys Val Gly Asp Gln
 610 615 620
 Val Trp Leu Phe Ile Asp Glu Pro Arg Arg Arg Pro Ile Met Ser Asn
 625 630 635 640
 His Thr Ala Thr His Ile Leu Asn Phe Ala Leu Arg Ser Val Leu Gly
 645 650 655
 Glu Ala Asp Gln Lys Gly Ser Leu Val Ala Pro Asp Arg Leu Arg Phe
 660 665 670
 Asp Phe Thr Ala Lys Gly Ala Met Ser Thr Gln Gln Ile Lys Lys Ala
 675 680 685
 Glu Glu Ile Ala Asn Glu Met Ile Glu Ala Ala Lys Ala Val Tyr Thr
 690 695 700
 Gln Asp Cys Pro Leu Ala Ala Lys Ala Ile Gln Gly Leu Arg Ala

705 710 715 720
 Val Phe Asp Glu Thr Tyr Pro Asp Pro Val Arg Val Val Ser Ile Gly
 725 730 735
 Val Pro Val Ser Glu Leu Leu Asp Asp Pro Ser Gly Pro Ala Gly Ser
 740 745 750
 Leu Thr Ser Val Glu Phe Cys Gly Gly Thr His Leu Arg Asn Ser Ser
 755 760 765
 His Ala Gly Ala Phe Val Ile Val Thr Glu Glu Ala Ile Ala Lys Gly
 770 775 780
 Ile Arg Arg Ile Val Ala Val Thr Gly Ala Glu Ala Gln Lys Ala Leu
 785 790 795 800
 Arg Lys Ala Glu Ser Leu Lys Lys Cys Leu Ser Val Met Glu Ala Lys
 805 810 815
 Val Lys Ala Gln Thr Ala Pro Asn Lys Asp Val Gln Arg Glu Ile Ala
 820 825 830
 Asp Leu Gly Glu Ala Leu Ala Thr Ala Val Ile Pro Gln Trp Gln Lys
 835 840 845
 Asp Glu Leu Arg Glu Thr Leu Lys Ser Leu Lys Lys Val Met Asp Asp
 850 855 860
 Leu Asp Arg Ala Ser Lys Ala Asp Val Gln Lys Arg Val Leu Glu Lys
 865 870 875 880
 Thr Lys Gln Phe Ile Asp Ser Asn Pro Asn Gln Pro Leu Val Ile Leu
 885 890 895
 Glu Met Glu Ser Gly Ala Ser Ala Lys Ala Leu Asn Glu Ala Leu Lys
 900 905 910
 Leu Phe Lys Met His Ser Pro Gln Thr Ser Ala Met Leu Phe Thr Val
 915 920 925
 Asp Asn Glu Ala Gly Lys Ile Thr Cys Leu Cys Gln Val Pro Gln Asn
 930 935 940
 Ala Ala Asn Arg Gly Leu Lys Ala Ser Glu Trp Val Gln Gln Val Ser
 945 950 955 960
 Gly Leu Met Asp Gly Lys Gly Gly Gly Lys Asp Val Ser Ala Gln Ala
 965 970 975
 Thr Gly Lys Asn Val Gly Cys Leu Gln Glu Ala Leu Gln Leu Ala Thr
 980 985 990
 Ser Phe Ala Gln Leu Arg Leu Gly Asp Val Lys Asn
 995 1000

<210> 172
 <211> 659
 <212> DNA
 <213> Homo Sapiens

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 tcagatggac cgattggatc gagaagaagc tttctatcaa tttgtaaata acctgagtga 300
 agaagattat aggcttatga gagataacaa tttgctaggc accccagggtg aaagtactga 360
 ggaagagttg ctgagacgac tacagcaaat taaagaaggc ccaccaccgc aaaactcaga 420
 tgaaaataga ggaggagact cttcagatga tgtgtctaat ggtgactcta taatagactg 480
 gcttaactct gtcagacaaa ctggaaatac aacaagaagt gggcaaagag gaaaccaatc 540
 ttggagagca gtgagtcgga ctaatccaaa cagtgggtga tttcagattc agtttagaga 600
 taaatgtaa cccgtaataa tgggagccaa aattcagaga atgaaaatga gccatctgc 659

<210> 173
 <211> 192
 <212> PRT
 <213> Homo Sapiens

<400> 173
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 35 40 45
 Leu Lys Pro Ser Ile Phe His Leu Phe Ile Asn Met Glu Asn Ser Asp
 50 55 60
 Ser Asn Asp Lys Gly Ser Gly Asp Gln Ser Ala Ala Gln Arg Arg Ser
 65 70 75 80
 Gln Met Asp Arg Leu Asp Arg Glu Glu Ala Phe Tyr Gln Phe Val Asn
 85 90 95
 Asn Leu Ser Glu Glu Asp Tyr Arg Leu Met Arg Asp Asn Asn Leu Leu
 100 105 110
 Gly Thr Pro Gly Glu Ser Thr Glu Glu Glu Leu Leu Arg Arg Leu Gln
 115 120 125
 Gln Ile Lys Glu Gly Pro Pro Pro Gln Asn Ser Asp Glu Asn Arg Gly
 130 135 140
 Gly Asp Ser Ser Asp Asp Val Ser Asn Gly Asp Ser Ile Ile Asp Trp
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 165 170 175
 Gly Asn Gln Ser Trp Arg Ala Val Ser Arg Thr Asn Pro Asn Ser Gly
 180 185 190

<210> 174
 <211> 610
 <212> DNA
 <213> Homo Sapiens

<400> 174
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 gtccgaggcc tcagaaatta ctattcctcc cagcaccccg gcagttccac aggctcccg 240
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 cccacagtg gaattggcaa acccactgca gccctgaga ggaggtcgaa tgggtaaagg 480
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 cttctaaaaa 610

<210> 175
 <211> 138
 <212> PRT
 <213> Homo Sapiens

<400> 175

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 35 40 45
 Ser Gly Thr Gly Ile Arg Ser Glu Ser Glu Thr Glu Ser Glu Ala Ser
 50 55 60
 Glu Ile Thr Ile Pro Pro Ser Thr Pro Ala Val Pro Gln Ala Pro Val
 65 70 75 80
 Gln Gly Glu Asp Tyr Gly Lys Gly Val Ile Phe Tyr Leu Arg Asp Lys
 85 90 95
 Val Val Val Gly Ile Val Leu Trp Asn Ile Phe Asn Arg Met Pro Ile
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 Ala Arg Lys Ile Ile Lys Asp Gly Glu Gln His Glu Asp Leu Asn Glu
 115 120 125
 Val Ala Lys Leu Phe Asn Ile His Glu Asp
 130 135

<210> 176
 <211> 805
 <212> DNA
 <213> Homo Sapiens

<400> 176
 gggacagcca agtctgtgac ttgcacgtac tcccctgccc tcaacaagat gttttgccaa 60
 ctggccaaga cctgccctgt gcagctgtgg gttgattcca ccccccgcc cggcaccgc 120
 gtccgcgcca tggccatcta caagcagtca cagcacatga cggagggtgt gaggcgctgc 180
 ccccaccatg agcgctgctc agatagcgat ggtctggccc ctctcagca tcttatccga 240
 gtggaaggaa atttgcgtgt ggagtatttg gatgacagaa acacttttcg acatagtgtg 300
 gtggtgccct atgagccgcc tgaggttggc tctgactgta ccaccatcca ctacaactac 360
 atgtgtaaca gttcctgcat gggcggcatg aaccggaggc ccatectcac catcatcaca 420
 ctggaagact ccagtggtaa tctactggga cggaacagct ttgagggtgcg tgtttgtgcc 480
 tgtcctggga gagaccggcg cacagaggaa gagaatctcc gcaagaaagg ggagcctcac 540
 cacgaagctg cccccaggga gcactaagcg agcactgccc aacaacacca agtctctctc 600
 cccagccaaa gaagaaancca ctggatngag aatatttcac cccttcanat tcgttgggcg 660
 tgagcgcttc cganaatggt ccgaagagct gnaagaaggc cttgggaact caaaggatgc 720
 ccaaggcttg ggaaaggagc caangggggg gaancaangg gctcaactnc aagccaacct 780
 gaaagttcca aaaaangggg ccagt 805

<210> 177
 <211> 626
 <212> DNA
 <213> Homo Sapiens

<400> 177
 ctaatttgtc tgttttattcc cacaaggtag ccaggggtgg gggcgccgag ccaagcccag 60
 caggccatgg gaccttccctc cggcgggggtg cacgctggat ttccgggtct gccccaccag 120
 caggtttgca ggcaggccgt catgagtgcg ggtggaaggc tccgaggcg tgggcagggg 180
 ctcgggcggg gccacacact tgtggagcta gaaatantgg ggcaggctct tctctatcac 240
 caggggctcc tccatgggtc cgtagcgctt caccacgcag ccgttcttgt cgatgaggaa 300
 ctgtgganan acggtgtcca aactgtgggg ccaccctgc aaggggctga ggctgccctt 360
 cctgtccgct gcccatctgg gccacggctg tggccagggg aaactgggtc cctaccccc 420
 acagccccct tacctttggt gaagtccac ttgatggcac tggaaaaanaa gcacatggac 480
 gtgagcgctc ccaggcagcc cccacagtc cccaaagctt gtctgtctc caaggaggcc 540

anaaagggttg tnagcttccc cgggtncctc cacangccac agtgccccc aanncccccc 600
aanagccatc tttaccccaa ggaggg 626

<210> 178
<211> 793
<212> DNA
<213> Homo Sapiens

<400> 178
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gcggcgggccc ctcttatgct gggaggatgc tggagagtag cggctgcaaa gcgctgaagg 120
agggcgctgct ggagaagcgc agcgacgggt tgttgagct ctggaagaaa aagtgttgca 180
tcctcacga ggaagggctg ctgcttatcc cgcccaagca gctgcaacac cagcagcagc 240
agcaacagca gcagcagcag cagcaacaac agcccgggca ggggcccggcc gagccgtccc 300
aaccagtggt ccccgctgtc gccagcctcg agccgcccgt caagctcaag gaactgcaact 360
tctccaacat gaagaccgtg gactgtgtgg agcgcaagg caagtacatg tactttactg 420
tgggtgatggc agaggggcaag gagatcgact ttcggtgccc gcaagaccag ggctggaacg 480
ccgagatcac gctgcagatg gtgcagtaca agaatcgta ggccatcctg gcggtcaaact 540
ccacgaggca gaagcagcag cacttggctc agcancagcc cccctcgag ccgcagccgc 600
agccgcagct ccaagcccca acccagcct tcagcctcaa gccngcaacc ccaagcccca 660
attcacaaac ccaagccct caagcccca cccaaagccc tcangcccca ngcaagntcc 720
aaccggttat ncggccatcc aacattcaan atccaanact ctcaangcct taactnccn 780
acccaanaac nct 793

<210> 179
<211> 786
<212> DNA
<213> Homo Sapiens

<400> 179
aatatcagag ttttaatttc aaccagctgg cacaacaatg aaagtgtcag actttctgaa 60
agtactcgag aaataatgaa taaattctta atgttttccc ctccaccgcc cttttttatt 120
ctccaagatt aggaattact acggattagg tttttgaaaa taaagtctcc tttttggaaa 180
atggctctaca ttcagaaatg tcttagaaca agcattttaa aaaaactaat aaataatcat 240
aaatcaaaat acattaaaat aaaattacag tacatcatcg ctctagaaa attcaccata 300
caagacgac ctttcaaagg ttcataaata aaagtcttct tgactcgaaa tcgtttcctg 360
catcgtgatg aaaagtatgc agaaaactaa gaagaatcgc aagttttcag taggggtgatg 420
tccaaactac ttgatctggt gcggggcgga gagactgttt tgcttttgat ccaagtgaag 480
acaatagaaa tgtgctcgtc ccacttctc aagtcctcaa aaccttgtct tgcccgggag 540
ctgccccctt cangcagagt tgggaggtgc tgcganaaaa ccggtgcccg tgccgctgcc 600
aatgcggctg tgggtgtggg tgcngtattt ggtgcccgat gcnggtgccg ggtnaagggtg 660
tggggtgcca antnaaggat gaaaatgtgg atnttngnat nttgattccg gatacgggggt 720
gggaacctng cngggggccn naaggcttgg ggttggggct naanggctgg ggttttttaa 780
ttgggg 786

<210> 180
<211> 791
<212> DNA
<213> Homo Sapiens

<400> 180
aggacctcag agaccagggc tctgtgattg tggccttcaa ggaaggggaa cagaaggaga 60
aggagggat cctgcagctg cgtcgcacca actcagccaa gccagtcga ctggcaccat 120
ccctcatggc ctcttctccg acttctatct gtgtgtgtgg gcaggtgcca gctgggggtg 180
gagttctgca gtgtgacctg tgtcaggact ggttccatgg gcagtgtgtg tcagtgtccc 240

atctcctcac	ctctccaaag	cccagtctca	cttcatctcc	actgctagcc	tggtgggaat	300
gggacacaaa	attcctgtgt	ccactgtgta	tgcgctcacg	acggccacgc	ctagagacaa	360
tcctagcctt	gctggttgcc	ctgcagaggc	tgcccgtgcg	gctgcctgag	ggtgaggccc	420
ttcagtgtct	cacagagagg	gccattggct	ggcaagaccg	tgccagaaag	gctctggcct	480
ctgaagatgt	gactgctctg	ttgcgacagc	tggtctgagct	tcgccaacag	ctacaggcca	540
aacccanacc	agaggaggcc	tcagtctaca	cttcagccac	tgctctgtgac	cctatcagag	600
aaggcagtg	caacaatatt	tcnaangtcc	aagggctgct	ggagaatgga	gacantgttg	660
accagtcctg	agaacatggc	tccaggaaag	ggctctgacc	tgagctacn	gtcctcactg	720
ttgccgcaat	ttgactggnc	ctgttttttg	ganctgcctg	aaggcaatcc	cggggctccc	780
cctggaggga	g					791

<210> 181

<211> 747

<212> DNA

<213> Homo Sapiens

<400> 181

agtatccaaa	catactcatt	gttttatttt	taacaaaaga	aatgaaatta	aagatagacc	60
acaggtagag	tcatagaatt	cttgtttttc	cctattcttt	ttggttaatta	caacgtacat	120
tgtcttcttt	tataataaga	cccaagggga	gaaaagaaaa	ggatgtacaa	tgaagggtaca	180
agttttgaag	cacccaaaata	ttttatgaca	gggacaaaaa	aacaaaaaac	aaacaaaaat	240
tgaagtacag	aaagaggggtg	gtggggggcaa	aaataaaaggt	acgcacttgg	gcttctctcaa	300
gatttgtttg	tccttattca	gactagaatg	aaactggttt	aggaaatcac	tcctgtatgc	360
tagcaggaat	gttgctggca	agacacttct	gagcatcggtg	gtgtggactt	tacgaaccaa	420
ccttttaaca	gtaactctag	gagagaggat	atcaaaaatt	ggcagtgaag	aattatagat	480
aggcaaaaag	ctccttctga	ggccaggcc	aggagatagt	angatttaag	aaacaaacaa	540
acaataacaa	ccacaaatgg	acctttgggtg	ccactgtcac	aactgttgct	catcagagta	600
ggagaattgt	ancaaaggca	ttaaagaagg	gacaagcaag	ctgaagagcc	tgaatccttg	660
gggttgtaag	ccnatttttg	gnttcctttc	aagaaaagggt	ctgttggnctg	gtggaanggg	720
tcanggaaca	ntatttcacg	ggtcngc				747

<210> 182

<211> 909

<212> DNA

<213> Homo Sapiens

<400> 182

aaacagagag	ccaaatcatg	agtgaactcc	cattcacaaat	tgcttccaag	ataataaaat	60
acctaggaat	ccaacttaca	aaggatgtga	aggacctctt	caaggagaac	tacaaaccac	120
tgctcaatga	aataaaaagag	gatacaaaaca	aatggaagaa	cattccatgc	tcattgggtag	180
gaagaatcaa	tatcgtgaaa	atggccatac	tgcccaagggt	aatgtataga	ttcaatgcca	240
tccccatcaa	gctaccaatg	actttcttca	cagaattgga	aaaaactact	caaaagtcca	300
tatggaacca	aaaaagagcc	cacattgcca	agtcaatcct	aagccaaaag	aaacaaagctg	360
gaggcatcac	gctacctgac	ttcaaaactat	actacaaggc	tacagtaacc	aaaacagcgt	420
ggtactggta	ccaaaacaga	gatataaatc	aatgcaacag	aacagagccc	tcagaaataa	480
tgccacatat	ctacaactat	ctgatctttg	acaaacctga	gaaaaacaag	caatggggaa	540
aggattccct	atttaataaaa	tggtgctggg	aaaactggct	agccatatgt	agaaagctga	600
aactggatct	cttctttata	ccttatacaa	aaattaattg	aagatggntt	aaaggactta	660
aacgttagac	ctaaaaccat	aaaaacccta	gaagaaaaac	ctaggcatta	ccattcangg	720
acataggctt	gggcaaggac	ttcctgtcta	aaacaccaan	agcaatggga	ncaaaaagcca	780
aaattgcaaa	tggggattct	aattaactaa	agggcttttg	cacagcnaag	aagctccatc	840
agagngaaca	ggaacntcaa	antgggagaa	attttgaacc	taccatcnga	naaggctaat	900
nccagaatc						909

<210> 183

<211> 708
 <212> DNA
 <213> Homo Sapiens

<400> 183

attatcatta	tactttaagt	tttaggttac	atgtgcacaa	tgtgcagggt	agttacatat	60
gtatacatgt	gccatgctgg	tgtgctgcac	ccattaactc	gttatcttagc	attaggtata	120
tctcctaattg	ctatccctcc	cgcctccccc	cacccacaaa	cagccccag	agtgtgatgt	180
tcccccttcct	gtgtccatgt	gttctcactg	ttcaattccc	acctatgagt	gagaatatgc	240
gggtgtttggt	ttttttgtcc	ttgccatagt	ttactgagaa	tgatgatttc	caatttcac	300
cctgtcccta	caaaggacat	gaactcatca	ttttttatgg	ctgcatagta	ttccatgggtg	360
tatatgtgcc	acattttctt	aatccagtct	atcattgttg	gccatttggtg	ttgggtccaa	420
gtctttgcta	ttgtgaatac	tgccgcaata	aacatacgtg	tgcatgtgtc	tttatagcag	480
catgatttat	antcctttgg	gtatatactc	agtaatggga	tggctgggtc	aaatggnatt	540
ccaantccan	atcccttang	aattgccaca	cggactccac	aanggttgaa	ctantttaca	600
gtcccancaa	cagngtnaaa	gggtccnaan	tcnccaaaat	cctctccaag	caccngttgt	660
tcccggactt	tttaanggat	tgncaatcc	aaccggngt	caaaagggt		708

<210> 184
 <211> 855
 <212> DNA
 <213> Homo Sapiens

<400> 184

agactcacag	tctgctgggtg	ggcagagaag	acagaaacga	catgagcaca	gcaggaaaag	60
taatcaaatg	caaagcagct	gtgctatggg	aggtaaagaa	acccttttcc	attgaggatg	120
tggaggttgc	acctcctaag	gcttatgaag	ttcgcattaa	gatggtgggt	gtaggaatct	180
gtcgcacaga	tgaccacgtg	gttagtggca	acctggtgac	cccccttcct	gtgatttttag	240
gccatgaggc	agccggcatc	gtggagagtg	ttggagaagg	ggtgactaca	gtcaaacacc	300
gtgataaagt	catcccgtc	tttactcctc	agtgtggaaa	atgcagagtt	tgtaaaaacc	360
cggagagcaa	ctactgcttg	aaaaatgatc	taggcaatcc	tcgggggacc	ctgcaggatg	420
gcaccaggag	gttcacctgc	agggggaagc	ccattcacca	cttccttggtc	accagcacct	480
tctcccagta	cacgggtgggtg	gatgagaatg	cagtggccaa	aattgatgca	gcctcgcccc	540
tggagaaagt	ctgcctcatt	ggctgtggat	tctcgactgg	gttatgggtc	tgcatgtaac	600
gttgccaagg	tcaccccagg	ctctacctgt	gctgtgtgtg	gcctgggaag	ggtcgcccta	660
tctgctgtta	tgggctgtta	aagcaactgg	agggcancag	aatcaattgc	ggtggacatc	720
aacaaggaca	aattttgcaa	agggcaaaaag	agttgggtgc	caatgaatgc	catcaaccct	780
caagnctnca	ngnaaaccca	tccaggnaag	tgctaaaaang	gaatttaccg	attggagggtg	840
ttggattttt	ccgtt					855

<210> 185
 <211> 865
 <212> DNA
 <213> Homo Sapiens

<400> 185

cacagatgtt	caatcaactg	atgaagcaag	tgctcaggact	tactgttgac	acagaggagc	60
ggctgaaagg	agttattgac	ctggtctttg	agaaggctat	tgatgaaccc	agtttctctg	120
tggcttacgc	aaacatgtgt	cgatgtctag	taacgctgaa	agtacccatg	gcagacaagc	180
ctggtaaacac	agtgaatttc	cggaaagctgc	tactgaaccg	ttgccagaag	gagtttgaaa	240
aagataaagc	agatgatgat	gtcttttgaga	agaagcagaa	agaacttgag	gctgccagtg	300
ctccagagga	gaggacaagg	cttcatgatg	aactggaaga	agccaaggac	aaagcccggc	360
ggagatccat	tggcaacatc	aagttttattg	gagaactctt	taaactcaaa	atgctgactg	420
agcccatcat	gcatgactgt	gtgggtgaagc	tgctaaagaa	ccatgatgaa	gaatccctgg	480
agtgcctgtg	tcgcctgtctc	accaccattg	gcaaagactt	ggactttgaa	aaagcaaagc	540

cacgtatgga	ccagtacttt	aatcaagatg	gagaaaattg	tnaaagaaag	aaaaacctca	600
tctagggatt	cgggttcatt	ttcaaagatg	ttatanacct	aaggctgttg	caattggggg	660
atctcgaaaag	agcagatnaa	gggcctnaan	ctatcgaaac	gattcacaaa	ganggctaaa	720
attgaaanaa	caagaatagc	caaagggaag	gnccaacaac	tcatggacca	anggagaaat	780
agaataccaa	ggtgttccaa	aaanttggtc	aaangnnggt	tggaaanacn	gttcaaaggg	840
ggccangaaa	aantccgggt	actgg				865

<210> 186

<211> 736

<212> DNA

<213> Homo Sapiens

<400> 186

aaatatttgt	tctatgtatt	tacaagcctt	aaagttgtct	taaagatttc	aagagtatta	60
agagtacttt	tctcagggtg	gcactttngt	tttttttaac	aattcttgga	gttctgtggg	120
ccacagcatt	tccttctgtt	tcaatgttat	gtatgttttg	attactattg	tgatttttta	180
aattttctga	agcaagctga	gaggcaggca	gaaagatttg	atgccaaaaa	aaaaaaaaatc	240
tttcttacct	tgttcacccc	aaactttctc	aaatctggac	taaatgctat	accttaaaac	300
aaacatgagg	tgcatcctga	aggggaggga	aattttattc	tctgcttttc	tattatacaa	360
gttgttttga	gaaactgcaa	attaaaaaat	tacactggca	tttgacgtcc	ttaaaataaa	420
ttaaaaagtt	tcaacttttt	tttttttttg	ctaaacattt	ttttaagtat	gagtccttgt	480
ttaaaaagaa	aagattaaaa	cagaaaaatat	tttctataaa	taatacatgt	attttggttt	540
tagtgctccc	gccctaagggt	ttgaagttaa	cttttancca	ngtacctttt	tcctccatga	600
tcaccttttt	ttctctttcc	cctctcccaa	ntccgtgcac	acgtgggggt	ttccggcaan	660
aattggcctt	gctgnactgt	gattgggcga	anaacgttga	aaaacctttt	taaaaaaaaa	720
tacttaaaat	tgggtt					736

<210> 187

<211> 946

<212> DNA

<213> Homo Sapiens

<400> 187

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ctgtagaccc	caaataccat	cccaagatta	tcgggagaaa	gggggcagta	attacccaaa	120
tcgggttgga	gcatgacgtg	aacatccagt	ttcctgataa	ggacgatggg	aaccagcccc	180
aggaccaa	taccatcaca	gggtacgaaa	agaacacaga	agctgccagg	gatgctatac	240
tgagaattgt	gggtgaactt	gagcagatgg	tttctgagga	cgtcccgctg	gaccaccgctg	300
ttcacgcccc	catcattggg	gcccgcggca	aagccattcg	caaaatcatg	gacgaattca	360
aggtggacat	tcgcttccca	cagagcggag	ccccagaccc	caactgcgtc	actgtgacgg	420
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ccccagcac	acgaanaagc	caanggnacc	tttcaaaagg	ctttnttggt	gccgggacca	780
acctgggacc	gccagcaacc	aatnaaaaaa	ggcncctgacn	ttaaccaagc	tcngagggaa	840
tttcccancc	tttggggggc	caaggtggct	cccaaagaac	cctccccntt	ngggggcccc	900
aaacnaatna	ttgttcaaaa	anggaacaaa	aaccctctct	aagccc		946

<210> 188

<211> 802

<212> DNA

<213> Homo Sapiens

<400> 188

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tgcggnnaa	aagtgatgaa	ggccaaagt	ctgactgaca	tgccgggtgg	accaaganct	120
ggagtcngtt	atcntaacac	gaatgccc	gaccttggtt	taatgttaaa	cantggagca	180
ngtctganc	gggcacggcc	angcctggag	gancggccgc	acacacanc	angcgcnagg	240
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tcngttcntt	ttgatcanta	ncntttgggg	ccccaaggga	nggtcntggg	anccacctga	420
nccccaagc	tgggaaattc	ctcaaagctg	cncatgtcaa	gagccttcnc	antgctgctg	480
gcggtccaag	gtgcgtccc	caccacaaag	cctctggaag	gngccntggc	ctcttctgt	540
gccgggggtt	tcatgtntac	ctgcancgcc	tactgtcca	ccaangtcag	ctaactgcag	600
gcnaagaca	ggaatnacag	ggtcagtctg	cccaacaacc	ccancatccc	ggcccgccct	660
ggctcaaacc	ctgcaacctt	gcctgccttc	cggaanac	aatttccac	ccttgtnccc	720
ctgaaanccn	cctggntctg	ggcctcaaa	ggcgttgg	ncttccanag	gncnccccca	780
gggntccca	angggccac	aa				802

<210> 189

<211> 807

<212> DNA

<213> Homo Sapiens

<400> 189

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agcgcccttt	gagctgtggg	gaggttcag	cagcagctac	agtgcgact	aagactccag	120
tgcatttcta	tcgtaacgg	gcgcggggga	gcgcagatcg	gcgccagca	atcacagaag	180
ccgacaaggc	gttcaagcga	aaacatgacc	gctgagccca	tgagtgaag	caagttgaat	240
acattgggtg	agaagcttca	tgacttcctt	gcacactcat	cagaagaatc	tgaagaaaca	300
agttctcctc	cacgacttgc	aatgaatcaa	aacacagata	aatcagtg	ttctggaagt	360
aactctgata	tgatggaaaa	cagcaaggaa	gagggaaacta	gctcttcaga	aaaatccaag	420
tcttcaggat	cgtcacgatc	aaagaggaaa	ccttcaattg	taacaaagta	tgagaatca	480
gatgatgaaa	aacctttgga	tgatgaaact	gtaaatgaag	atgcttctaa	tgaaaattca	540
gaaaatgata	ttactatgca	nagcttgcca	aaaggtacag	tgattgttca	gccagagcca	600
gtgctgaatg	aagacaaaga	tgattttaaa	ggggcctgaa	tttagaagca	gaagttaaaa	660
tgaaaactga	naatctcaaa	aaacgcggga	gaanatgggc	ttcatgggga	ttgtgangcc	720
tgcactggcn	tggtggacaa	caaggtcaat	caatttcaaa	aaggttccat	ttatagacaa	780
cccttcaatg	caaggtcnta	tttgta				807

<210> 190

<211> 608

<212> DNA

<213> Homo Sapiens

<400> 190

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agattggctt	taatttcttc	taaaagcatc	ttcttggcaa	ttctattctc	aggatcattg	120
tcgtcatcat	catcatccac	tgtgacaggc	actgatctag	ataaggcttc	atctcctgaa	180
gattggcaaa	atccagtatg	tgaagacagc	actaaatttt	cagtcacagg	cttaattttc	240
tgttcatcgc	tgttcccttc	acctatagaa	ttctgatcat	catcttctat	atcagaagaa	300
gatgaggatg	taatgtcagc	ttgttccctt	ttagtgttg	ttcttaggga	gtttctcttt	360
ttctccttga	caatgactgc	cttcttttta	gatgaagttc	tttgccttct	ctttttacta	420
tcttcangaa	ctttccctcag	catcagatga	tgatgangcc	actttgtatt	tccttagtat	480
ttctctttga	acttaaat	cttctttccc	tcaattogag	tcttttcagt	caccttatca	540
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tccttgaa						608

<210> 191
 <211> 786
 <212> DNA
 <213> Homo Sapiens

<400> 191
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 ggagcaagct cagtactctc agagaggatg gaaggaaaac atctcatcgg tactccaagg 660
 ttctggangg ccatttggga aaaccaaacc ctcgggctcn acaaccctgt ccangcctgt 720
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<210> 192
 <211> 819
 <212> DNA
 <213> Homo Sapiens

<400> 192
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 cagatttgtg catgtttcct tcaaactctca gtctgtactg tcattaaaaa gatcatggaa 180
 tctatgttgt tcctcatgat ggaatagtaa aaaaactgca ttccactgac aaaaaaata 240
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 atagccttta acaagcgtct tttagcttgg tcagggttgt atcatttgtt tggaaagtac 360
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<210> 193
 <211> 744
 <212> DNA
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<400> 193
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 ctgcagtgca gcagccctct acccagggtc caccttcagt tattcagcag ggtgctcctc 180
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 ctccccagcc acaaggagta gaatcagtag ctcaaggaaat tgtttcacag cagttgcctg 360
 cagttagttc tttgccctct gctagtagta tttctgttac aagtcagggt agttcaactg 420

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acaatcatta	gtcaggcaca	ttggaagcca	aattgaagat	gccaggcggt	gcagcggagc	660
cctccttaag	ttggcttacc	tcaagactaa	tcagttgggtg	acaattgggg	ggaatgttca	720
gcaagtttca	agattgggaa	gtta				744

<210> 194

<211> 567

<212> DNA

<213> Homo Sapiens

<400> 194

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tgcagaaaacc	cctactggga	aatccatttc	attagttaga	actgagcatt	tttcaaagta	180
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ctagatttca	ggattacaca	aagttagtaa	ctgtgccaaa	ttcttaaaat	ttcttttaggt	300
gtggtttttg	tcatgtagca	gtttttatgt	agatcnatat	ntaaaagtcc	acacctcttc	360
agacangcca	atgaaacnac	taaatttcaa	tctgtacaan	ctaaatagta	attacagtcc	420
tctangtgmn	caangatact	tacaccacat	anacaaatnt	acnntacgca	naacaacctt	480
catggggaag	gatagcccta	ggtccccagc	tancctgtca	ccatttttgt	cactctcata	540
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<210> 195

<211> 771

<212> DNA

<213> Homo Sapiens

<400> 195

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ccaagaaaaga	ancanaaaaag	aaagcaaaaag	cagaagctaa	acggaaggag	caagaagcta	180
aagaaaaaca	aagacaagct	gaattagaag	ctgctcgggt	agctaaggag	aaagaagagg	240
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ttaagaagga	aaggcaaaaa	tttcgaaact	catgcaagac	ctggaatcat	ttttctgata	360
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tggcaagctt	acagtgcctt	aatgaaacac	tcacatcatg	cacaaaagaa	gtnggaaagg	480
ctgctttgga	aaaacagata	gaagaaataa	atgagcaaata	cagaaaagag	aaagagggaag	540
ctgaggctcg	tatgcgacaa	gcatctaaga	acacagagaa	atcaactggt	ggaagggtgga	600
aaatggaagt	aaaaattggg	cacaaagatg	ntctacaatt	actaatttna	aagctgtgaa	660
tcctgttncc	tgctggaaca	aantcaagat	gggaagttat	tgccaantac	atgaacatac	720
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<210> 196

<211> 561

<212> DNA

<213> Homo Sapiens

<400> 196

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tccttgtatc	gtttcatgca	gtccttcttt	gtcctgccag	gcaccgcttc	tgctattttt	180
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gcgttgtctg cttgaggtag cactccatgt tcttttttga acttatcaaa tgccttttta 360
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 tctttggnan gttcttttga ctccaagagg aagaangnt ntgtcatgtn antangcaan 480
 aacgtcccat ctggaanttt tgttcnacca gggaacanac tcacaagctt taactaagta 540
 antgtngnat naccgnncgn c 561

<210> 197

<211> 691

<212> DNA

<213> Homo Sapiens

<400> 197

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 cacagtgtan tatgaataac agtttcaccc cagctcctat gatcatggag ataccagaat 180
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 ttatggaccc tcatgccatg ccttatagcc attctcctgc tgtgacttcc tatgcaacca 360
 gtgtttctct gtccaataca ggactggctc agctggctcc atctcatccc ttagctggga 420
 ctctcaagc acangccacc atgacgccac ccccaactt ggcattccact accatgaacc 480
 tcacatctcc tctgcttcag tgcaacatgt ctgccacca cattggcatt cctcacacgc 540
 aggagattgc aagggcaaat gccagtgaag gggcacattt ccatccgctc caagtttggc 600
 ggcaactgcc tctgcnctg ctaccanna ngcagctggt atgggcccgn tccccaatcg 660
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<210> 198

<211> 646

<212> DNA

<213> Homo Sapiens

<400> 198

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 cctactgtgc tgggtggctcg tctgtccctc ttctcattag ccactcacag gagagggtgt 180
 tgtgcaactc gattcacagg ggatgaactc aggatctcaa aagacataca aaaactanag 240
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 gcgccatctc ttccaacata aaatanactg ttccaatggt ttgtcagtta tttttcaaat 360
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 gggactgcta tttgagtttt atcagtcaaa ggctcaagca tcaanaccct cagttancat 480
 ttcaaagtac atactangaa acancgaggc tgggtggcgt tgtgtgcgtt anggctgatt 540
 caccaggtgg taaanacaaca aagnggttaa gnctccnctt tttggattgt taattgncca 600
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<210> 199

<211> 811

<212> DNA

<213> Homo Sapiens

<400> 199

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 gatgaaatta tttctaagac aaagcaagta attcaggggc tgggaagcttt gaagaatgag 180
 cacaattcca ttttacaag tttgctggag acactgaagt gtttgaagaa agatgatgaa 240
 agtaatttgg tggaggagaa atcaaacatg atccggaagt cactggagat gttggagctc 300
 ggctgagtg aggacaggt tatgatggct ttgtcaaact acctgaatgc tgtggagtcc 360

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gatgaactgg	ccaacacgca	gcagaaactg	cagaagagtg	agcagtcgtg	ggctcaactg	480
gaggaggaga	agaagcatct	ggagtttatg	aatcagctaa	aaaaatatga	tgacgacatt	540
tccccatccg	aggacaaaga	caactgattct	accaaagagc	ctctggatga	ccttttcccc	600
aatgatgaag	acgacccagg	gcaaggaatc	cagcagcagc	acagcagtg	agccgagggt	660
gccagcaag	gcngctacna	agattccccg	gcggctgcgg	acgctccaca	acctgggtga	720
ttcagttcgc	ctcnnccagg	ggcgcctacc	aaggtaacct	gttgccccct	cctggcaaaag	780
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<210> 200

<211> 763

<212> DNA

<213> Homo Sapiens

<400> 200

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agttcacaga	gaggtgcagc	tctgacaaga	tcctagaggc	tgctagacac	agcgggcagc	180
actggagaga	gaagggagc	tgccggaggc	gccacccgtc	atgcaggaga	cagtgtgaga	240
gtcacggcg	gctagggcat	gggacgctga	gcaagtcagt	taaccagccc	gagcttcatt	300
ttcctcattt	cctccccctc	gtcagggcc	ctctcgtact	tgaccacgtc	cacgttgagg	360
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tctgcagctt	caaatttgcc	ttgacgtctg	taaagtgtcc	caagggtttt	tagagtgggt	540
gtaacagttg	gnctatcaac	tttgcanct	ttgtaccaac	cgccatactc	tccaaaaaga	600
tgtcccatcc	ttttgctttc	ctttgcattc	ttctctttcc	tcaacaatgc	atccaaatgg	660
gtttaatttc	aacatctaca	gaaccaaact	ccctttcatg	tgacacaagt	agaatcnctt	720
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<210> 201

<211> 717

<212> DNA

<213> Homo Sapiens

<400> 201

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ttacacagga	tgaaattatt	tctaagacaa	agcaagtaat	tcaggggctg	gaagctttga	120
agaatganca	caattccatt	ttacaaagtt	tgctggagac	actgaagtgt	ttgaagaaag	180
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ggctacggga	tgaactggcc	aacacgcagc	aagaaactgc	agaagagtga	gcagtctgtg	420
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gacgacattt	ccccatccga	gggacaaaga	caactgattct	accaaagagc	ctccggatga	540
ccttttcccc	aatgatgaag	acgacccag	ggcaaggga	tccancagca	gcacagcaan	600
ttgcagccgc	ggctgcccga	gcaaggcggc	tacgagattc	ccgccgcggc	tgccggacgc	660
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<210> 202

<211> 647

<212> DNA

<213> Homo Sapiens

<400> 202

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tactggggca	tatcctaggg	agaccgggag	tccgagcggg	gccccaggg	ctctaagtac	180
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aatcgctctt	aatttttaaa	ctcgtgtatt	acacagtaaa	tggattttan	taatacagtt	360
tatattacta	agtacatatc	tggcaaagct	acatgtatac	agaaatcagg	aaccccccca	420
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gcgccaaccc	gtcatgccag	gggacagtgt	ganagtacag	ggncgggcta	ngccaatggg	600
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<210> 203

<211> 786

<212> DNA

<213> Homo Sapiens

<400> 203

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tggaggagga	gcagcaggcc	ctccagaaga	agctgaaggg	gacagaggat	gaggtggaaa	180
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<210> 204

<211> 738

<212> DNA

<213> Homo Sapiens

<400> 204

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aaggaaggca	anatctgctt	caacaacaat	tggccttctt	cncggccngc	tccaattttc	720
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<210> 205

<211> 818

<212> DNA

<213> Homo Sapiens

<400> 205

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cagtttgatc	tcctcttcat	atttatcttc	tttgggtggaa	tactcctcct	ctgaggccat	300
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nctngcncca	attttctccn	ggggcctncc	tttcangggg	tnaagaanaa	atttcaaatt	780
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<210> 206

<211> 927

<212> DNA

<213> Homo Sapiens

<400> 206

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tggaggagga	gcagcaggcc	ctccagaaga	agctgaaggg	gacagaggat	gaggtggaaa	180
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ccttggccag	tgccaaggag	gagaacgtcg	agattcacca	gaccttgga	cagaccctgc	840
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<210> 207

<211> 910

<212> DNA

<213> Homo Sapiens

<400> 207

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<210> 208

<211> 745

<212> DNA

<213> Homo Sapiens

<400> 208

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<210> 209

<211> 965

<212> DNA

<213> Homo Sapiens

<400> 209

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<210> 210

<211> 867

<212> DNA

<213> Homo Sapiens

<400> 210

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gctgtccttt ctttccgtaa gccattctg gttcaatctc cagtcgagcc ttttctcctt      420
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<210> 211

<211> 972

<212> DNA

<213> Homo Sapiens

<400> 211

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<210> 212

<211> 817

<212> DNA

<213> Homo Sapiens

<400> 212

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<210> 213

<211> 756

<212> DNA

<213> Homo Sapiens

<400> 213

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<210> 214

<211> 728

<212> DNA

<213> Homo Sapiens

<400> 214

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<210> 215

<211> 710

<212> DNA

<213> Homo Sapiens

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canaacccaa	agaacatatt	cgtataattg	aaaaattcta	ggtgcttcn	aattgacctt	180
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<211> 824

<212> DNA

<213> Homo Sapiens

<400> 216

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<210> 217

<211> 749

<212> DNA

<213> Homo Sapiens

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<210> 219
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<210> 220
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 <212> DNA
 <213> Homo Sapiens

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<210> 221

<211> 833

<212> DNA

<213> Homo Sapiens

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cggatttgat	togattcata	gaggagctga	aaggtggaac	aaaaaagggg	aagccaaata	360
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aaaggggtga	tccagaacgg	cagagagaga	tggaagaaga	ggaggatgag	gatgaggatg	480
aggatgaaga	tgaggatgaa	cggcagttac	tgggagaatt	tgagaangaa	ctggaaggga	540
tcctgcttcc	gtcagaccga	gaccggctcc	gttcggaggt	gaangctggc	atggagccgg	600
gaactggnaa	acatcatcca	ggagacanga	gaaaganctg	ggacccanat	ggggctgaag	660
aanggatcag	aatccgggat	cgggcaatgc	tggctctcaa	aatcaactct	caacaaantc	720
attaaaaaga	ctggagggga	aaacaagagt	tccaaancct	ggtgaannaa	gcncataaaa	780
aagaagggttg	tcccaaaaaa	gnctcccca	tcaanccaac	cctncaggga	aaa	833

<210> 222

<211> 745

<212> DNA

<213> Homo Sapiens

<400> 222

ggattgatgg	tccagttggt	tatttagaaa	cctgattggt	caagaacatg	gtgggtgctt	60
cacacctttt	tcaactgggat	tgtgctggag	gtgataggca	gcattctacc	atttcctcag	120
caacagaggt	gaaggctcct	caactcagaa	gcacaaattg	taggggacag	ggtgggcagg	180
gaaagggaga	aggaaatccc	aaggcaattc	aatagaagag	ggtaaaacga	ctccaaacat	240
cactaagggc	aggtaggggc	ctgcttgctc	agtgcctgct	aagtgtcctg	ccctccttgc	300
tctctctacc	cacctccact	caaaagatcc	tactgaatct	ccaggtaggc	agcagggaat	360
atcctatcat	taggggacaa	taacaggaaa	agccacagag	gagaggaaga	ggattgagtg	420
agagttcagg	agagcaaata	tcacaggccc	ggtgaggtct	caaggtggct	gccagcaggg	480
gcagcaagca	ttcacccagg	gccccacac	ccacagagtt	gcccagang	tccacaagct	540
cagctccact	ctgctgtttg	gccctcaagg	gttcagggtt	ggggaagtgg	ggaagaggca	600
ngccagtcca	ggaagatctg	gattccgtga	angggatcaag	tgtagtgttg	gtctcagaag	660
tcaaatntc	caagtccctt	gttgccctcc	ccacctggag	aagccccana	cccgnggta	720
attgctcncc	anctccttct	gccgc				745

<210> 223

<211> 747

<212> DNA

<213> Homo Sapiens

<400> 223

actacatcga	tgcggtggac	gagcccttgt	cctgctctta	tgtgctgacc	attcgcactc	60
ctcggtcttg	ccccaccct	ctcctccggc	ccccaccag	tgctgcaccg	caggccatcc	120
tctgtcacc	ttccctacag	cctgaggagt	acatggccta	cgttcagagg	caagccgact	180
caaagcagta	tggagataaa	atcatagagg	agctgcaaga	tctaggcccc	caagtgtgga	240
gtgagaccaa	gtctgggggtg	gcaccccaaa	agatggcagg	tgcgagcccg	accaaggatg	300
acagtaagga	ctcagatttc	tgggaagatgc	ttaatgagcc	agaggaccag	gccccaggag	360
gggaggagg	gccggctgag	gagcaggacc	caagccctga	ggcagcagat	tcagcttctg	420
gtgctcccaa	tgatttttcag	aacaacgtgc	aggtcaaagt	cattcgaagc	cctgctgatt	480
tgattcgatt	catagaggag	ctgaaagggtg	gaacaaaaaa	ggggaagcca	aatataggcc	540
aagagcagcc	tgtggatgat	gctgcagaag	tcctcagag	ggaaccagag	aangaaaggg	600
gtgatccaga	acggcagaga	gagatgggaa	ngaagangan	gatgaggatg	aggatgaggg	660
atgaaagann	aaggatgaaa	cgggcaagtt	actggggaan	aattttgana	aagggaactg	720
ggaaagggat	tcctggcttt	cgttca				747

<210> 224

<211> 618

<212> DNA

<213> Homo Sapiens

<400> 224

gatggtccag	ttgtttatatt	agaaacctga	ttgttcaaga	acatggtggg	tgcttcacac	60
ctttttcgct	gggattgtgc	tggagggtgat	aggcagcatt	ctaccatttc	ctcagcaaca	120
gagggtgaagg	ctcctcaact	cagaagcaca	aattgtaggg	gacagggtgg	gcagggaag	180
ggagaaggaa	atcccaaggc	aattcaatag	aagagggtaa	aacgactcca	aacatcacta	240
agggcaggtg	ggggcctgct	tgctcagtgc	ctgctaagt	tcctgccctc	cttgcctct	300
ctaccacact	ccactcaaaa	gatcctactg	aatctccagg	tangcancan	ggaatatcct	360
atcattaggg	gacaatanca	ggaaaagcca	cagaggagag	gaagaggatt	gagtganaag	420
ttcangacag	caaattatca	caggcccggt	gaggtctcaa	ngtgngctgc	caacaagggg	480
caancagcat	tcaccangg	gccccacacc	cacnnnagtt	gccccagagg	tcacancctc	540
ancctccan	ctgcengttt	ggcctcaag	gggttccaan	gttcngaaa	gtgggggagg	600
aaggcanccc	antcccag					618

<210> 225

<211> 765

<212> DNA

<213> Homo Sapiens

<400> 225

caaacatcag	agactgcatg	ctggagagaa	acttgaagaa	tgtgagaaaa	ccttcagcaa	60
ggatgaggag	cttagaaaag	agcagagaa	tcaccaggaa	aagaaagttt	attggtgtaa	120
tcagtgtagt	aggaccttc	agggcagctc	agatctcacc	agacatcagg	taactcatac	180
aagagagaaa	ccatatgaat	gtaaagaatg	tgggaaaact	caatcagagc	tcagaccttc	240
tgagacatca	tagaattcac	agtggagaaa	aaccttacgt	atgcaataaa	tgtggggaat	300
cttttaggag	cagctcagat	cttattaaac	accatcggtg	tcatactgga	gagaaacctc	360
atgaatgtag	tgaatgtggg	aaagtcttta	gccagagggtc	ccaccttgct	acacaccaga	420
aatccacac	tggagagaag	ccctatcagt	gcaactgaatg	tgaaaaagcc	ttcaggcggc	480
gttactcct	tattcaacgt	cggagaattc	atagtgtgga	gaaaccctat	gaatgtaagg	540
aatgtgggaa	actcttcagt	tggcacacag	ctttcctcaa	acatcagaga	ctgcatgctg	600
gagagaaaact	tgaagaatgt	gagaaaacct	tcagcaagga	tganggagct	taggggagag	660
cagaaaattc	accanggaag	agaaagcctt	attggngta	atcagtgtgg	tanggctttc	720
caagggcagc	tcangacctc	atcgggccat	caggtaactc	aatac		765

<210> 226
 <211> 791
 <212> DNA
 <213> Homo Sapiens

<400> 226
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 gtgtatgggc ctccaccccc caacttctcc atccccctca tccctatggg tgtgctgcat 120
 tgcaacgtcc ctgaacacca taacttagag aatgaagttt ctagattaga agacataatg 180
 cagcatttaa aatcaaagaa gcgggaagaa aggtggatga gagcatccaa gcggcagtcg 240
 gagaaagaaa tgggaagaact gcatcataat attgatgac ttttgcaaga gaagaaaagc 300
 ttagagtgtg aagtagaaga attacataga actgtccaga aacgtcaaca gcaaaaggac 360
 ttcattgatg gaaatgtaga gagtcctatg actgaactag aaatagaaaa atcactcaaa 420
 catcatgaag atattgtaga tgaaattgag tgcattgaga agactcttct gaaacgtcgc 480
 tcanagctca gggaagctga ccgactcctg gcagaggctg agagtgaact ttcattgact 540
 aaagaaaaga caaaaaatgc tgttgaaaag ttcactgatg ccaagagaag tttattgcaa 600
 actgagtcag atgctgaggg aattagaaaag gagagctcan gaaactgctg ttaanctcgt 660
 caaanctgat cagcagctaa gatcgctcca agctgatgca aaaggatttg gancancaca 720
 angatcaagc aagaagaaat cttgaaaaga aattaacnaa aatttntnca gcaaaagact 780
 cagacttcaa a 791

<210> 227
 <211> 687
 <212> DNA
 <213> Homo Sapiens

<400> 227
 gattgttatc ttttattttc atatgaaaaa tagattttta gcaaaattca aaaataactc 60
 gacactataa aaanagaggg ccttaagtac attctttttg ttaataagat ttaccagttt 120
 gtaggttcaa atatgcagtt aaaatcactg ttttttttta aacatgttac gaagattaaa 180
 aaaaaaaagg ctcagccaca tgttggttta aattcccata tgcaactatt cccatattgta 240
 ctatgtacaa gtgatttata aaaacattgg cattaatggt acaggcaaag taaactacag 300
 tggagtttca naatctcagt tcaactgcac ttgattaaaa aaaccatgtg acattccaat 360
 tatgaagtca gtgaggtagt ggaggtgttt tcttggaata tatttacaca agacagtatt 420
 cctcatctgg ctgaggcatt cttttccgga ttttgccaa gttganagtc ctctgtgagg 480
 gaagactcca agctgagaca gactgggtga tgacgctgaa tctgcaaagg tgccgtgtga 540
 ccaattcccc ctaanagcat cctacttgct tccncaaact gtgntaaagt gccctctgtc 600
 ctgccgcttt cttttaatna aaacttctgg cttngcttgg ggcanacagt gtcgganttg 660
 gggccttgag tcnngcttcc cggggaa 687

<210> 228
 <211> 810
 <212> DNA
 <213> Homo Sapiens

<400> 228
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 gcagtgaggg ggccggcggg cgtgggccga gtggccgcgg gcgccatgga gggggtgctg 120
 tacaantgga ccaactatct gagcgttggt cagcctcgat ggttctctct ctgtggggga 180
 atattgtcct attatgattc tctgaagat gcttgaaaag gttgcaaagg gagcatacaa 240
 atggcagtc gtgaaattca agttcattct gtagataata cacgcattgga cctgataatc 300
 cctggggaac agtatttcta cctgaaggcc agaagtgtgg ctgaaagaca gcgggtggctg 360
 gtggccctgg gatcagccaa ggcttgctg actgacagta ggaccagaa ggagaaagag 420
 tttgctgaaa aactgaaaa cttgaaaacc aaaatgtcan aactaagact ctactgtgac 480
 ctcttgttcc ancaagtaga ttaaaacata agaagtgacc acaactggtg tgtccaattc 540

tgaggtaaag	gagtcttcca	ctctggttgt	ttcgtangag	ggaattgatg	tgggaaacttt	600
gctgaaatca	anctgntata	ctttttctga	aagaccttgg	taagaattca	tgcanatngc	660
aaattgcagc	cttnaanctc	ctgaagcctn	cttctaaccg	gcactccaac	canggaatna	720
anctnaagct	gggccaatgg	ctccaaaagt	ccaacnaaag	gttaaaanat	cccagctcaa	780
atttgggcng	caaacaaaag	gcaatccaac				810

<210> 229

<211> 552

<212> DNA

<213> Homo Sapiens

<400> 229

gtaaatttgt	ttgagttcat	tgtagattct	ggatattagc	ccttttgtca	gatgagtaga	60
ttgcaaaaat	tttctcccat	tctgtagggt	gcctgttcac	tctgatggta	gtttcccttg	120
ctgtgcggaa	gctctttagt	ttaattagat	cccatttgtc	aatttcgggt	tttgttgcca	180
ttgctttcgg	tgtttttagac	atgaagtcc	tgcccatgcc	tatgtcctga	atggttttcc	240
taggttttct	tctagggttt	ttatggtttt	aggtctaaca	tttaagtctc	gaatccatct	300
tgaattaatt	tttgtataag	gtgtaaggaa	gggatccact	ttcagctttc	tacgtatggc	360
tagccagttt	tcccancacc	atattattaaa	tagggaatcc	tttccccant	tcctgttttt	420
gtcangtttg	tcaaagatca	natggctgta	natatgcanc	attattttccg	agggctctgt	480
tcngttccat	tggtctacat	ttccgttttg	gttcnngtac	catgctgttt	tttgttacng	540
gtanaccttg	gt					552

<210> 230

<211> 842

<212> DNA

<213> Homo Sapiens

<400> 230

ctcatcagtt	agaagaaaaa	gaaaatcaaa	ttaagagcat	gaaggctgat	attgaaagtc	60
ttgtaacaga	aaaagaagcc	ttacagaagg	aaggaggcaa	tcagcaacag	gctgcttctg	120
aaaaggagtc	ttgtataaca	cagttgaaga	aagagttatc	tgaaaacatc	aatgctgtca	180
cattgatgaa	agaagagctt	aaagaaaaaa	aagttgagat	tagcagtctt	agtaaacaac	240
taactgattt	gaatgttcag	cttcaaaaata	gcatcagcct	atccgaaaaa	gaagcagcca	300
tttcatcact	aagaaagcag	tatgatgaag	aaaaatgtga	attgctggat	caggtgcaag	360
atattatctt	taaagttgac	actctgagta	aagagaaaat	ttctgctctt	gagcaggtag	420
atgactggtc	caataaatcc	tcagaatgga	agaagaaagc	acagtcaaga	tttacacagc	480
atcaaaacac	tgttaaagaa	ttgcagatcc	agcttgagtt	aaaatcaaag	gaagcttatg	540
aaaaggatga	gcagataaat	ttattgaagg	aagagcttga	tcagcaaaaat	aaaagatttg	600
attgttttaa	gggtgaaatg	gaagacgaca	agagcaagat	gggagaaaaa	ggagtctaata	660
ttagaaacag	agttaaagtc	tcaaacagca	agaattatgg	gattagagga	ccatattanc	720
caagaaaact	atattggaaat	tagagtcctt	aaatngaaag	ttccttaaaa	aattacaatc	780
aacaaaaagg	atattggacc	acaaagnaat	tgggtcaaaa	aaccttcaac	aantttcaag	840
ga						842

<210> 231

<211> 781

<212> DNA

<213> Homo Sapiens

<400> 231

atatagtaaa	taaactttat	ttatctgttt	ctcagagatg	acaactgcaa	caatcacaga	60
tttgcataca	atacagttat	gtattggcta	ttcacaatct	acagtagtgt	tttttctct	120
gaaaaatata	agtacaaaag	ctaagtaaac	aatgagggtac	tgccatttgg	gattttttac	180
atgtcttagc	ttaaagaact	ggtcttttagc	aaatattcaa	cagatcaacc	tgaataaaat	240

agtcaattaa	atgctcta	ttatcagaaa	aaatccacta	agtttcacct	caaaatgtat	300
tgcacaagtc	tttttaaaaa	atcaccctaa	aaataaatag	gaaaggtaag	ccgttcttta	360
aaaagaatgg	atgaaaggaa	tattatgtaa	gcccataaag	cagggttaagt	tatcaaaaata	420
tctttttaaac	aacataaaac	tcttcccaag	agaaaaactga	agaaaaaact	atcaccatttt	480
ctccactgat	aaaatctatt	ttaaaggcag	tctgcaactt	atctgtgggc	cagattttttc	540
ttgggtcttt	tggctacatg	aggggccctg	aatgacaact	tcattctcaa	agagtagcaa	600
agtgtggaca	agttttccaa	gcagcangtc	acccaatgtc	actcttcctc	aagatgaagg	660
atcggagcca	tgacacatgt	ttaactaagc	acagaccgga	tgggtttacc	cagaagatac	720
cactggcaan	ggtgaagtaa	acatcaggcc	gaggcaacct	tccccntttc	aaaaantttt	780
c						781

<210> 232

<211> 767

<212> DNA

<213> Homo Sapiens

<400> 232

ggttatatagt	aaataaactt	tatttatctg	tttctcagag	atgacactgc	caacaatcac	60
agatttgc	acaatacagt	tatgtattgg	ctattcacaa	tttacagtag	tgttttttcc	120
tctgaaaaat	ataagtacaa	aagctaagta	aacaatgagg	tactgccatt	tgggattttt	180
tacatgtctt	agcttaaaga	actgggtctt	agcaaatatt	caacagatca	acctgaataa	240
aatagtcaat	taaatgctct	aatttatcag	aaaaaatcca	ctaagtttca	cctcaaaatg	300
tattgcacaa	gtctttttta	aaaatcaccc	taaaaaataa	taggaaagg	aagccgttct	360
ttaaaaagaa	tggatgaaag	gaatattatg	taagcccata	aagcagggtta	agttatcaaa	420
atatctttta	aacaacataa	aactcttccc	aagagaaaac	tgaagaaaaa	actatcacca	480
tttctccact	gataaaatct	attttanagg	cagtctgcaa	cttatctgtg	ggccagattt	540
ttcttgggtct	tttggctaca	tgagggggccc	tgaatgaaaa	cttcattctc	aaaggagtag	600
caagtgtggg	acagttttcc	aagcagcagt	cacccaatgt	cactcttctt	caagatgaaa	660
gatcggagnc	atgacacatg	ttaacctaa	ncangactg	gaggggtttac	ncangaagat	720
acactgcgaa	ggtgaaagtt	aaacatcaag	ccgaggaacc	tccccctt		767

<210> 233

<211> 879

<212> DNA

<213> Homo Sapiens

<400> 233

gggagtttaa	tacacagctg	gcacaaaagg	aacaagagct	ggaaatgacc	ataaaaagaaa	60
ctatcaataa	ggcccaggag	gtggaggctg	aactttttaga	aagccatcaa	gaagagacaa	120
atcagttact	taaaaaaatt	gctgagaaag	atgatgatct	aaaacgaaca	gccaaaagat	180
atgaagaaat	ccttgatgct	cgtgaagaag	aaatgactgc	aaaagtaagg	gacctgcaga	240
ctcaacttga	ggagctgcag	aagaaatacc	agcaaaagct	agagcaggag	gagaaccctg	300
gcaatgataa	tgtaacaatt	atggagctac	agacacagct	agcacagaag	acgactttta	360
tcagtgattc	gaaattgaaa	gagcaagagt	tcagagaaca	gattcacaa	ttagaagacc	420
gtttgaagaa	atatgaaaag	aatgtatatg	caacaactgt	ggggacacct	tacaaagggtg	480
gcaatttgta	ccatacggat	gtctcactct	ttggagaacc	taccgaattt	gagtattttgc	540
gaaaagtgtc	ttttgagtat	atgatgggtc	gtgagactaa	gacctgggca	aaagttataa	600
ccaccgtact	gaagttccct	gatgatcaga	ctcagaaaat	tttgggaaaa	gagaagatct	660
cggctgatgt	ttacttcacc	tcgcagtgg	atcctcngag	taaaccatca	gtcgtgccta	720
agtttacatg	tgtcatgggt	ccgattcttc	atcctttgaa	gaaagagtg	acattgggggt	780
naccggctgc	cttgggaaaa	ctgtccanac	nttgcnaacn	ccttggggaa	atggaagntt	840
ttccanttca	aggggccctt	caangnttgc	ccaaaagag			879

<210> 234

<211> 780

<212> DNA

<213> Homo Sapiens

<400> 234

aaacttttatt	tatctgtttc	tcagagatga	cactgccaac	aatcacagat	ttgcatacaa	60
tacagttatg	tattggnnng	gcacaattta	cagtagtggt	ttttcctctg	aaaaatataa	120
gtacaaaagc	taagtaaaca	atgaggtact	gccatttggg	atTTTTTaca	tgtcttagct	180
taaagaactg	gtcttttagc	aatattcaac	agatcaacct	gaataaaata	gtcaattaaa	240
tgctctaatt	tatcagaaaa	aatccactaa	gtttcacctc	aaaatgtatt	gcacaagtct	300
ttttaaaaaa	tcaccctaaa	aataaatagg	aaaggtaagc	cgttctttta	aaagaatgga	360
tgaaaggaat	attatgtaag	cccataaagc	aggtttaagt	atcaaaatat	cttttaaaca	420
acataaaaact	cttcccaaga	gaaaactgaa	gaaaaaacta	tcaccatttc	tccactgata	480
aaatctattt	taaaggcagt	ctgcaactta	tctgtgggcc	agatttttct	tgggtcttttg	540
gctacatgag	gggccctgaa	tgaaaacttc	attctcaaa	agtagcaagt	gtggacaagt	600
tttccaagca	gcagtcanc	aatgtcactc	ttcttcaaga	tgaaagatcg	gagccatgac	660
acatgttaac	taagcacaga	cntgatggtt	tactncagaa	gattaccact	gcnaagggtga	720
aagttaaaca	tcaagncgag	catncntctc	tttccaaaa	ttttccggng	tccggattca	780

<210> 235

<211> 780

<212> DNA

<213> Homo Sapiens

<400> 235

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gagaggagct	ccaaatggac	cagcaggcaa	agaaacatct	gcaagaggag	tttcatgcat	120
cttttagagga	gaaagatcag	tatatcagtg	ttctccaaac	tcagggtttct	ctactgaaac	180
aacgattacg	aaatggcccc	atgaatgttg	atgtactgaa	accacttctc	cagctggaac	240
cacaggctga	agtcttcact	aaagaagaga	atccagaaag	tgatggagag	ccagtagtgg	300
aagatggaac	ttctgtaaaa	acactggaaa	cactccagca	aagagtgaag	cgtcaagaga	360
acctacttaa	gcgttgtaag	gaaacaattc	agtcacataa	ggaacaatgt	acactattaa	420
ctagtgaaaa	agaagctctg	caagaacaac	tggatgaaag	acttcaagaa	ctagaaaaga	480
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cagatgacta	cccaagggag	aggaattacg	ggaacaagan	agaaaagtcc	gaaagaactg	720
cntttgaggg	aacttgaaaa	agccttgagt	acagnccaaa	aanacagnng	aagccaccgg	780

<210> 236

<211> 711

<212> DNA

<213> Homo Sapiens

<400> 236

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ctgacaattt	ctgtgtgagt	atctcaattt	cttctctctg	tccttctctc	atttgtaaaa	120
tcatattttt	cttttccacc	aagatttgct	ttgtctgttc	ctgttctttg	ttaccatctt	180
caagtttgga	ctcatagact	tgggttaaa	attttacttt	ttgctccatt	tcactatttt	240
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gctcatgtgt	ggcactctgg	taagactgaa	aaacgtccag	cttagcagat	gcctgctgga	480
gttccccttc	agacctttta	atatctgcct	ccaaattttt	tacatgagcc	tgatgctctt	540
tcaaagtgtt	gtcccttttc	ttcaagagaa	gctcaagttg	nttaanttga	tcttttaaa	600
ccttctcaan	tcttccggga	tanaaaacnt	cgtgttcttt	naatgagaac	ggtcaacntg	660

ccggctgggt gataantttt ccgttcance anccttgggg ctccaaattc c 711

<210> 237
 <211> 658
 <212> DNA
 <213> Homo Sapiens

<400> 237
 atagtaaata aactttatatt atctgttttct cagagatgac actgccaca atcacagatt 60
 tgcatacaat acagttatgt attggctatt cacaatttac agtagtggtt tttcctctga 120
 aaaatataag tacaaaagct aagtaaaca tgaggtactg ccatttgagg ttttttacat 180
 gtcttagctt aaagaactgg tcttttagcaa atattcaaca gatcaacctg aataaaatag 240
 tcaattaaat gctctaattt atcagaaaaa atccactaag tttcacctca aaatgtattg 300
 cacaagtctt tttaaaaaat caccctaaan ataaatagga aaggtaagcc gttcttttaa 360
 aagaatggat gaaaggaata ttatgtaagc ccataagagc aggttaagtt atcaaaatat 420
 ctttttaaca ncataaaaact cttcccanga gaaaactgaa gaaaaaacta tcaccatttc 480
 tccactgata aaatctattt taaaggcagt ctgcanccta tctgtgggcc aagatttttc 540
 ttggnctttt ggctacatga gggggccctg gaatgaaaaa cttcattccc aanggagttt 600
 gcnaggtgtg ggacagggtt tccaaggcaa gcaagtnagc caaatngtca gctcttcc 658

<210> 238
 <211> 678
 <212> DNA
 <213> Homo Sapiens

<400> 238
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 agatttgcat acaatacagt tatgtattgg ctattcaciaa tttacagtag tgttttttcc 120
 tctgaaaaat ataagtacaa aagctaagta aacaatgagg tactgccatt tgggattttt 180
 tacatgtctt agcttaaaga actggtcttt agcaaattt caacagatca acctgaataa 240
 aatagtcaat taaatgctct aatttatcag aaaaaatcca ctaagtttca cctcaaaatg 300
 tattgcacaa gtcttttttaaaaatcacc taaaaataaa taggaaaggt aancggttct 360
 ttaaaaagaa tggatgaaag gaattattatg taagcccata aagcagggtta agttatcaaa 420
 atatctttta aacaacataa gaactcttcc caaggagaaa actgaannaa aaaactatca 480
 ncatttcnnc actgataaaa tctantttta aggggnagtcn gcaacttanc tgtgggccag 540
 atttttccgt ggggcttttg ggctacantn agggggccct gaatgaaaaa nttcaattcc 600
 ncaaatgnng tagcaaatg tgggncangt ttttccaaag cagncaantt cancccnana 660
 tgtcactcct tctttcaa 678

<210> 239
 <211> 1402
 <212> DNA
 <213> Homo Sapiens

<400> 239
 gggagttttaa tacacagctg gcacaaaagg aacaagagct ggaaatgacc ataaaagaaa 60
 ctatcaataa ggcccaggag gtggaggctg aactttttaga aagccatcaa gaagagacaa 120
 atcagttact taaaaaaatt gctgagaaag atgatgatct aaaacgaaca gccaaaagat 180
 atgaagaaat ccttgatgct cgtgaagaag aaatgactgc aaaagtaagg gacctgcaga 240
 ctcaacttga ggagctgcag aagaaatacc agcaaaagct agagcaggag gagaacctg 300
 gcaatgataa tgtaacaatt atggagctac agacacagct agcacagaag acgactttta 360
 tcagtgattc gaaattgaaa gagcaagagt tcagagaaca gattcacaat ttagaagacc 420
 gtttgaaaga atatgaaaag aatgtatatg caacaactgt ggggacacct taaaaggtg 480
 gcaatttgta ccatacggat gtctcactct ttggagaacc taccgaattt gatttttgc 540
 gaaaagtgtc ttttgagtat atgatgggtc gtgagactaa gacctggca aaagttataa 600

ccaccgtact	gaagttccct	gatgatcaga	ctcagaaaaat	tttgaaaga	gaagatgctc	660
ggctgatgtt	tacttcacct	cgcagtggta	tcttctgagt	aaaccatcag	tctgtgctta	720
gttaacatgt	gtcatggctc	cgatcttcat	cttgaagaag	agtgcattg	ggtagctgct	780
gcttggaana	ctgtccacac	ttgctactct	ttgagaatga	agttttcatt	cagggccct	840
catgtagcca	aaagaccaag	aaaaatctgg	cccacagata	agttgcagac	tgcttttaaa	900
atagatttta	tcagtggaga	aatggtgata	gttttttctt	cagttttctc	ttgggaagag	960
ttttatgttg	tttaaaagat	attttgataa	cttaacctgc	tttatgggct	tacataatat	1020
tcctttcatc	cattcttttt	aaagaacggc	ttacctttcc	tatttatatt	tagggtgatt	1080
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ttttgtactt	atatttttca	gaggaaaaaa	cactactgta	aattgtgaat	agccaataca	1320
taactgtatt	gtatgcaa	ctgtgattgt	tggcagtgct	atctctgaga	aacagataaa	1380
taaagtttat	ttactatata	ac				1402

<210> 240

<211> 760

<212> DNA

<213> Homo Sapiens

<400> 240

gtgcagtttc	tcttatatc	ctcacatatg	tgctttcatt	catctttcgc	aagtggagaa	60
aaaataatgg	cttttggtct	tttggctttt	ttattatctt	aatatgtgta	tcacacaatta	120
tggtatcaac	tcaatatgaa	aaactcaact	taattttgtg	catgattttc	ataccttctt	180
tcactttgct	ggggatgtc	atgttattga	tccagctcga	ctttatgaga	aacttggaca	240
gtctggacaa	tagaataaat	gaagtcaata	aaaccattct	tttaacaacc	ttaataccat	300
accttcagag	tgttattttc	ctttttgtca	taagtggtct	ggaaatgaag	tatggaaatg	360
aaataatgaa	taaagaccca	gttttcagaa	tctctccacg	gagtagagaa	actcatccca	420
atccggaaga	gcccgaagaa	gaagatgaag	atgttcaagc	tgaaagagtc	caagcagcaa	480
atgcactcac	tgctccaaac	ttggaggagg	aaccagtcac	aactgcaagc	tgtttacaca	540
aggaatatta	tgagacaaag	aaaagttgct	tttcaacaag	aaagaagaaa	atagccatca	600
gaaatgtttc	cntttgtgtt	aaaaaagggtg	aaagttttgg	ggattaccta	ggacacaaatg	660
ggagctggta	aaagtacttc	cattaaaatg	ataacntggg	tgacaaaagc	caaactgcan	720
ggagtggttg	gtgttacaaa	ggnagcagan	gcacnnggta			760

<210> 241

<211> 745

<212> DNA

<213> Homo Sapiens

<400> 241

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cncnggtatt	acatcaatac	agctataaca	ttaatgcagc	aattatataa	cacaaaagtg	120
ctataatgac	atgggaaatg	ttcatgaact	gtgaggtgaa	aagatacaga	aatgactat	180
gcctacngat	actacctttg	aaaaaggatc	cataaaaaat	acattgaata	taagttggct	240
aaagaaaata	ttaactgcgg	tactttctta	cagattangg	ctancttctt	ccatataact	300
tcaatatgta	ctaaaattca	catgcattta	ttttataatc	agaatgtcat	tataattaaa	360
tgttangetg	tgccattttca	tcagttttatc	anaccttctt	atagtcaatg	tcacattaaa	420
ttagaatccg	agtaataaan	gtttaaaaat	anctgataca	tttgaagttc	aggctaaaaa	480
cctcatattt	ttatttgtaa	aatgtttctca	ntgttagctt	tattgataat	aaccgataac	540
caacctataa	ttgtangatt	tttaaattat	ttttaagcac	aaantagacc	catgttgggg	600
atgaataaca	tgctngatgt	tgtnaatttt	ggctcnacnac	ttttcccaaa	aatttccttg	660
tttccttcan	ccnaaatttt	taaaantgaa	aactgtatca	attatggaan	ggtttattaa	720
aangtttnc	tttggttaacc	ngaag				745

<210> 242
 <211> 818
 <212> DNA
 <213> Homo Sapiens

<400> 242
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 agaacctgct gaaattaaga tcatcagaga agcatataag aaggcctttt tatttggttaa 120
 caaagggtctg aatacagatg aattaggtca gaaggaagaa gcaaagaact actataagca 180
 aggaatagga cacctgctca gagggatcag catttcatca aaagagtctg aacacacagg 240
 tcctgggtgg gaatctgcta gacagatgca acagaaaatg aaagaaactc tacagaatgt 300
 acgcaccagg ctggaaattc tagagaaggg tcttgccact tctctgcaga atgatcttca 360
 ggaggtgccc aagttatata cagaatttcc acctaaagac atgtgtgaaa aattaccaga 420
 gcctcagtct ttagtttcag ctctcagca tgctgaagta aatggaaaca cctcaactcc 480
 aagtgcaggg gcagttgctg cacctgcttc tctgtcttta ccatcacaaa gttgtccagc 540
 agaagctcct cctgcttata ctctcaagc tgctgaaggt cactacactg tatcctatgg 600
 aacagattct ggggagtttt catcagttgg agaggagttt tataggggaat cattctcagc 660
 caacggcctc ttnagaacct taagggtctg gattcangat gaaattgatt ttgataccaa 720
 atgggagtag annttttttt tgtaaactct gcaangggga ngttatgcan cttcgtancc 780
 ccggggtacc ttcnaattgt gaagggtttt ggnntaaa 818

<210> 243
 <211> 799
 <212> DNA
 <213> Homo Sapiens

<400> 243
 aatttcttga agtacttttt taatccaatt aagctgataa taatcacttc gaattttaat 60
 acaatacaat catgttccca aatttccnag gtcataaca atacagtctc aatacaaaag 120
 acgtaataat ctatttttat tcatttttaa tcaaagaaac cattccattt cctaacaac 180
 aggtaagtta caaaagtagt ccatttttact tttcatcagt ctttccctgt tttgaacaag 240
 tctttttgag aattcttagt tttagttttt gtttagctta cacactgaaa attttgagaa 300
 gcatctaaaa aaatccacaa ttagtgcaaa aagaggggac aatactttta gtcattcctt 360
 ctataaaaaa aattaagggtt actaaatgcc aattttttaag caaatatata gtttcttatt 420
 tgccctctga aagacagcag atataaaaa agttcaatat taggtttaac aagggttgaa 480
 caacacatgt actatcagct ttattttacc tgcaaaaata ttttagctac acttggaaaa 540
 aaaataaact tgagaatata acttcacatt tctaaggcca gatgcaagaa tacttaatct 600
 tttcctttta aatagaagac atgccataaa atttatgaaa agttaatttg taggaatggn 660
 atacatttaa aaaatacngg ttaaacngg tgagggaatt ccacatttgg cctatttaac 720
 aaaaatttta aaccaatttt caaaaggggc tttggggtaa aaagtngatt cccaagcaac 780
 ntcaancant ttaaccttc 799

<210> 244
 <211> 726
 <212> DNA
 <213> Homo Sapiens

<400> 244
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 tctacttcac cagcagcagc gttaattcat ctgcctacac tatttacatg ggaaaagata 120
 aatatgaaaa tgaagatctg atcaagcatg gctggcctga agatatctgg tttcatgtgg 180
 acaaactctc ttgggtcat gtataccttc gattacataa gggagagaat atagaagaca 240
 tcccaaagga agtgctgatg gactgtgccc accttgtgaa ggccaatagc attcaaggct 300
 gcaagatgaa caacgttaat gtggtatata cgccgtgggtc taacctgaag aaaacagctg 360
 acatggatgt ggggcagata ggctttcaca ggcagaagga tgtaaaaatt gtgacagtgg 420

agaagaaagt	aaatgagatc	ctgaaccgat	tagaaaagac	caaagtcgag	cggttcccag	480
acctancagc	agagaaagaa	tgcagagatc	gtgaagagag	gaatgagaaa	aaagcccaaa	540
ttcaggaaat	gaaaaagaga	gaaanagaag	aaatgaagaa	gaanagggaa	atggatgaac	600
ttangagcta	ttcatcacta	atgaaagttt	gaaaatatgt	cttcanatca	ggatggcaat	660
ggattcagat	gaattcatgt	taaaaggaga	aaaggngaaa	aaggaccttt	gaaaaatttg	720
aatgtt						726

<210> 245

<211> 592

<212> DNA

<213> Homo Sapiens

<400> 245

ccagattaaa	aaaatggat	tttattataa	cttttaaaat	tgcggaacat	cagactgaat	60
atcatcagac	acatacacia	aaccactcat	ctctaaagtc	attttctata	ccctctcaaa	120
atttggccag	tgagttttgc	ctcagggaa	tttccagttc	aaccccatat	accaacatgg	180
aataaatgga	aacactagcc	ttttggtttt	gcccanaagtt	ccaaagtgtc	attacaggtg	240
gaatatctgc	tgcaggaagt	cattcttgc	gctgtgggtg	tgagtaaaat	gcttagttcc	300
ttctaaaatc	ataattgcaa	tatggacttc	tgcttcacgc	tgcattcctaa	ggcacaaatc	360
aggtaacctc	catctcccaa	atgatcaaca	ggagcactcc	atcctatttt	accctcaatg	420
cnganaaatt	acncctgggc	ccanaagttg	tcacataggt	ggcttgggtt	acttgggggt	480
caggcaacaa	ctgccacagg	ccccagcttg	atgaanacca	tcnatttctt	taaaatatgt	540
tggnnactaa	gatggaggcc	tccggcncan	agggaancan	nggacataaa	ac	592

<210> 246

<211> 821

<212> DNA

<213> Homo Sapiens

<400> 246

aggatgaaga	gctggagagc	gccgaggagc	acgagcgcag	ctgtcggggc	cgcgagtcgg	60
acgaagacac	tgaggatgct	agtgaactcg	acctggcaaa	gcatgatgaa	gaagactatg	120
tagaaatgaa	ggaacagatg	tatcaggaca	aactggcttc	tctcaagagg	cagttgcaac	180
aactgcaaga	aggtaacatta	caggaatatc	agaagagaat	gaaaaaacta	gatcagcagt	240
acaaagagag	gatacggaat	gcagaactct	tcctccagct	ggaaactgaa	caagtggaac	300
gaaattacat	taaagaaaag	aaggcagcag	tgaaagaatt	tgaagacaag	aaggttgagc	360
tgaaagagaa	cctgattgct	gagctagaag	aaaagaagaa	aatgattgaa	aatgaaaagc	420
tgacaatgga	actgactgga	gattctatgg	agggtgaacc	tatcatgacc	agaaagtgtc	480
ggaggcgacc	aaatgatccc	gtcccatccc	cagacaagag	gaggaaacct	gctccagccc	540
agctaaacta	tttggttaaca	ggatgaacag	atcatggagg	atctgagaac	attaaataag	600
cttaagtcac	ccaagagacc	agcatctcca	tcctctcctg	agcacttgcc	tgcaacaccc	660
gccggaatct	ccaagcccca	gaggttcnaa	agccccggat	anaagaatgg	caaacctgtt	720
actatgacaa	aaagatgggt	accacaagag	ccaaggccat	cctatcctgg	angtcaaagg	780
gacaaaccan	gaaactgaag	cctgcctnat	taagtttccg	t		821

<210> 247

<211> 639

<212> DNA

<213> Homo Sapiens

<400> 247

gttacacaaa	gcattttattt	ctctgagaag	gccgagagcc	acgagaattc	atcatctcct	60
gctaggacct	ctgccccaa	cttctgggca	aatagtgaat	tggacgcgac	agggaaagta	120
gctacgtgat	ccactaatca	gattcaaaac	atgaaaatgc	actggagagt	gtatcccttc	180
ctgctcttct	ccatggtaga	gagacttaaa	gataatcaat	aaaaatagct	gtcccttcaa	240

actcagagga	ggttttcaaa	aacaagtata	agcaaaaaat	aaagaaataa	aaggaaagta	300
aatcaaacc	cccaatacgc	ctgaaagtaa	aacagtctca	tggtagactga	tgtctggaan	360
aagttgaggc	agaaaagact	gacaaagttg	gaangcatcc	cggccacaaa	agtgccnaa	420
aagaattcan	tgcagtgtct	tccatttcca	aggetgagta	actattccca	gntaagttaa	480
catttttcna	nttaaggana	nanogaanac	anntncatnt	ctanatccca	ctccagaaat	540
anggtcaatg	agaangangc	actgtannna	aagtcaagna	gctggancnc	ccgggcggnt	600
tnaccaaga	gcccggcgct	nnaagcctgg	gccaagct			639

<210> 248

<211> 846

<212> DNA

<213> Homo Sapiens

<400> 248

aacaggatgt	caaaaattaa	actgcgcttt	ccatcacaat	agaggacgat	atgttgatgg	60
ccttttctta	cctccgagca	aaactgtgtt	gcccactgtg	cctgagtcac	cagaagagga	120
agtgaaggct	agccaacttt	cagttcagca	gaacaaattg	tctgtccagt	ccaatccttc	180
ccctcagctg	cggagcggtta	tgaaagtaga	aagttccgaa	aatgttctta	gccccacgca	240
tccaccagtt	gtaattaatg	ctgcagatga	tgatgaagat	gatgatgatc	agttttctga	300
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acgagtgact	tctgtccgga	aacctgcagt	caatataaag	caaggtgaat	gtttgaattt	420
tggaataaaa	actcttgagg	aaattaagtc	aaagaaaatg	aaggaaaaat	ctaagaagca	480
aggtgagggt	tcttcaggag	tttccagttc	tttactccac	cctgagcccg	ttccaggtcc	540
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agaacccttg	gttagattga	gtcttactga	gagactgggg	aaacgaaaat	tttcagcagg	660
cggtgacagt	gatcctccat	taaagcgtag	cctggcacan	aggctaaggg	aagaaagttg	720
aagctccaga	aactaacant	gacaaaacac	caangaaagc	tcaagtttcc	aagtccccct	780
aaaggggcga	attaggtcatg	tcagccngga	ttcaagataa	tnagggatgc	aacaagatta	840
aaggtt						846

<210> 249

<211> 763

<212> DNA

<213> Homo Sapiens

<400> 249

gactttctta	catcagtttt	attttaaaca	caaacaagta	tttctctttc	tgtaagggca	60
aatggttcaa	ataatgcgga	acacgaaaca	ttgactaata	caagtgtctt	aaatatgaaa	120
caaaattatt	ttttaaaaaa	gcaaaaagaat	aaagaatata	tacaaaaggg	acctggaatc	180
tgtaagctga	ttccaaaaat	gaaataagta	gaaaatccat	ggtgaaacct	gaacattcta	240
cctctgtctt	ggagaagggc	tatcatacaa	cattcagtc	gctgaagatg	gattggtaga	300
ggtgtgtcta	tacataaact	tcagtcattt	ttgcttgtgc	agaatcatcc	caatcttccc	360
aagactgaat	gggcagtcct	gtggctttct	tccttttcca	tattcccaac	aaggctacgt	420
gaagttcaac	tcttgatgag	ccgcttacaa	cagcagttcc	ttaggagcca	acatgacagg	480
tgggtcagat	ttccctatga	gaaacaaaac	tggccacct	cagcaaaaata	tcaaaatggg	540
taagtccttc	cttctctctc	ctcctgatta	tatacaacat	atctcctttc	aagactatta	600
tttccatcat	gccttatctc	ttcacaaaac	taaaccttga	ngtgatatga	angaaaccaa	660
catcaagaaa	agaaaactca	attcagaaat	gaanaaaacg	ggcaggtata	caatacaccc	720
cagagcatct	caatatcccc	tgggacagnt	acaattcagt	ggt		763

<210> 250

<211> 899

<212> DNA

<213> Homo Sapiens

<400> 250

attcaagtca	agagatgtga	gaccatgaga	gagaagcaca	tgcagaaaca	gcaggagagg	60
gaaaaatcag	tcttgacacc	tcttcgggga	gatgtagcct	cttgcaatac	ccaagtggca	120
gagaaaccag	tgtctactgc	tgtgccagga	atcacacggc	acctgaccaa	gcggcttccc	180
acaaagtcac	cccagaaggt	ggaggtagaa	acctcagggg	ttggagactc	attattgaat	240
gtgaaatgtg	cagcacagac	cttggaaaaa	aggggtaaag	ctaaacccaa	agtgaacgtg	300
aagccatctg	tgggttaaagt	tgtgtcatcc	cccaaattgg	ccccaaaacg	taaggcagtg	360
gagatgcacg	ctgctgtcat	tgcgctgtg	aagccactca	gctccagcag	tgtcctacag	420
gaacccccag	ccaaaaaggc	agctgtggct	gttgtcccgc	ttgtctctga	ggacaaatca	480
gtcactgtgc	ctgaagcaga	aaatcctaga	gacagtcttg	tgtgcctcc	aaccagtc	540
tcttcagatt	cctcaccccc	ggaggtgtct	ggcccttcc	catcccaa	gagcatgaaa	600
actcgcgcac	tcagctctgc	ctcaacaagg	aaagccccc	ctctctgtgg	aggatgattt	660
tgagaaacta	atatgggaga	tttcaaggag	gcaaaattgg	naactganat	tgacctggat	720
tctgggaaaa	gatgaagatg	acccttccgg	cttngngcct	atcaannaaa	ngattgntan	780
cctgaaaggg	tggtaattga	nggacncctt	naaaaaaaaa	atccnccaaa	aaaactnngg	840
ccttaanttc	naccaaatgg	taacaatttn	acctgagaat	gnttaatttc	ctttaggcc	899

<210> 251

<211> 755

<212> DNA

<213> Homo Sapiens

<400> 251

cctacatcag	ttttatttaa	aacactaaca	agtattttctc	tttctgtaag	ggcaaatggt	60
tcaaataatg	cggaacacga	aacattgana	nagacaagtg	ctttaaatat	gaaacaaaat	120
tattttttta	aaaagcaaaa	gaataaagaa	tatatacaaa	agggacctgg	aatctgtaag	180
gtgattccaa	aaacgaaata	agtagaaaat	ccatggtgaa	acctgaacat	tctacctctg	240
ctttggagaa	gggctatcat	acaacattca	gtcagctgaa	gatggattgg	tagagggtgtg	300
tctatacata	aacttcagtc	atttttgctt	gtgcagaatc	atcccaatct	tccaagact	360
gaatgggcag	tctgtggct	ttcttccttt	tccatattcc	caacaaggct	acgtgaagtt	420
caactcttga	tgagccgctt	acaacagcag	ttccttagga	gccaacatga	cagggtgggtc	480
agatttccct	atgagaaaca	aaactggcca	cctacagcaa	aatatcaaaa	tgggtaagtc	540
cttccctcct	cttccctcctg	attatataca	acatatctcc	tttcaaagac	tattatttcc	600
atcatgctta	ntccttcaca	aatctaaacc	ttgaggtgat	atgaaggaaa	ccaacatcan	660
gaaaagaaaa	ctcaattcag	aatgaagaa	aacgggcang	tatacaattc	anccccagag	720
caacccaata	atccctgggc	aaaagttcaa	ttcaa			755

<210> 252

<211> 753

<212> DNA

<213> Homo Sapiens

<400> 252

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tattttttta	aaaagcaaaa	gaataaagaa	tatatacaaa	agggacctgg	aatctgtaag	180
gtgattccaa	aaacgaaata	agtagaaaat	ccatggtgaa	acctgaacat	tctacctctg	240
ctttggagaa	gggctatcat	acaacattca	gtcagctgaa	gatggattgg	tagagggtgtg	300
tctatacata	aacttcagtc	atttttgctt	gtgcagaatc	atcccaatct	tccaagact	360
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caactcttga	tgagccgctt	acaacagcag	ttccttagga	gccaacatga	cagggtgggtc	480
agatttccct	atgagaaaca	aaactggcca	cctacagcaa	aatatcaaaa	tgggtaagtc	540
cttccctcct	cttccctcctg	gattatatac	aacatatctc	ctttcaagac	tattatttcc	600
atcatgnta	atccttcaca	aatctaaaac	cttgaggggtg	atatgaaagg	aaaccaacat	660
canagaaaag	aaaactcaat	tcaagaaaa	taagaaaacc	tggcaaggta	tacaaatata	720

ccccaggag catcccaaata aatccctggg aaa

753

<210> 253

<211> 793

<212> DNA

<213> Homo Sapiens

<400> 253

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caaaattatt	ttttaaaaaa	gcaaaaagaat	aaagaatata	tacaaaaggg	acctggaatc	180
tgtgaagnga	ttccaaaaac	gaaataagta	gaaaatccat	ggtgaaacct	gaanattcta	240
cctctgcctt	gganaagggc	tatcatacaa	cattcagtc	gctgaanatg	gattggtaaa	300
ggtgtgtcta	tacataaaact	tcagtcattt	ttgcttgtgc	anaatcatcc	caatcttccc	360
aagactgaat	gggcagtcct	gtggcctttc	tccttttcca	nattcccaac	aaggctacgt	420
gaagttcaac	tcttgatgag	ccgcttaca	cagcagttcc	ttaggagcca	acatgacagg	480
tgggtcagat	ttccctatga	gaaacaaaac	tggccaccta	cagcaaaata	tcaaatggg	540
taagtccttc	cttcctcttc	cncctgatta	tatacaanat	atctcctttc	aagactatta	600
tttccatcat	gcttattcct	tcacanattc	aaaccttgan	gtgatatgaa	nggnaaccaa	660
catcangaaa	agaaaactca	attcagnaat	gaangaaaac	tgggagggtat	ttaatanacc	720
cccangnnga	atccaaatac	cctggnaana	gttcaattca	antgtacngc	naaagnccat	780
aantaantat	tgg					793

<210> 254

<211> 625

<212> DNA

<213> Homo Sapiens

<400> 254

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tattttttta	aaaagcaaaa	gaataaagaa	tatatacaaa	agggacctgg	aatctgtaag	180
gtgattccaa	aaacgaaata	agtagaaaat	ccatggtgaa	acctgaacat	tctacctctg	240
ctttggagaa	gggctatcat	acaacattca	gtcagctgaa	gatggattgg	tanagggtgtg	300
tctatacata	aacttcagtc	atttttgctt	gtgcagaatc	atcccaatct	tccaagact	360
gaatgggcag	tcctgtggct	ttcttccttt	tccatattcc	caacaaggct	acgtgaagtt	420
caactcttga	tgagccgctt	acaacancaa	gttccttang	agccaacatg	acaggtgggg	480
tcangatttc	cctatgagaa	acaanactgg	ccacctacag	caaaaatatn	aaaatggggg	540
aagtccttcc	ttcctcttcc	tcctgaatta	tatncaacat	ntctcctttt	caagacnatt	600
anttccatca	gggcttaatc	cttca				625

<210> 255

<211> 907

<212> DNA

<213> Homo Sapiens

<400> 255

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tggccaagcg	cgctcggcgc	tgcgacgctg	gcgggccccg	tcagctagag	cccggggtac	180
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gtgacattaa	ggcatctaca	gagatgaggt	taagaagatt	ccagtcagtg	gaaagtggag	420
caaataacgt	tgtcttcatc	aggacacttg	ggatagagcc	tgagaaattg	gtgcatcata	480

ttctccagga	tatgtacaaa	accaagaaaa	agaagactcg	agttatTTTTg	cgaatgttac	540
ccatctcagg	cacatgcaag	gctTTTTtag	aagatatgaa	aaaatatgca	gaaacatttt	600
tggaacctg	gtttaaagct	ccaaacaaag	ggacatttca	gatttgtgtac	aaaatctcga	660
nataacagtc	atgtnaatag	agaagaagtt	atcaagagaa	tttgcangga	atagtgtgca	720
acctcaattc	agnaaataaa	gtgggtntca	acaatccaca	agtacacaat	ngtaatanaa	780
atcatcaaan	ctgtcngttc	cctganngtt	tgtaaagga	ttacaagggt	ggtttannaa	840
aattcaatcn	ccaagaaggt	tggtnaanaa	nccctaang	ggntccttca	naggcnttaa	900
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<210> 256

<211> 794

<212> DNA

<213> Homo Sapiens

<400> 256

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gacctctggt	tatcagatat	gatgtcacaa	aanagagata	ttggcctttg	ttctggcagg	120
ctcctagcaa	tagaaaaagt	tttctttgaa	tttcatcatt	tacaaatctt	acaaatgcta	180
cagcatgaca	aatatttagtg	aaacctgttg	actcatcatc	ctggatagag	aagctgctac	240
ttttcagtta	atgacacaaa	acctTTTTg	catcatatga	catatcatca	gtaaatcaac	300
ttattgagaa	taaagtctct	tcaactttgt	actgcatctt	gccccagcat	tttaattgtta	360
ttagattctc	accaaccatg	catatTTTTc	tttcttgaga	taagttctgc	tactaaataa	420
tttgcttctt	aaacctTTTTg	actaaagggtg	atttctgaac	aaaagcctta	ctgtTTTTga	480
tagtccaaaa	gccatttgaa	aataatgaat	atcctttctt	gtcaagtggc	tgtgatttat	540
tgttacaatt	gctaagtttt	gtaagttgca	tgtcacagac	aatgcacaat	gggacaagan	600
aaccttggac	ctgagtcac	ataaatacce	cttgagaagt	tanctTTTTc	tttaattaaga	660
caagaatttc	ctttggtgtc	cccttggttg	cactaagtat	acttgaaagt	ntnctccagn	720
angactggaa	gttcttcaat	caaccaanct	ttttcaagaa	aatgtccngt	agtttcaang	780
gcctaaaaat	gggt					794

<210> 257

<211> 885

<212> DNA

<213> Homo Sapiens

<400> 257

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ccctgccca	gcagactact	cagcctggcg	gcgggaagcg	caaaggcaag	gctcagtatg	120
tgctggccaa	gcgcgctcgg	cgctgcgacg	ctggcgggcc	ccgtcagcta	gagcccgggc	180
tacagggcat	cctcatcacc	tgcaatatga	acgagcgcaa	gtgcgtggag	gaggcctaca	240
gcctcctcaa	cgaatacggc	gacgacatgt	atggggcaga	aaagtttaca	gacaaggatc	300
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ttggtgacat	taaggcatct	acagagatga	ggttaagaag	attccagtca	gtggaaagtg	420
gagcaaataa	cgttgtcttc	atcaggacac	ttgggataga	gcctgagaaa	ttggtgcatc	480
atattctcca	ggatatgtac	aaaaccaaga	aaaagaagac	tcgagttatt	ttgcgaatgt	540
tacccatctc	aggcacatgc	aaggcttttt	tagaagatat	gaaaaaatat	gcagaaacat	600
ttttggaacc	ctgggtttta	agctccaaac	aaaggacat	ttcagattgt	gtacaaatct	660
cgaaataaca	gtcatgtgaa	tngagaaaga	agttatcaga	gaaattggca	aggaatagtt	720
gtgcacccctc	aattcagaaa	attaaagggtg	ggntctcaac	caatccacag	ttcacagntg	780
gtagttagaa	atcaatcaaa	acctgtcngt	ttgcccgaan	ttgnttgta	aaagaattca	840
angttgggtt	tanaaanaat	naaatcccc	aagaagggtg	gtgaa		885

<210> 258

<211> 798

<212> DNA

<213> Homo Sapiens

<400> 258

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cttcactgta	tcttcaagtt	tttgatatca	gnagcactgt	ggagaaagca	gtgtgctata	120
atgtcaacat	caggattttct	tttttttttt	ttaataacgc	aaaatgactt	atggagacaa	180
ccactgatgg	ggcaccagga	gtgtagatac	cagacctctg	gttatcagat	atgatgtcac	240
aacattatat	attggccttt	gttctggcag	gctcctagca	atagaaaaag	ttttctttga	300
atttcatcat	ttacaaatct	tacaaatgct	acagcatgac	aaatattagt	gaaacctgtt	360
gactcatcat	cctggataga	gaagctgcta	cttttcagtt	aatgacacaa	aacctttttt	420
gcatcatatg	acatatcatc	aagtaaatac	acttattgag	aataaagtct	cttcaacttt	480
gtactgcata	ttgccccagc	attttaatgt	tattaagatt	ctcaccaacc	atgcataatt	540
tcctttctctg	agataagttc	tgctactaaa	taatttgctt	cttaaaccct	ttgactaaag	600
gtgattttctg	aacaaaagcc	ttactgtttt	tgataagtcc	caaaaagcca	tttgaaaaat	660
aatgaatatc	ctttcntgtc	aagtggctgt	gaatttaatg	ttacaattgc	caagttttgt	720
aagttgcatn	gtcacangac	aatgcacaat	ggggacaagg	agaaccttgg	gcttgagtcc	780
acaataanta	ccccttga					798

<210> 259

<211> 831

<212> DNA

<213> Homo Sapiens

<400> 259

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gcgcacacca	tggcggtccc	tgcccagcag	actactcagc	ctggcggtcg	gaagcgcaaa	120
ggcaaggctc	agtatgtgct	ggccaagcgc	gctcggtgct	gcgacgctgg	cgggccccgt	180
cagctagagc	ccgggctaca	gggcatcctc	atcacctgca	atatgaacga	gcgcaagtgc	240
gtggaggagg	cctacagcct	cctcaacgaa	tacggcgacg	acatgtatgg	gccagaaaag	300
tttacagaca	aggatcagca	gccctctgga	agtgaggagg	aggatgatga	tgcgagggct	360
gccttgaaga	aagaagttgg	tgacattaag	gcatctacag	agatgaggtt	aagaagattc	420
cagtcagtgg	aaagtggagc	aaataacggt	gtcttcatca	ggacacttgg	gatanagcct	480
gagaaattgg	tgcatcatat	tctccaggat	atgtacaaaa	ccaagaaaaa	gaagactcga	540
gttattttgc	gaatgttacc	catctcaggc	acatgcaang	ctttttttaga	agatatgaaa	600
aaatatgcan	aaacattttt	ggaancctgg	tttaaagctc	caaacaaagg	gacatttcag	660
attgtgttca	aatctcgaaa	ataacagtca	tggtgaatag	aagaagaagt	tatcagagaa	720
nttggaagg	aataatgntg	caacctcaat	tcagaaaata	aaagtggatt	tcaccaattc	780
cacagtncac	aantggtagt	agaaatcatc	aaaagcctntc	tgtttgcccc	a	831

<210> 260

<211> 772

<212> DNA

<213> Homo Sapiens

<400> 260

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gacctctggt	tatcagatat	gatgtcacia	cattatatat	tggcctttgt	tctggcaggc	120
tcctagcaat	agaaaaagtt	ttctttgaat	ttcatcatct	acaaatctta	caaagtctac	180
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tagattctca	ccaaccatgc	atattttcct	ttcctgagat	aagttctgct	actaaataat	420
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agtccaaaag	ccatttgaaa	ataatgaata	tcctttcttg	tcaagtggcn	gtgatttatt	540
gttacaattg	ctagttttgt	nagttgcatg	tcacagacaa	tgacacaaatg	gacangagag	600

cctgggactg	agtccacata	ataccnttga	gaagtannct	ttcttttatta	agacagaant	660
tctttgtgtc	ccttggttgc	caagtntact	gaagtntcnc	aagaaggact	ggangtcntc	720
ataancaacc	tttttagaat	gtccgtattc	ctaaggccca	aaaangggtc	cc	772

<210> 261

<211> 753

<212> DNA

<213> Homo Sapiens

<400> 261

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atggcgggcc	ctgccagca	gactactcag	cctggcggcg	ggaagcgcaa	aggcaaggct	120
cagtatgtgc	tggccaagcg	cgctcggcgc	tgcgacgctg	gcggggcccc	tcagctagag	180
cccgggctac	agggcatcct	catcacctgc	aatatgaacg	agcgcaagtg	cgtggaggag	240
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aaggatcagc	agccctctgg	aagtgaggga	gaggatgatg	atgcggaggc	tgccttgaag	360
aaagaagttg	gtgacattaa	ggcatctaca	gagatgaggt	taagaagatt	ccagtcagtg	420
gaaagtggag	caaataacgt	tgtcttcac	aggacacttg	ggatagagcc	tgagaaattg	480
gtgcatcata	ttctccagga	tatgtacaaa	accaagaaaa	agaagactcg	agttattttg	540
cgaatgttac	ccatctcagg	ccatgcaag	gcttttttag	aaagatatga	anaaatatgc	600
anaaaacatt	tttggaaccc	tgggtttaaa	gctccaaaca	aagggaacatt	tcagaattgt	660
ggtacaaatc	tcgaaatanc	agtcatgtta	antagagaan	naagtttttc	agaagaattt	720
ggcaaggaat	nagtnntgca	accctcaatt	tca			753

<210> 262

<211> 659

<212> DNA

<213> Homo Sapiens

<400> 262

aataacgcaa	aatgacttat	ggagacaacc	actgatgggg	caccaggagt	gtagatacca	60
gacctctggt	tatcagatat	gatgtcacia	cattatatat	tggcctttgt	tctggcagge	120
tcctagcaat	agaaaaagtt	ttctttgaat	ttcatcattt	acaaatctta	caaagtctac	180
agcatgacaa	atattagtga	aacctgttga	ctcatcatcc	tggatagaga	agctgctact	240
tttcagttaa	tgacacaaaa	ccttttttgc	atcatatgac	atatcatcag	taaatcaact	300
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tagattctca	ccangccatg	catattttcc	tttcctgaga	taagtctctg	tactaaagaa	420
tttgcttctt	aaaccttttg	actaaagggt	atctctgaac	aaaagcctta	ctgtttttga	480
nnagtccana	agccatttga	aaaataatga	atatcctttc	cttgtcaagt	ggcngtgatt	540
tantgttaca	atttgcnaag	ttttgtaagt	tgcatgggtc	cagnanaatg	cacantnggg	600
acanngagan	cntgggncng	aagtccacat	tatanccctt	tgagnaangt	agctttccc	659

<210> 263

<211> 673

<212> DNA

<213> Homo Sapiens

<400> 263

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tttaaggggt	ctgtcatgga	aggtgctctt	ccaggaaact	ctgtgatgga	ggtcacagcc	120
acagacgcgg	acgatgatgt	gaacacctac	aatgccgcca	tcgcttacac	catcctcagc	180
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gctgctgacc	ttcaagggtga	gggtttaagc	acaacagcaa	cagctgtgat	cacagtcact	360
gacaccaacg	ataatcctcc	gatcttcaat	cccaccacgt	acaaggggtc	gggtgctgaa	420

aacgaggcta	acgtcgtaat	caccacactg	aaagtgactg	atgctgatgc	ccccaatacc	480
ccagcgttgg	gaggctgtat	acaccatatt	gaatgatgat	ggtgggacaa	tttgtcgtca	540
ccacaaatcc	agtgaacaac	gatggcattt	tgaaaaacag	caaagttgaa	gtcaagtgat	600
tttgtctggt	cngaatacat	tggtgcctcn	gttgggagaa	aggnttccaa	cacatacccc	660
gggatnngtt	att					673

<210> 264

<211> 661

<212> DNA

<213> Homo Sapiens

<400> 264

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acctccaact	gcatctccta	ctctgaaatn	cctcttgagc	agccaagggg	ggccagttct	120
gctcctcatt	ttcctgaaga	anaatctcag	cctgaaagaa	tatagagcta	ggtgacatat	180
gggtggccaa	cgctttctcc	tcaagttcca	anagagtggg	caattagtga	aattccatca	240
gtcatgttaa	aataactttt	caccaggtan	acatccttct	ttcaatgcta	gaggacagt	300
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aacgcgggag	tgctgaacac	atgccctcgg	aagggaccct	gaagacccaa	gtgacctgca	420
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gagccaggtc	tacggcaggg	aacatgatct	tcttctccag	cttctgtgga	aggaacanga	600
aatttttcat	gatgtcntcc	agctcttcta	nggccaactg	ggcatgganc	ttggccacgt	660
c						661

<210> 265

<211> 659

<212> DNA

<213> Homo Sapiens

<400> 265

ccatccaana	taactttatt	ccattttgca	ttatttgata	actatttcct	tccccctccc	60
acctccaact	gcatctccta	ctctgaaatg	cctcttgagc	agccaagggg	ggccagttct	120
gctcctcatt	ttcctgaana	anaatctcag	cctgaaagaa	tatanagcta	ggtgacatat	180
gggtggccaa	cgctttctcc	tcaagttcca	ananagtggg	caattagtga	aattccatca	240
gtcatgttaa	aataactttt	caccaggtan	acatccttct	ttcaatgcta	gaggacagt	300
aaaaatgtag	attaatgaga	tctgtaactg	tcttctctta	actgtacacc	cctcaggctg	360
aacgcgggag	tgctgaacac	atgccctcgg	aagggaccct	gaagacccaa	gtgacctgca	420
ccataaaacc	accccgaggg	tcagccatgc	tgccagcact	caaaaagcag	cagggccacc	480
tgctggaana	actgggcacg	gctctgggtg	cctggccctg	cctgcctcct	ccacgtcctt	540
gganccagg	ctacggcnagg	accatgatct	tcttctccan	cttctgtgga	aggaacanga	600
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<210> 266

<211> 620

<212> DNA

<213> Homo Sapiens

<400> 266

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acctccaact	gcatctccta	ttntnaaatg	cctcttgagc	agccaagggg	ggccagttct	120
gctcctcatt	ttcctgaana	anaatctcag	cctgaaagaa	tatagagcta	ggtgacatat	180
gggtggccaa	cgctttctcc	tcaagttcca	ananagtggg	caattagtga	aattccatca	240
gtcatgttaa	aataactttt	caccaggtan	acatccttct	ttcaatgcta	gaggacagt	300
aaaaatgtag	attaatgaga	tctgtaactg	tcttctctta	actgtacacc	cctcaggctg	360

aacgcggggag	tgctgaacac	atgccctcgg	aagggaccct	gaagacccaa	gtgacctgca	420
ccataaaaacc	accccgaggg	tcagccatgc	tgccagcact	caagaagcag	cagggccacc	480
tgctggaaga	cctgggcacg	gctctgggtg	cctggccctg	cctgcctcct	ccacgtcctt	540
ggagccaggt	ctacngcang	aacatgatct	tcttctccac	ttctgtggaa	ggaacaggaa	600
ntttttcatg	atgtcatcca					620

<210> 267

<211> 745

<212> DNA

<213> Homo Sapiens

<400> 267

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tgctcagctta	tgaccctcaa	attccaacac	gggctgctgc	cctgcgtact	ctttcccact	180
ggatagagca	gagagaagca	aaagcccttg	agatgcaaga	gaagcttctc	aagatattct	240
tggaataactt	ggaacatgaa	gacacttttg	tatatctatc	tgcaattcag	ggggttgccc	300
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<210> 268

<211> 676

<212> DNA

<213> Homo Sapiens

<400> 268

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gctcctcatt	ttcctgaana	anaatctcag	cctgaaagaa	tatagagcta	ggtgacatat	180
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aaaaatgtag	attaatgaga	tctgttaactg	tcttctctta	actgtacacc	cctcaggctg	360
aacgcggggag	tgctgaacac	atgccctcgg	aagggaccct	gaagacccaa	gtgacctgca	420
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<210> 269

<211> 737

<212> DNA

<213> Homo Sapiens

<400> 269

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gtgtcatcca	acgggaatgc	agttgaggat	ccaatggaga	ttttgatcac	ggtaaccgat	180
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gctcttccag	gaacctctgt	gatggaggtc	acagccacag	acgcggacga	tgatgtgaac	300
acctacaatg	ccgccatcgc	ttacaccatc	ctcagccaag	atcctgagct	ccctgacaaa	360
aatatgttca	ccattaacag	gaacacagga	gtcatcagtg	tggtcaccac	tggtcaggac	420
cgagagagtt	tccttacgta	tacctgggtg	gttcaagctg	ctgaccttca	aggtgagggg	480
ttaagcacia	cagcaacagc	tgtgatcaca	gtcactgaca	ccaacgataa	tcctccgata	540
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caacactgaa	aagtgactga	tgcctgatgc	cccccaatta	nccanccgt	gggaagctgt	660
ntacaccata	tngaaatgat	gatgggtggg	cnaatttgn	cgttcaccaa	caaatnccan	720
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<210> 270

<211> 726

<212> DNA

<213> Homo Sapiens

<400> 270

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atctttcatg	atgtctccan	ctcttctagg	gccactgggc	atggancttg	ggcnctcat	660
cgggtcccaa	anacactact	gcttcancag	gtgggtanaa	atccttgaag	angggctcac	720
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<210> 271

<211> 814

<212> DNA

<213> Homo Sapiens

<400> 271

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gctcctcatt	ttcctgaaga	agaatctcag	cctgaaagaa	tatagagcta	ggtgacatat	180
gggtggccaa	ccgcttctcc	tcaagttcca	agagagtggg	caattagtga	aattccatca	240
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gaaggacggg	ggctcaacaa	cccaagtanc	ctttccnggg	ctgaatcccc	ngaagcaagc	780
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<210> 272

<211> 862

<212> DNA

<213> Homo Sapiens

<400> 272

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cccagacagg	cctgcagtca	aatgctccaa	tcattcctca	aggagtcaat	gagcccagca	180
ctactacaag	tcagaaatct	ggaagcgtaa	ccacagaaca	gctccaagag	gttcttttgt	240
cagcttatga	ccctcaaatt	ccaacacggg	ctgctgccct	gcgtactctt	tcccactgga	300
tagagcagag	agaagcaaaa	gcccttgaga	tgcaagagaa	gcttctcaag	atattcttgg	360
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<210> 273

<211> 677

<212> DNA

<213> Homo Sapiens

<400> 273

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gctcctcatt	ttcctgaaga	agaatctcag	cctgaaagaa	tatagagcta	ggtgacatat	180
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ccataaaaacc	accccgaggg	tcagccatgc	tgccaagcac	tcaagaggca	gcagggccac	480
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ttggggccaa	gtctaaggga	agggaccaat	gatcttcttc	cccaaacttc	tgtggagggg	600
aaaaaaggaa	ntttttcaag	gnngtcatcc	nangetcttc	caaggggnca	aatggggggc	660
antggaacct	tgggcaa					677

<210> 274

<211> 863

<212> DNA

<213> Homo Sapiens

<400> 274

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catcaccatc	tctacccatg	gagcctttgc	cactgaggcc	gtcagcatgg	ctgcccacaa	180
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anggcattag	ggagacatgg	tctcaaagta	accgagaacc	tttgattcat	accttctctga	780

aggggaatta gagattctga atggtgctca cagggccaac aaccttggcn aaccttgggg 840
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<210> 275

<211> 821

<212> DNA

<213> Homo Sapiens

<400> 275

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gctcctcatt ttctgaaga agaatctcag cctgaaagaa tatagagcta ggtgacatat 180
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gtcatcgggc tccagacaca ctacgtgctt cancaagggt gtaaaagatt cttganggac 720
ggngctcanc acctcagtaa notttctggc tgagtcccc gaaagcaaca gcacaancca 780
catgtntngg aaacctgcg ttacttngaa cttcaacaac c 821

<210> 276

<211> 722

<212> DNA

<213> Homo Sapiens

<400> 276

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cagaaaagat ctggaagggg aaatagaaga gcagcaacaa accagtcag aaagaccac 480
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gtcagaaatc tggaagcgtt accacagaac agctccaaga gggttcntttg tcagctttat 660
gaacctcaaa ttccaacacg gggctgggtgc ctgcgttact cnttcccact gggntagaag 720
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<210> 277

<211> 805

<212> DNA

<213> Homo Sapiens

<400> 277

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aaaaatgtag	attaatgaga	tctgtaactg	tcttctctta	actgtacacc	cctcaggctg	360
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gcacgtcatn	cgggctccag	acacactacg	gtgcttcaac	aagggnggta	nagattcttg	720
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aagtacaaac	cacatgtttt	gggaa				805

<210> 278

<211> 1358

<212> DNA

<213> Homo Sapiens

<400> 278

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aattttaagtc	tatccgtgag	accatgaagg	agaagggctt	gctgggggag	ttcctgagga	180
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<210> 279

<211> 702

<212> DNA

<213> Homo Sapiens

<400> 279

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caggaagagc	ttttacagtt	gaaagctata	caccaagaag	agggtgaaaga	gttgatgtgc	300
cagattgaag	catcagctaa	ggaacatgaa	gcagagataa	ataagttgaa	cgagctaaaa	360
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<210> 280

<211> 874

<212> DNA

<213> Homo Sapiens

<400> 280

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<210> 281

<211> 730

<212> DNA

<213> Homo Sapiens

<400> 281

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ggcccaggct	ctcgccacac	atcctgggan	aactgccata	ggccctagaa	ggagggatga	180
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agcttcttca	ggaagcctcc	aactgatcct	catccttgat	gccacaaaac	ttgtccacca	480
cgtccccatt	cttcatggcc	agcacagtgg	gcaccgctga	cacctcatac	tcaatggcga	540
agtctgtgtg	gtcntcaata	tccaccttgg	ccatcaccac	cttcccgtgc	tgcttgacca	600
ccatcttctc	taacctccgn	cccangatct	tcagggtcca	caccactgtg	cgtggaaatc	660
cacaaccact	ggtgtctcct	gtttgaacac	tccgtcttga	aantcngtcc	ntcctgnata	720
ttaaagggtg						730

<210> 282

<211> 699

<212> DNA

<213> Homo Sapiens

<400> 282

agaactcaga	gctgctcttc	ctctgtggcc	agttggggac	cagcatcatg	aagtggatgg	60
tggtgggtct	ggctctgcct	cagctcttgg	aggcagcagt	ggtcaaagtg	cccctgaaga	120
aatttaagtc	tatccgtgag	accatgaagg	agaagggtct	gctgggggag	ttcctgagga	180

cccacaagta	tgatcctgct	tggaagtacc	gctttgggtga	cctcagcgtg	acctacgagc	240
ccatggccta	catggatgct	gcctactttg	gtgagatcag	catcgggact	ccaccccaga	300
acttcctggt	cctttttgac	accggctcct	ccaacttggt	ggtgccctct	gtctactgcc	360
agagccaggc	ctgcaccagt	cactcccgt	tcaaccccag	cgagtcgtcc	acctactcca	420
ccaatgggca	aaccttctcc	ctgcagtatg	gcagtggcag	cctcacccgc	ttctttggct	480
atgacaccct	gactgtccag	agcatccaan	gtccccaacc	aggagtccgg	cttgagttag	540
aatnagcctg	ggtaccaact	togtctaagc	gcanttttga	tgggatcaag	ggcctgggcc	600
taacctggct	ctgtcccgtt	ggattaaggc	caccacaagc	tatntagggc	nattnggntc	660
aaggatgggt	gtcnctttat	nnagcccccg	tnctttcaa			699

<210> 283

<211> 759

<212> DNA

<213> Homo Sapiens

<400> 283

gaaattgaga	actgatttaa	tactaaagtt	ctgaataaag	gtgtgcactt	tatgattgat	60
tctatctttt	tgcacaagtt	ggatactcca	gtttcccatc	ccaacatggt	gttcgcaatg	120
tgtgagaacg	tgatgaaaga	cgatatcccc	gtttacacac	aaattcaact	gattcacctg	180
ttctcgaata	aagcttctgt	ttggctgtcc	accttaatgc	tatgttataa	ttttccataa	240
tttctcggga	tattacacac	ggatgtaagc	attttgggtg	ttctgacct	tgtccatttc	300
tacatgttat	togcttggtt	ccctcaagtt	gatacaagtt	ctggcattgg	tactcaactg	360
atgaagctgg	agcatatact	gacaacggga	atgaagtaat	gtccccattg	tcaatagggt	420
gagggggccc	acatttttct	gtagaatctt	tgcattgagg	tggttccgtc	cagtttccat	480
ttaaacacat	cactttcttca	tccccaaaca	tttcataagg	gtcctacat	tgataacgta	540
ctctctcacc	agatggatat	ttactcatct	gtctcgacac	tatataagca	ttttgtactg	600
tgggcggatt	ccacangang	tgtctctgca	tgttgggctt	cctgtccact	gctattaatg	660
catgtttacat	tactggctcc	accattttgt	aatatgttgc	acaagtttta	gtccttgctc	720
accccccttat	acacatcctt	ctctctccat	gggtttggc			759

<210> 284

<211> 764

<212> DNA

<213> Homo Sapiens

<400> 284

ggaccgcgat	gacgcagact	ggagggaggt	gatgatgccc	tattcgacag	aactgatatt	60
ttatattgaa	atggatcctc	cagctcttcc	accaaagcca	cctaagccaa	tgacttcagc	120
agttccaaca	tggaatgaag	gacagttctg	tttctcttca	ggatgcagaa	tggtagtggg	180
gggatatttc	aagggaggag	gtaaatgaca	aattgcggga	tatgccagat	gggaccttct	240
tggtcgcaga	tgctcaaca	aaaatgcagg	gagattatac	tttgactttg	cggaaggagg	300
gcaataataa	gttaataaag	atctatcacc	gggatggtaa	atatggcttt	tctgatcctc	360
tgacatttaa	ttccgtgggt	gagctcatta	accactatca	ccatgaatct	cttgctcagt	420
acaatcccaa	acttgatgtg	aagctgatgt	acccaagtgt	ccagatacca	acaggatcag	480
ttggtaaaa	gagataatat	tgatgcagta	ngtaaaaaac	tgcaagaata	ccactctcaa	540
gtatcaggag	aagagtaaag	gagtatgata	ngctgtatga	agaatatact	agaacatccc	600
aaggaaatac	agatgaagag	gactgcaata	gaaagctttt	aatgaaaaca	ttaaaatatt	660
tggaaagagca	ntgtcacaca	caaggaacca	acattnccaa	agaatatatt	gagnggattt	720
cncaaaaanaa	ggggaaatga	aaagggggan	ttgaacgaaa	ttta		764

<210> 285

<211> 586

<212> DNA

<213> Homo Sapiens

<400> 285
gcattgcacc ttttctttac ccatacaaac aagttacaaa ggtttcaaac aacagntcat 60
tcttttaggct aaggaaacac catacaagca ccaacttcat tttangattc aaagtcacc 120
atccccacaa aaagaatgct attccncatc tcagagaaac aggcaggaag gacanaaggg 180
gttagttaca gtgatcaatt ttagcgtttg ctaaaacnca caaattcnag nctttttaag 240
ttcaagtttt ggtacagaag tatacattca actatgagtg ccacgttttc ccatcaaaca 300
ttggntctggc aacaaactgt tttgttggct tctgaacata atactttctc anagggaggg 360
gctggtgaaa tgctgaancc taaattatgt tggnaagaaa caaagtacct tcanntgaag 420
gtttttttta acanctnngc ttaaattatt taaatgaaan cccaagcctc ccnatttncc 480
tttggtngcc ttttncanaa aatcccattc natcacaaaa ccctaaaaag ccttcttcgt 540
nggggggaaa aaananactg ccaaangcaa aaacaaaaac ncccaa 586

<210> 286
<211> 666
<212> DNA
<213> Homo Sapiens

<400> 286
gcctggagtt cagtgggtgc agcctgcttg cgagctgagg ccagacaggg ggggcctac 60
ggacggaaaa gaaaagttga ttacaaacgg gaccatattt tgcttcgaaa tggaaccagc 120
agtttagcgag ccaatgagag accaagtcgc acggactcat ttgacagagg acactcccaa 180
agtgaatgct gacatagaaa aggttaacca gaatcaggcc aagagatgca cagtgatcgg 240
gggctctgga ttcctggggc agcacatggt ggagcagttg ctggcaagag gatatgctgt 300
caatgtattt gatatccagc aagggtttga taatccccag gtgcggttct tctgggtga 360
cctctgcagc cgacaggatc tgtaccagc tctgaaagggt gtaaacacag ttttccactg 420
tgctgcaccc ccaccatcca gtaacaacaa ggagctcttt tatagaagtg aattacattg 480
gcaccaagaa tgtcattgaa acttgcaaag aggtctgggt tcagaaactc attttaacca 540
gcagtgccat gtcattcttg agggcgtcga tatcaagaat ggaactgaaa gaccttcct 600
nagccattga aaccaattga cctactacac aaganactaa agatcttaca ngagaaggca 660
atttct 666

<210> 287
<211> 782
<212> DNA
<213> Homo Sapiens

<400> 287
gacagagaac aaatcggtat aatatgaagc tgcctgcttc aagaaatcca aatccagttc 60
catgaaggaa gaaatgtctg tttttgccgc cctcatcgtc acggaaagag taggggtgcgc 120
tctctgcta gcagaaggag tcacaggctc agagcaaact cattcaaagg atgttatttc 180
atcaatccac aggggaagga gtgactggct gagcaacgtg tcgagagagc ccagcctcca 240
gtgtccctca cttgaccctc cgcagggtggc gaaagctctg cacggctctc tccatagcat 300
catccatggt cactagtggc tggtagccca tggccttttt ggctctctcg cagctgtagt 360
agtggaatgt gccagccagt gcgacccgca tgggtgtgaa ggtgggctgc agctggatga 420
caggactgat caccatcacc agcagggata gcaggagggc caggtagtag gccaccagt 480
aggggatgtg gtacttgggg gcctcataat tgaggcctgt caaggatgcg agacaggaat 540
gtccaaaaag ggatgggctc atcattggtg atgtgaaatg ccttcccacc cagtgtcgag 600
tctcngggan anctgctctg ccgccaagat tgtccatggg accaagggtt tcacaaaggt 660
gaaagtccac caagttcctc ccaatttcca atcacgaaac ttcaaccttg ccgttcctgg 720
ctgcctccat gaaggatggg ttacaaactg ccgggttccc tttggggccg aaaaattgcc 780
aa 782

<210> 288
<211> 707
<212> DNA

<213> Homo Sapiens

<400> 288

gtgggtccag	cgccgggtttt	gaccgccaca	ttaccattttt	ttcaccogag	ggtcgggtctt	60
accaagtaga	atatgctttt	aaggctatta	accaggggtg	ccttacatca	gtagctgtca	120
gagggaaaga	ctgtgcagta	attgtcacac	agaagaaagt	acctgacaaa	ttattggatt	180
ccagcacagt	gactcactta	ttcaagataa	ctgaaaacat	tggttgtgtg	atgaccggaa	240
tgacagctga	cagcagatcc	caggtacaga	gggcacgcta	tgaggcagct	aactggaaat	300
acaagtatgg	ctatgagatt	cctgtggaca	tgctgtgtaa	aagaattgcc	gatatttctc	360
aggtctacac	acagaatgct	gaaatgaggc	ctcttggttg	ttgtatgatt	ttaattggta	420
tagatgaaga	gcaaggccct	caggtatata	agtgtgatcc	tgagggttac	tactgtgggt	480
ttaaagccac	tgacgaggga	gttaaacaac	ctgagtcaac	cagcttcctt	gaaaaaaaaa	540
tgaagaagaa	atgtgattgg	acatttgaac	agacagtggg	aactgcaatt	acatgcctgt	600
ctactgttcc	atcaattgan	ttcaaacctt	cagaaataga	aattgggagt	aatgacagtt	660
gaaaatccta	aattcangan	tcctacagaa	gcagagattg	atgctca		707

<210> 289

<211> 673

<212> DNA

<213> Homo Sapiens

<400> 289

atggcaccat	cacaacaaag	gaacttgga	ctgtcatgag	gtcactgggt	cagaacccaa	60
cagaagctga	attgcaggat	atgatcaatg	aagtggatgc	tgatggtaat	ggcaccattg	120
acttccccnn	atttttgact	atgatggcta	gaaaaatgaa	agatacagat	agtgaagaag	180
aaatccgtga	ggcattccga	gtctttgaca	aggatggcaa	tggttatata	agtgcagcag	240
aactacgtca	cgatcatgaca	aacttaggag	aaaaactaac	agatgaagaa	gtagatgaaa	300
tgatcagaga	agcagatatt	gatggagacg	gacaagtcaa	ctatgaagaa	ttcgtacaga	360
tgatgactgc	aaaatgaaga	cctactttca	actccttttt	ccccctcta	gaagaatcaa	420
attgaatctt	ttacttacct	cttgcaaaaa	aaaaaaaaaat	aagncanaaa	annnataaaa	480
aaaaaaacnc	gagagtactt	ctaaagcggc	cgcgggccna	togatatttc	accgggtgg	540
ggtaccaggt	aagtgtccca	attcgcccta	taggggagtc	gtattacaat	tcacggggcc	600
gtcgttttta	aaacgtcntg	acgggggaaa	accctggngt	taccaactta	atcccccttg	660
caacaaatnc	ccc					673

<210> 290

<211> 573

<212> DNA

<213> Homo Sapiens

<400> 290

gcaagaggta	agtaaaagat	tcaatttgat	tcttctanag	gggggaaaaa	ggagttgaaa	60
gtaggctctc	attttgcagt	catcatctgt	acgaattctt	canagttgac	ttgtccgtct	120
ccatcaatat	ctgcttcnct	gatcatttca	tctacttctt	catctgttag	tttttcnccn	180
aagtttgtca	tgacgtgacg	tagttctgct	gcactgatat	aaccattgcc	atccttgtca	240
aagactcgga	atgcctcacg	gatttcttct	tcactatctg	tatctttcan	ttttcnagcc	300
atcatagtca	aaaattcggg	gaantcaatg	gngccattac	catcagcatc	cacttcattg	360
atcatatcct	gnaattcaan	cttctgttgg	gttntgaccc	antgaccnca	nggacaagtt	420
ccaagttccc	tttggttgtg	aaggggtgcca	nctcgtgccc	gaattccttt	gggntccnac	480
gangggtcna	accctgcana	gnggccgcga	ancctccaan	cttttggttc	ccctttanat	540
ngagggttaa	atttcgaact	ttggnntttt	tcc			573

<210> 291

<211> 819

<212> DNA

<213> Homo Sapiens

<400> 291

aaagaagaac	tattttattat	tagagaaaagt	ccagagtcca	gaaaaagaag	gctgaatcca	60
gagtggaaag	acagatacaa	tgccctagga	gggtgcaggg	tcaagaggaa	gaggggagcc	120
cacgtgtcga	ggcagcaagt	ctaggcggca	gtggcaaagc	ctactctgtt	gttgcccaag	180
tcgtagacgg	aatagtagga	cctgaggaag	acatccccga	ggatccacag	gggctggccg	240
ttctgggagg	acaggtaggt	gggctcgact	cccacgggtc	agtagccgtt	gttactgagg	300
atataggagg	aaggtggcag	agggaactcc	acaccattga	tgatgaaggt	caagctgggc	360
agattctgaa	tgctgttaca	gttcacgaga	aactgtccat	actcatcctc	ctggggccct	420
gtggcctgca	gaagagcact	catgtactgc	tggggcacag	tgagcagaga	ggtgcctgtg	480
tccacgatgg	cctggcaacc	ctcagaacac	cagccggagg	cctggccgcc	gatgaggaac	540
tcttcaatgc	caatctgccca	gtagagttcc	tgggtgacan	gcgccagta	gatctgcccc	600
gtgtacangc	tgctatccac	acccccaaag	gacaaccgct	cccccgctgg	gagccctgct	660
ggttgctgan	gtaaaccctg	aanacggggc	tggttnaggg	cgccctcctg	cacatgccct	720
gcatactgtg	gtggcctcat	ccacggnena	aaccanggta	aggcaaggcc	catgatgcca	780
tcaaactgcc	ataacaaatt	tgtacaaggc	tcaatccca			819

<210> 292

<211> 664

<212> DNA

<213> Homo Sapiens

<400> 292

ctcgcgctcg	cgctgggtggc	ggtcgcctgg	gtccgcgcgcg	aggaagagct	aaggagcaaa	60
tccaagatct	gtgccaatgt	gttttgtgga	gccggccggg	aatgtgcagt	cacagagaaa	120
ggggaaccca	cctgtctctg	cattgagcaa	tgcaaaccctc	acaagaggcc	tgtgtgtggc	180
agtaatggca	agacctacct	caacctactgt	gaactgcctc	gagatgcctg	cctcactgga	240
tccaaaatcc	aggttgatta	cgatggacac	tgcaaagaga	agaaatccgt	aagtccatct	300
gccagcccag	ttgtttgcta	tcagtccaac	cgtgatgagc	tccgacgtcg	catcatccaa	360
tggctggaan	ctgagatcat	tccagatggc	tggttctcta	aaggcagcaa	ctacagtgaa	420
atcctagaca	agtatttttaa	agaactttga	taatgggtgat	tctcgcctgg	actccaagtg	480
aattcctgaa	gtttgtggga	acangaatga	aactgccatc	aatattacaa	cgtttccagn	540
accaagggag	aacaacaagt	ttgcctaang	ggactccggt	ngttgatgcc	tctcaatttg	600
aactggtctg	gatgaaaaat	gcctgattgg	gnaattnaag	cttcccaant	agttttncca	660
aatg						664

<210> 293

<211> 719

<212> DNA

<213> Homo Sapiens

<400> 293

cactttaatt	tctttattca	tcaatagtat	ccgaaaagga	agaatcagga	gttacaaaaa	60
caagttaaatt	gcaatatana	agcctactaa	atacaaatac	aagttcacaa	acacatatgc	120
aacagaaaact	tgtttanatt	gtttcttgaa	gtttgactac	ttaaaaacat	aggtgtaaag	180
gaaagacatt	cagactgggtc	cacgtgggct	tgtagcagg	canaggaacc	ctgctttcca	240
aaaactgata	tagtccaaag	tcacggcatg	tgggaatgtt	tccatggaca	ctggatctta	300
acagatgcta	tagtgtttac	aaaactacac	acacagagaa	agcccaagga	agcctgcagg	360
ctaagcccta	tgcttttaga	gggctgaagg	aaccaaaccct	agtttaatcc	tgtttgtttg	420
ctccatgcaa	aactttatgg	aagactcccc	agactaggct	atttagcagc	ttccatgaat	480
ggtcctcaga	tcatgtgatt	ctacggcata	nacgacagct	gccctattta	cacagaagct	540
gcagaactca	agaagaatgt	ggatttgctc	ttggganttc	aatgttgagc	ggtanantaa	600
tcttgggatg	ataaccatgt	tctaaatgac	tagtgaanaa	acctgtgggt	tcttgctttt	660
aacaaattgg	tgtactcttg	cccctcccat	aatgtccaag	ggctgggtaa	aacctttga	719

<210> 294
 <211> 762
 <212> DNA
 <213> Homo Sapiens

<400> 294
 agctaaggag caaatccaag atctgtgcc aatgtgtttt tggagccggc cgggaatgtg 60
 cagtcacaga gaaaggggaa cccacctgtc tctgcattga gcaatgcaaa cctcacaaga 120
 ggcctgtgtg tggcagtaat ggcaagacct acctcaacca ctgtgaactg catcgagatg 180
 cctgcctcac tggatccaaa atccagggtg attacgatgg aactgcaaa gagaagaaat 240
 ccgtaagtcc atctgccagc ccagttgttt gctatcagtc caaccgtgat gagctccgac 300
 gtcgcatcat ccagtggctg gaagctgaga tcattccaga tggttggttc tctaaaggca 360
 gcaactacag tgaaatccta gacaagtatt ttaagaactt tgataatggg gattctcgcc 420
 tggactccag tgaattcctg aagtttgttg aacagaatga aactgccatc aatattacaa 480
 cgtatccaga ccaggagAAC aacaaagttg cttaggggac tctgtgttga tgccctcatt 540
 gaactgtctg gatgaaaatg ctgattggna actcagcttc caagagtttc tcaaagtgcc 600
 ctcaaaccga tctttcaacc ctctgagaa agaagtgtgc cctgngaggg attaaacgta 660
 atgcagatgg agnctgagac cnaaggtgga ccngttnacc gcctgtgtcc ggtgccgggt 720
 ggaaattggg tcnngtncag ccatgaacct gttacgggaa ag 762

<210> 295
 <211> 708
 <212> DNA
 <213> Homo Sapiens

<400> 295
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 caagttaaat gcaatataga agcctactaa atacaaatac aagttcaca acacatatgc 120
 aacagaaact tgtttanatt gtttcttgaa gtttgactac ttaaaaacat aggtgtaaag 180
 gaaagacatt cagactgggtc cacgtgggct tgtagcagg cagaggaacc ctgctttcca 240
 aaaactgata tagtccagag tcacggcatg tgggaatgtt tccatggaca ctggatctta 300
 acagatgcta tagtgtttac aaaactacac acacagagaa agcccaagga agcctgcagg 360
 ctaagcccta tgcttttaga gggctgaagg aaccaaacct agtttaatcc tgtttgtttg 420
 ctccatgcaa aactttatgg aagactcccc agactaggct atttagcagc ttccatgaat 480
 ggtcctcaga tcatgtgatt ctacggcata gacgacagct gccctattta cacagaagct 540
 gcagaactca agaggaaatg ggatttgctc ttgggagttc aatggtgcag ggtaaaagta 600
 gtctggatg ataaccatgt tccaaatgac taagtgaaga gacactgtgg gttcctgcct 660
 tttacaaaaa tgggggtact cctgcccctc ctccccanaa atgtocaa 708

<210> 296
 <211> 652
 <212> DNA
 <213> Homo Sapiens

<400> 296
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 caagttaaat gcaatataga agcctactaa atacaaatac aagttcaca acacatatgc 120
 aacagaaact tgtttanatt gtttcttgaa gtttgactac ttaaaaacat aggtgtaaag 180
 gaaagacatt cagactgggtc cacgtgggct tgtagcagg cagaggaacc ctgctttcca 240
 aaaactgata tagtccagag tcacggcatg tgggaatgtt tccatggaca ctggatctta 300
 acagatgcta tagtgtttac aaaactacac acacagagaa agcccaagga agcctgcagg 360
 ctaagcccta tgcttttaga gggctgaagg aaccaaacct agtttaatcc tgtttgtttg 420
 ctccatgcaa aactttatgg aagactcccc aagactaggc tatttagcag ctccatgaa 480
 tggctcctcag atcaagtgt tctacggnat anacgacaag ctgcctatt tacacagaag 540
 ctgcangaac tcaagaggga atgtgggatt gccctgggg agttcaatgg ttgcanggggt 600

aaaagttant cttgggntga ataaccaggt ttctaaaatg accaaattga aa 652

<210> 297

<211> 879

<212> DNA

<213> Homo Sapiens

<400> 297

cactttaatt	tctttattca	tcaatagtat	ccgaaaagga	agaatcagga	gttacaaaaa	60
caagttaaat	gcaatataga	agcctactaa	atacaaatac	aagttcacia	acacatatgc	120
aacagaaaact	tgtttagatt	gtttcttgaa	gtttgactac	ttaaaaacat	aggtgtaaag	180
gaaagacatt	cagactgggtc	cacgtgggct	tgtagcagg	cagaggaacc	ctgctttcca	240
aaaactgata	tagtccagag	tcacggcatg	tgggaaatgtt	tccatggaca	ctggatctta	300
acagatgcta	tagtgtttac	aaanctacac	acacagagaa	agcccaagga	agcctgcagg	360
ctaagcccta	tgcttttaga	gggtgaagg	aaccaaacct	agtttaatec	tgtttgtttg	420
ctccatgcaa	aactttatgg	aagactcccc	agactaggct	atttagcagc	ttccatgaat	480
ggctcctcaga	tcatgtgatt	ctacggcata	gacgacagct	gccctattta	cacagaagct	540
gcagaactca	agaggaatgt	ggatttgctc	ttgggagttc	aatgttgagc	ggtagaagta	600
gtcctggatg	ataacccatgt	tccnaaatga	ctagtgaaga	gacactgtgg	tttctgcct	660
ttaacaaaant	gggtgtactcc	ttgccctcct	ccaatanagt	ccaaagggct	ggtaaaaacc	720
ctttgattaa	agggctgctg	cctgttgagt	ttcccaangg	nacttgggac	anggganccg	780
catttcaaga	ccggaacaaa	ttgggagttt	tgaaaaaagt	ttttaaatng	ggaatggggt	840
acataaaaaan	gcttgaaatg	gctaaaaacaa	aggngggaa			879

<210> 298

<211> 697

<212> DNA

<213> Homo Sapiens

<400> 298

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gtgaaaacaa	ctatggaaa	tatatcta	acgtctacgc	agtctctcac	agcagaaaca	120
aaggacatag	ctttggaacc	taaggaacaa	aaacatgaag	acaggcagag	caatacacct	180
tctcctcctg	ttagtacctt	ttcatcagg	acttctacca	ccagtgat	tgaagtttta	240
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aattcaagat	gatgaattgt	caggcaagg	gatatgcttt	agtgcctatt	ataagtta	540
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tgaaacatta	agttatacca	ctgaggaagc	agaaatggga	agaaaagtgg	gcgaaagtgg	660
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<210> 299

<211> 510

<212> DNA

<213> Homo Sapiens

<400> 299

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taattttttta	ctttaacnnc	taatgttont	tttcctgaac	nntaattaan	aaatgttgaa	420
atatttaaatg	tnaaanantc	caantttccg	tntgttaaca	ttacnctcc	aatgttcnta	480
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<210> 300

<211> 625

<212> DNA

<213> Homo Sapiens

<400> 300

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tgctgaaagt	cagccanaan	cactttctga	caaggaanat	gtttgcaata	cagttgaatt	360
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naanngcagt	ancatttccn	tccttgaaan	gattnngttt	actcaaagga	attngnnnaa	540
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<210> 301

<211> 792

<212> DNA

<213> Homo Sapiens

<400> 301

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ggtaccacaaa	ggtaccacnt	tttatacaaa	cttaattgtg	aaanctgggt	gaaataaatt	240
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gtgtgacnct	tacttttttaa	ggaaaaaaat	tagtttataaa	tttaatancc	acanatttaa	360
taattttttta	ctttaacact	taattgtacat	tttcatganc	agtaattaaa	atatnttgaa	420
atttttaaatn	tgaaaaaattt	caaagtttca	gtatnttaac	attacncttc	aaatgttctt	480
aatatatata	taaacactta	caaattataa	atacaactag	ttgtntntct	acaatacata	540
tntgaacacc	attctttcttc	tctagccatn	tttatntgan	gataaaagtaa	taaatctctg	600
tgctattcaa	gggaaaaaaa	atgaatgctt	taaaaataaa	atctttataaa	aataattcca	660
aaaataaagt	tcaaatattg	cacaaaaata	atttaactgt	aaatattact	ncntagtgtg	720
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<210> 302

<211> 738

<212> DNA

<213> Homo Sapiens

<400> 302

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ttcagatcaa	aatttttttt	aagttttaa	cattcactct	ttaaattttca	gacagtgtca	300
gtgtgactct	tacttttttaa	ggaaaaaaat	tagtttataaa	tttaatagcc	acagatttaa	360

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ctggtgctat	tcaaggnaaa	aaaatggaat	gccttaaaaa	aataaaatcc	ttaaagaata	660
ggttcaaaaa	ataaagttca	aaatantngc	ccaaaaataa	attaacnngg	taatattaac	720
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<210> 303

<211> 635

<212> DNA

<213> Homo Sapiens

<400> 303

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ggttgaaatc	aaacactgaa	cctcagagtc	caccaatagc	ctctcctaaa	gcaatcacia	420
agccagttn	gaggactgtg	gtcgatgaat	ctgaaaatct	cttcagtgcc	tttctctcgc	480
caactgatgt	ccagaccatt	cagaagagtc	cagtgggtatc	aaaacctcca	ncataatcac	540
aacnaccang	nagaangaan	tgaaaancan	ottacatgaa	tccttgacac	ttggncaan	600
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<210> 304

<211> 847

<212> DNA

<213> Homo Sapiens

<400> 304

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tacaggcgca	caccaccacg	ccaggcta	ttttgtatct	ttagtagaga	tggggtttca	180
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tatgtgcaag	taaaggcagt	taaataactt	tcagtaataa	aatgcatcac	aatatttcac	360
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ccatttgcaa	aatcattata	aataaatttt	cncaattatc	caatcacaa	tctagataac	780
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<210> 305

<211> 767

<212> DNA

<213> Homo Sapiens

<400> 305

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cggctgagga	ggggcgatga	gttggttcaa	cgctcccag	ctctccagct	tcgctaagca	240
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gaatcccttg	cacattggcc	aatcaagaac	tcctgaaaca	actgaatcac	aagtaaaaag	660
actccctcct	tgtgtgtttc	aaggggaaaa	ctctgggcaa	caaggtactt	catcacctaa	720
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<210> 306

<211> 1659

<212> DNA

<213> Homo Sapiens

<400> 306

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gaatcccttg	cacattggcc	aatcaagaac	tcctgaaaca	actgaatcac	aagtaaaaag	660
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ttgaatttct	gaatgaaaaa	gcnggaaaaa	agggangctc	agttattatc	tcttagtaag	1620
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<210> 307

<211> 831

<212> DNA

<213> Homo Sapiens

<400> 307

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ctcctcaaag	gatatgaagc	cccacagatt	gccttacgtt	gtgggattat	gctgagagaa	480
tgtattcgac	atgaaccact	tgccaaaatc	atcctctttt	ctaatacaatt	cagagatttc	540
tttaagtacg	tggagttgtc	aacattttgat	attgcttcag	atgcctttgc	tactttcaag	600
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<210> 308

<211> 833

<212> DNA

<213> Homo Sapiens

<400> 308

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gagacgactg	actgtgacag	gggccgggga	gctcttcaag	gggccgtttt	cttcaagtct	180
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<210> 309

<211> 1320

<212> DNA

<213> Homo Sapiens

<400> 309

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<210> 310

<211> 1030

<212> DNA

<213> Homo Sapiens

<400> 310

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<210> 311

<211> 546

<212> DNA

<213> Homo Sapiens

<400> 311

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tggaggacct	gcaaaatgta	tactcgggtt	gtttttcttt	ttaaaaatat	tgtnaaacag	360
gcaagtgagg	cttaacagca	ttatggttca	ttacnngggt	tgggntatat	acctttttca	420
gcttctgtna	tgagcaagtt	gtgttttcaa	tccccacttt	caatgtctat	gggaagggcg	480
cnttttgcctn	tgttttgttt	tgtctttaaa	ncntttttaa	acnngggaca	canatggang	540
cgggcc						546

<210> 312

<211> 518

<212> DNA

<213> Homo Sapiens

<400> 312

aaaattatta	ntntaaaagg	ggaaataggt	nggattncen	tnttnagggc	aataattntg	60
gggaggaatg	gggtggggct	nacccctgna	acccatnata	aacctattct	nctnagggtg	120
ctgggaaana	attgggggtct	ggaataaaanc	tncaaagggg	tcnccngctt	cactaaaacc	180
ttggcaacta	aggctcattt	ttccaaaggg	gttnctnang	tcnnctccct	ntnaaatcnt	240
tttattatnc	caggggtggct	gttgctaang	cttnggtggg	aaancangaa	nttntgctn	300
ctnctgctgc	tggtgctgct	gggcantnca	agggaaaacc	cccccgacaa	actgggataa	360
ngtgacctgn	ttgcncacnt	ctngggccct	attncntac	ctgnccctgna	aatncttccc	420
nctctgcccc	ctttactnnt	gccaannctt	tcccccccg	ttaggataaa	aattccccctn	480
aacctccnac	ctttgggttan	cggggggtccc	ctncccc			518

<210> 313

<211> 660

<212> DNA

<213> Homo Sapiens

<400> 313

gccaagctgt	gaatacggcc	caggggtgtg	gcctgaaagt	ggcctgtgtc	tcagccgccc	60
tatcggaaga	gtcagtggtc	ggagacagt	gtgtgtacga	ggcttccgtg	cagagactgg	120
gtgcttcaga	agctgctgca	tttgacagt	acgaatcgga	agcagtgggt	gcgacccgaa	180
ttcagattgc	cctgaagtat	gatgagaaga	ataagcaatt	tgcaatatta	atcatccagc	240
tgagtaacct	ttctgctctg	ttgcagcaac	aagaccagaa	agtgaatata	cgcgtggctg	300
tccttccttg	ctctgaaagc	acaacctgcc	tggtccggac	ccggcctctg	gacgcctcaa	360
gacactctag	tggtcaatga	gggtgttctg	gtatccatgt	cctatccaag	cccttcacca	420
agaagacctt	aagagtcgat	gtctgtacca	ccgacaggag	ccatctggga	aaagtgcctg	480
ggaggcgccc	aaatnagcct	ggcgagggtc	tgccggtctg	ggggaaaagt	cgactcgctn	540
gtacaacctt	ctcagctaca	aatacttgaa	gaaacaagac	aangggactc	aagccantgg	600
gagtcattgg	ccctggcctc	angggctgcc	aacaacgggc	cccgtgttct	ggccccgttt	660

<210> 314

<211> 516

<212> DNA

<213> Homo Sapiens

<400> 314

gaaaggccac	tttattgatg	gagataaaaac	tgaatggagt	tccccacagc	cctccccctca	60
ctcatgttag	tggcttnact	gggcatctga	gaccagcgtg	gcctgtcacc	cacatanact	120
aggetgctta	gcccacccag	cctatcacac	tgcccgtctc	acgttgggca	gccacataaa	180
aacacgtcac	agctcaanaa	natccgtgga	tgacactctg	aatccccccc	aatggtttct	240
gtgcattttt	ttaatattgt	acaaaatatg	ttacttagga	aaaattagct	gtactgtgac	300
aagtgcggga	cgctctatta	ggattaccgt	ccccaggca	ttacttctta	ttgcagtaag	360
acctctaaaa	ggtggagctg	tncaaaccac	aaaaaatcta	aacgatttta	agaanagcag	420
caactcaata	ctgctttagt	tcatttaaat	tttctttccc	aaaaatacac	tcctaaatat	480
acaaactata	caatcttatt	attttaatgc	tggttt			516

<210> 315

<211> 677

<212> DNA

<213> Homo Sapiens

<400> 315

tcagaatggc	agattcagga	gagagtttgt	gccagaatag	cattgaagaa	cttgatgggtg	60
tccttacatc	catattcaaa	catgagatac	catattatga	gttccagtct	cttcaaactg	120
aaatttggtc	tcaaaacaaa	tatactcatt	tcaaagaact	tccaactctt	ctccactgtg	180
cagcaaaatt	tggcttaaaag	aacctggcta	ttcatttgc	tcaatgttca	ggagcaacct	240

gggcatctaa	gatgaaaaat	atggaggggtt	cagacccccc	acatatattgct	gaaaggcatg	300
gtcacaaaaga	actcaagaaa	atcttcgaag	acttttcaat	ccaagaaatt	gacataaata	360
atgagcaaga	aaatgattat	gaagaggata	ttgcctcatt	ttccacatat	attccttcca	420
cacagaaccc	agcattttcat	catgaaagca	ggaagacata	cgggcaagag	tgcaaattgga	480
gctgaggcaa	atgaaatgga	aggggaaggn	aaacagaatg	ggntcaggca	tggagaccaa	540
acacagccca	ctaagagggtt	ggcagtgaga	gttctgaaag	accagtatga	tgacttgtan	600
gtgttcaatc	cctggnggct	gattcaagaa	aaataattcc	acaagggtgc	tattcntngt	660
ttttacaaga	cntcctt					677

<210> 316

<211> 843

<212> DNA

<213> Homo Sapiens

<400> 316

agcttttaaac	attcaattta	tttgtggcat	ttgtacatga	aaattatatg	acgataacat	60
tgctttctat	tctaagctag	taaattgttt	ctaagaaata	atagattgat	aaaattgcaa	120
gtcttaatac	aaaggtaggt	tatgaaaatg	tatattaatt	tgagatatag	aaaagttttc	180
aaataataat	gttttcaggg	ttatatgcaa	atagacacta	aataagacaa	ggtttctgca	240
aacatgatgt	aacaataatg	actggaactc	tgaatgtgag	aaattcagaa	aatgaaccag	300
ctacttaaaa	agcaaaaatg	tgctaagtaa	atttgtattt	tcatggttat	tctaaggaga	360
ggaggaataa	tctgttgagg	ttagtgccct	caagcagacc	ccataacttt	gctacaccgc	420
atttaacttc	tctgtgctgt	tttcttttaa	ttttcaaaat	ggaaattagc	tgtttccattg	480
gtgaagtgca	ttgtaaaatg	agagaatttt	caaataatgc	aattactcta	tggtattctg	540
ttttaatagt	aatataacca	tatgaagcag	gtataatgag	aataaatttt	gccataaaca	600
aattctgaaa	tctgaanttt	gtttctgctg	tcatagtatg	aattcgcttt	aaagananca	660
ggcaatccaa	attcaacttg	ctcacctgaa	aacaaaatgt	ccgtanatcg	tgagttcata	720
taataacctc	cttaatgatc	ttcctgcaca	naaaccaaatt	tcttttcaac	ttgggggtcaa	780
caagaaccta	ttgctgaatt	ttcatataaa	actatttccct	gttggcagtt	tctaccccc	840
gga						843

<210> 317

<211> 835

<212> DNA

<213> Homo Sapiens

<400> 317

acaagacacg	cctgcgtagt	ggtagtgccc	tcctgcagtc	ccagtctagt	actgaggacc	60
cgaaggatga	gcctgcggag	ctaaaaccag	attctgagga	cttatcctcc	cagtcctcag	120
cttcaaaggc	atctcaggag	gatgccaatg	aaatcaagtc	taaaacgggat	gaagaagaac	180
gagaacgaga	aaggagggag	aaggagaggg	aacgagaaaag	agaacgggag	aaggagaagg	240
agagagaacg	agagaagcag	aagctaaaag	agtcagaaaa	agagagagat	tctgctaagg	300
ataaagagaa	aggcaaacat	gatgatggac	ggaaaaagga	agcagaaatt	atcaaacaat	360
tgaagattga	actcaagaag	gcacaggaga	gccaaaagga	gatgaaacta	ttgctggata	420
tgtaccgttc	tgccccaag	gaacagagag	acaaaagtca	gctgatggca	gctgagaaga	480
agtctaaggc	agagttggaa	gatctaaggc	aaagactcaa	ggatctggaa	gataaagaga	540
agaaagagaa	caaagaaaat	ggctgatgaa	ggatgccttg	aggaagatcc	gggcagtgga	600
gggacaagat	agaataccta	cagaagaagc	taagccatgg	gcaagcagga	agaagaagca	660
ctcctctctg	aatgggatg	tcacaaggcc	aagcctttga	agacatgcag	gagcaaaaat	720
atccgntttg	attgcagcaa	nttgccggga	anaanggatg	atgccaaatt	ttcaaagccc	780
aatgtcaaaa	gccgttttca	agttccaaat	ccagnttcac	naagnttgcc	ttaaa	835

<210> 318

<211> 582

<212> DNA

<213> Homo Sapiens

<400> 318

caaactgaat	cctgctttaa	ttcaagcttg	nggagaacaa	agtcctacag	aaacattcca	60
nanaatthtc	nggaaaagag	ggatcacaa	aaccctgtaa	aaaggagact	ganagtaatt	120
canagctcac	caagttcncn	ccgtatcaaa	tttcanaaat	acccacaaga	tttcttcacc	180
anctcantcc	tgactcaacc	tcttcaatct	ttanttcatt	agaagacaaa	gggtcanatt	240
atthaaaaatt	antcnantcc	caagaaattt	aaagacttga	agtagtagag	cattcaaaac	300
ttaaataact	ttaacaagaa	agccanctga	tcttaacaag	ttacncngcn	antaaatggg	360
aaatagactg	aatcanccta	nacataattt	cattagggnt	gcaaaccacc	cangggaaag	420
tagcacaatt	ataccanttt	gtaatccaca	ttcacaagaa	gtttgcnaca	caaatagaaga	480
aaactttgng	cccatagaca	acttatthttt	taaaatatca	ctccccaaaa	gtagccatgt	540
ttccactthtt	ggtccctthtt	ccanatcaaa	aataccaact	tg		582

<210> 319

<211> 827

<212> DNA

<213> Homo Sapiens

<400> 319

gaagccattc	gatgttcatc	agattggcca	tttcagccat	accttgtgtt	tgatgttgga	60
gatggttcag	aaagacggga	taatgactca	tatataaatg	ttcaagaaat	aaaactgggtg	120
atggaaataa	ttaagcttat	taaagacaaa	agaaaggatg	ttagthttcg	aaacattggc	180
ataataactc	attacaaggc	ccagaagacg	atgattcaga	aggatttgga	caaagagttc	240
gatagaaaag	gaccagcaga	agtagacact	gtggatgcat	tccagggtcg	gcagaaggat	300
tgtgttattg	ttacgtgtgt	cagagcaaat	agcatccaag	gttcaattgg	attcctggca	360
agtttgaga	gattgaatgt	caccatcaca	cgagccaagt	acagcctctt	catcctcgga	420
catttgagga	ccctgatgga	aaaccagcat	tggaatcagc	tgattcagga	tgctcagaag	480
cgtggtgcca	ttattaagac	ctgtgacaaa	aactatagac	atgatgcagt	gaagattctg	540
aaactcaagc	ctgtgctgca	gagaagtctc	actcancctc	ctaccatagc	cccaaagggg	600
tccaaacccc	aaggggtggnt	tgcccaagca	ncaagctaga	cagttggatt	ttgccaaaga	660
caatcctggg	tgccggcttc	tccaatacca	aaacaaccc	cgggactccc	aagggaaaat	720
tacncctaac	ggthttacctt	caaagggacc	ctgaaaagac	ccncctgggt	caatgaccaa	780
cnttcanggg	nccacgaan	tggtgaaaa	agggatgggc	aatttag		827

<210> 320

<211> 598

<212> DNA

<213> Homo Sapiens

<400> 320

aaatthttaa	aggatthttgt	tatttgctat	acaaatatac	atthtcaactt	ttacaacatt	60
cactccagtc	tgacctcctt	gtctatagaa	gactaagaga	tcaacatttc	cagtctctga	120
cttcaaggac	attattacgg	atacacaatg	ccctctgaaa	gctthttgcaa	atgacagaaa	180
atactgaaga	tgaccagagg	ctcaggtgtt	aaggatgcat	tttccatgtt	ttccaacagc	240
acacaaaactc	cttacaataa	acaagcttat	ctagatgggtc	ccacgagctg	gtcatcttca	300
gtttacaata	tgctgtggct	gctggcccat	gtcactgggc	tttccataaa	aagctthctt	360
ttcttgggaa	ctgctgtcct	cctgctccaa	gtgtcctctt	gtccaccta	gagttcctcc	420
tggtgtgatg	ggtctcggaa	ccacacttct	cctgctcccc	ttcactgaaa	gccctggcct	480
ctctcctgtg	acagagctcc	tcttccgggt	catcacattt	gctctgacac	gtgggnagcc	540
tcggggaaact	gggcanctgg	gaggntccgt	thttthtttg	gaaggthttgt	tggtctgcc	598

<210> 321

<211> 808

<212> DNA

<213> Homo Sapiens

<400> 321

gcataccac	catccacgag	gatgaggtgg	ccaagaccca	gaaggcagag	ggaggtggcc	60
gcctgcaggc	tctgcgttcc	ctgtctggca	ccccaaagtc	catgacctcc	ctatccccac	120
gttctctctct	ctctctcccc	tccccacct	gttccccctct	catggctgac	ccccctctgg	180
ctggtgatgc	cttctcaaac	tccttggagt	ttgaagaccc	ggagctgagt	gccactcttt	240
gtgaactgag	ccttggtaac	agcgcccagg	aaagataccg	gctggaggaa	ccaggaacgg	300
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cogtgcagag	actgggtgct	tcagaagctg	ctgcatttga	cagtgcagaa	tcggaagcag	480
tgggtgcgac	ccgaattcag	attgccctga	agtatgatga	gaagaataag	caatttgcaa	540
tattaatcat	ccagctgagt	aacctttctg	ctctgttgca	ncaacaaaga	ccagaaagtg	600
aatatccgcg	tggctgtcct	tccttgcctct	gaaaagcaca	aactgcctgt	tccgggaccc	660
gggctctgga	cgcctcaaac	actccaagtg	ttcaatgaag	gtgttctggg	tatccatggt	720
ccctatccaa	accnttaac	aagaaagacc	tttaanaaag	tcfaatgtcc	ngtnaccaac	780
cggacaaggg	agccaatctt	gggaaaaa				808

<210> 322

<211> 629

<212> DNA

<213> Homo Sapiens

<400> 322

agcaaaataa	atgtcactat	atcaagataa	agaataacat	taggtgtgaa	ctagcatagg	60
tgattcatgg	gaaacgaaat	ggcaaatctg	aaaggaattc	tgggaaccat	cgtactaggt	120
tacattgcct	ttttgcctgt	agagaaccca	tgaggagagg	ggttctcagc	cttcccagtg	180
gaaccttctct	cttagttgca	ctggcattgg	gggatctcat	tgctgggcct	aggtccaggc	240
agggcgagctc	ctggggccca	agggcgggct	cactcaccag	ctgtcttcca	gtgtctgtgt	300
gctgtcctctg	ccctcctgcc	tcttctccaa	ctccactgct	gtctgttcca	acagagcaag	360
acacagcgtc	cgtgtctggca	ngccctgaag	caagggccat	gactccact	ggcttgagct	420
ccctgtctctg	tttcttcaag	tattttgtan	ctgagaaagt	tgtaccaanc	gaatcnacct	480
ctccccaaaga	cggggaagac	ctcccgccaa	ggctgatttg	gggcgcctcc	caagcactct	540
tccaaaatgg	ctcccgctcg	ttgggacana	catecnactt	tttaangcct	tccggggnaa	600
agggctgggn	taaggacatt	gggtncccc				629

<210> 323

<211> 798

<212> DNA

<213> Homo Sapiens

<400> 323

aacatttctg	tgatcaacat	tgettactgc	gtttctactg	tcaacaaaat	gagcccaaca	60
tgacaactca	gaaaggacct	gaaaacttac	attatgatca	gggttgctcag	acatctcgaa	120
ccaaaatgac	aggttcagca	ccacccccct	ctccaacacc	taacaaagag	atgaagaaca	180
aagcagttct	ttgcaaacct	ttaacaatga	caaaagctac	ttactgtaaa	cctcacatgc	240
agaccaaatac	ttgtcagaca	gatgatactt	ggaggacaga	atatgttcca	gtgcctatcc	300
ctgtgcctgt	gtatatccca	gttctctatgc	acatgtacag	tcagaatatt	cctgttccta	360
ctacagttcc	tgttctctgtg	ccagttcctg	tttttctgcc	tgctccattg	gacagcagtg	420
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acatcaacag	tgtaattatt	gaaacagata	taattgggttc	agaccttttg	agaactctg	600
accagagac	acagtccagc	atgcctgatg	taccatatga	accagatttg	gatatcgaa	660
tagattttcc	cagagctgct	gaaggagcct	tgatatggga	aaatgaattt	ttattaccaa	720
ccngtttttg	ggcgaaagaa	tatgaaggaa	caagcccaaa	cctcgattct	aaaaaaaaag	780

ggagccaagg agaaaagg

798

<210> 324

<211> 754

<212> DNA

<213> Homo Sapiens

<400> 324

aaaaggacac	taagggtttta	ataaggggaa	caaaaaattg	ttttcaccag	catagattca	60
cattacagta	caccaatatt	gacagcattc	tcttgtctat	ttttggtaca	gaagatggta	120
tctctctaca	taaccttgta	aggcttcagt	aactaaaatg	taaaaccaaa	caaaacaaaa	180
ccccaaaaca	aaacaaaaac	cccagcctat	tagtttacag	tttattttta	aaattccgaa	240
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gtttcttact	acaagaaaaa	aattatacat	ggcacattct	cattcatatt	ctgtaatgta	420
aaaagttaca	aacataccta	atcaaataaa	taataataaa	aaaagaattt	gaatgtattt	480
gttaagtatc	ctaaaaccac	tacatagaat	aatggcaact	ttcactcaca	gattattttac	540
atggtaatac	ccagcgtggg	tacactgcta	caaaactcaa	aacagaagga	gtaaacttga	600
aatgtttttc	ataataaaga	cttagcanca	tgactatcct	aatgccgttt	tatcccgaat	660
gcttctggca	acgttccctt	ttaatccggg	gtctcatcca	attcaaaaaa	tggccttttac	720
caaaaaatat	cctttttaca	gaaagaaacc	cggt			754

<210> 325

<211> 854

<212> DNA

<213> Homo Sapiens

<400> 325

ggtcaggggt	gagagctgga	atctctgcac	gggccttggg	aaacgactgt	cttcttctgc	60
caaaatgtca	ggaattggaa	ataaaagagc	agctggagaa	cctggcacct	ccatgcctcc	120
tgagaagaag	gcagctgttg	aagattcagg	gaccacagtg	gaaacaatta	agctaggagg	180
tgtctcttca	acggaggaac	tagacattag	aacactgcaa	accaaaaaatc	gcaagctggc	240
agaaatgttg	gatcagcggc	aggccattga	agatgaactt	cgtgagcaca	ttgaaaaact	300
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gtttgatgaa	aacatccgta	tcatecttaa	acgttatgat	ctggagcagg	gcttgggaga	420
cctactcaca	gaacgaaaag	cccttggtgt	gcctgaacca	gaaccagact	ctgatagcaa	480
tcaggagcgt	aaagatgacc	gagagagagc	agttccagtg	aagagatgga	gtctcagctg	540
caggaacgtg	tggagtcttc	ccgccgagcc	gtgtcccaga	ttgtgactgt	ttatgataaa	600
ttgcaagaaa	aagtggagct	cttatcccgg	gaagctaaac	agtgggagat	aatctgatag	660
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cctccaaagt	tgcaagaggt	aaaattgggg	naaaagccga	attcaccaan	tttccggtcc	840
tggaagtcca	anga					854

<210> 326

<211> 760

<212> DNA

<213> Homo Sapiens

<400> 326

caaactgaat	cctgctttta	ttcaagcttg	tggagaacaa	agtccctacag	aaacattcca	60
cagaattttc	tggaaaagag	ggatcacaa	aaccctgtaa	aaaggagact	gagagtaatt	120
catagctcac	caagttctct	ccgtatcaaa	tttccagaat	accacacaga	tttcttcacc	180
agctcagtc	tgactcaacc	tcttcaatct	ttattttcatt	agaagacaaa	gggtcatatt	240
atttaaaatt	attctagtct	caagaaattt	aaagacttga	agtagtagag	cattcaaaac	300

ttaaataact	ttaacaagaa	agccagctga	tcttaacaag	ttactctgct	agtaaattggg	360
aaatagactg	aatcatccta	gacataatct	cattagggct	gcaaaccacc	caggggagag	420
tagcacaatt	ataccatttt	gtaatccaca	ttcacaagaa	gtttgctaca	caaatagaaga	480
aaactttgtg	cccatagaca	acttatcttt	taaaatatca	ctccccaaaa	gtagccatgt	540
ttccactttt	gttccctttt	ccacatcaaa	aataccaact	tgatttcttc	aggaggaatg	600
gacaatccaa	gtttatacaa	gtgggctggg	aaaaagaaaa	cactgaaaag	tctaaaagca	660
caagataaac	aaagcctggg	aagggaagac	agttaagagt	tatttgcttc	caantcaatc	720
cnaaaacca	anggcttgta	attaacaagt	cctttccggc			760

<210> 327

<211> 852

<212> DNA

<213> Homo Sapiens

<400> 327

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gcagacccaa	tcttgtcaga	cagatgatac	ttggaggaca	gaatatgttc	cagtgcctat	120
ccctgtgcct	gtgtatatcc	cagttcctat	gcacatgtac	agtcagaata	ttcctgttcc	180
tactacagtt	cctgttccctg	tgccagttcc	tgtttttctg	cctgctccat	tggaacagcag	240
tgagaagatt	cctgcagcaa	ttgaggagct	aaaaagcaag	gtttcttcag	atgctcttga	300
tacagagttg	cttacaatga	cggatatgat	gagtgaagac	gaggggaaaa	cagagacaac	360
caacatcaac	agtgtaatga	ttgaaacaga	tataattggt	tcagaccttt	tgaagaactc	420
tgacccagag	acacagtcca	gcatgcctga	tgtaccatat	gaaccaagat	ttggatatcg	480
aaatagattt	tcccagagct	gctgaggagc	ttgatattga	aaatgaattt	ttattaccac	540
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aaactaagmn	acttggatga	aagatcntcc	gggnaattag	aatgagttaa	aatccttcca	780
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<210> 328

<211> 799

<212> DNA

<213> Homo Sapiens

<400> 328

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tctctctaca	taaccttgta	aggcttcagt	aactaaaatg	taaaacccaa	caaaacaaaa	180
ccccaaaaca	aaacaaaaac	cccagcctat	tagtttacag	tttattttta	aaattccgaa	240
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cccagtaaaa	gagccccctt	ccaaggaagc	tttgcaacag	tagagttgtg	caatatggat	360
gtttcttact	acaagaaaaa	aattatacat	ggcacattct	cattcatatt	ctgtaatgta	420
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aatgttttcc	ataataaaga	tctagcaaca	tgactatcca	atgctgtttt	atcccgattg	660
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<210> 329

<211> 978

<212> DNA

<213> Homo Sapiens

<400> 329

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<210> 330

<211> 1017

<212> DNA

<213> Homo Sapiens

<400> 330

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<210> 331

<211> 799

<212> DNA

<213> Homo Sapiens

<400> 331

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caggagcttt	ttagaaaagt	togaagtatc	ttaaataaat	tgacaccaca	gatgttcaat	180
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aattttccgga	agctgctact	gaaccgttgc	cagaaggagt	ttgaaaaaga	taaagcagat	420
gatgatgtct	ttgagaagaa	gcagaaagaa	cttgaggctg	ccagtgtctc	agaggagagg	480
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<210> 332

<211> 881

<212> DNA

<213> Homo Sapiens

<400> 332

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tggcggctgc	ctgggtccgc	gccgaggaag	agctaaggag	caaatccaag	atctgtgcca	180
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acctcaacca	ctgtgaactg	catcgagatg	cctgcctcac	tggatccaaa	atccagggtg	360
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tgtgcccttg	gaggatgaaa	cgtatgccan	atggagcttg	aaancgaggt	ggactgtaan	840
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<210> 333

<211> 810

<212> DNA

<213> Homo Sapiens

<400> 333

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<210> 334

<211> 808
 <212> DNA
 <213> Homo Sapiens

<400> 334
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 ctaagcccta tgctttttaga gggctgaagg aaccaaacct agtttaatcc tgtttggttg 420
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 ttaacaaatt ggnggactct tggcccttct tcccatagng tccaagggtt ggtaaaacct 720
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 atttcaaact ggaccaagtg gaggtttg 808

<210> 335
 <211> 758
 <212> DNA
 <213> Homo Sapiens

<400> 335
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 agagaagacc aggtgtccag agagtggacg aaggtgggtg gaacactgta caaggggcca 180
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 gaggtgtgga tgtggagagg aacagccttg agctgaaccg aaataaaciaa gggagtcagc 660
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 tgganaggaa gtccaaatct atcatggtta attttttc 758

<210> 336
 <211> 785
 <212> DNA
 <213> Homo Sapiens

<400> 336
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<210> 337

<211> 643

<212> DNA

<213> Homo Sapiens

<400> 337

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 ctctcttgac tatgagtaaa ggagaaaagg ctngactgga aaatggacc ccaaatggcctt 600
 accggaaaga aaggggacagc ctgatnccaa aatttcccca aat 643

<210> 338

<211> 831

<212> DNA

<213> Homo Sapiens

<400> 338

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<210> 339

<211> 758

<212> DNA

<213> Homo Sapiens

<400> 339

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<211> 840

<212> DNA

<213> Homo Sapiens

<400> 340

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<210> 341

<211> 793

<212> DNA

<213> Homo Sapiens

<400> 341

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aacagaaaact	tgtttanatt	gtttcttgaa	gtttgactac	ttaaaaacat	aggngtaaag	180
gaaagacatt	canactgggtc	cncgngggct	tgntagcagg	cagaggaacc	ctgctttcca	240
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<210> 342

<211> 906

<212> DNA

<213> Homo Sapiens

<400> 342

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ttgttgctct agcagagaga gactaaacat tgtcgtagt ttaccagatc cgtgatgccca      780
cttacctgtg tgtttggtta caacaaacca acatcatgga ggtccctgga ttgaaaaagg      840
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<210> 343

<211> 875

<212> DNA

<213> Homo Sapiens

<400> 343

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tgcacatcac tggcagagaa ctgaggtcca aaatagctga aacctttgga cttcaagaaa      180
attatatcaa aattgtcata aataagaagc aactacaact agggaaaacc cttgaagaac      240
aaggcgtggc tcacaatgtg aaagcgatgg tgcttgaact aaaacaatct gaagaggacg      300
cgaggaaaaa cttccagtta gaggaagagg agcaaaatga ggccaaactc aaagaaaaac      360
aaattcagag gaccaagaga ggactagaaa tactggcaaa gagagcagca gagacagtgg      420
tggatccaga aatgacaccg tacttagaca tagctaacca gacaggcaga tcaatcagaa      480
ttcccccatc agaaagaaaa gcccttatgt tagctatggg atatcatgag aagggcagag      540
ctttcctgaa aagaaaagaa tatggaatag ccttgccatg tctgttggaac gctgacaaat      600
atttctgtga gtgttgacga gagctgctgg acacagtgga taactatgcc cgtcttcagc      660
tggatatagt gtggtgttac ttgcgctggt aacagctgga atgccttgat gatgcagaaa      720
aaaaattaac ttggnccaga aatgctttta aaattggtcc ggagaaatcn tcgaaactgg      780
tccccntaaa nggaattgtg gggaaaagag aangtctggt tctaagactn tacttacttt      840
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<210> 344

<211> 629

<212> DNA

<213> Homo Sapiens

<400> 344

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cgcgatgatc atcctgtctt cagtcagtgc cttctggaag ggagggaaaag tcttggtatgc      180
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tcccactggg cacacatcta cagaggagtg cgtggcgtag tgaggacggg tactgctgga      300
gccgacacac agcgaactac atacttttag aaagagcctc tgtcacatgg ctagaacaac      360
aacaacaaca aagaaaaccc acaaaaaacc tggagaaaat atatctaat ctctgatagg      420

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tctcttagct	agcagtgagt	tcagtatgac	agcacagagt	ctaaaaatat	taattaaata	480
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aatgctgaat	atatataaag	cctgccactc	aatctttgaa	tttcnggggg	cgcaatttta	600
ctgaactaag	anccctaaaa	caactggcg				629

<210> 345

<211> 724

<212> DNA

<213> Homo Sapiens

<400> 345

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ctttcatttt	aaaaagttat	atttaatttt	tgggggcctt	aattaaaatt	taacatttaa	180
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gcaaatnctg	acttcatttg	tgttttaaac	acgattatat	gaatttttct	tttttaatta	300
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aaaaaaataa	aggaaacttat	ttccttccta	aggtctcagc	tagtttctta	ngtcttttct	480
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caaacttatt	cttgantgtt	aatttagtgt	tgcaggtana	acaggcaaag	cagttcacgc	600
accaggcctt	attaagagca	gagaccccca	tcaccttcta	taacacgatt	gcagtgggaa	660
gcaaacatca	ccaaatagct	gggttatagn	gagtttcaca	atatgccag	gcctttcctt	720
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<210> 346

<211> 907

<212> DNA

<213> Homo Sapiens

<400> 346

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tactgatgca	gaaagacgat	cagtgatgga	tgcaacacag	attgctggtc	ttaattgctt	180
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tcaagtttct	gtatgtgcat	ttaatagagg	aaaactgaaa	gttctggcca	ctgcatttga	360
cacgacattg	ggaggtagaa	aatttgatga	agtgttagta	aatcacttct	gtgaagaatt	420
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ggagtgtgag	aaactcaaga	aattgatgag	tgcaaatgct	tcagatctcc	ctttgagcat	540
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gatgtgcaat	gatctcttag	ctagagtggg	gccaccactt	cgtagtgttt	tggaaacaaa	660
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<210> 347

<211> 711

<212> DNA

<213> Homo Sapiens

<400> 347

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ttnttgtctg	aatccgaagg	cncagctgng	tctgtaccct	gctcancagc	ctggggggcct	120
gggttgtctc	cttgnccatc	cactgggtcca	ttctgctctg	cattttttttg	ttcctntttt	180
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ttctgcaaAT	ttagcttggt	attcatccac	tccattgctt	catttgggct	tttttctacc	360
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tnaaattcct	ggaaacgtat	nttaataggt	tgacctaaat	tttttaattc	agccaactta	540
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ccagtttcaa	agtaaaactg	ttacgancat	nttcactnnc	aaacttctca	tattcnccac	660
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<210> 348

<211> 862

<212> DNA

<213> Homo Sapiens

<400> 348

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attcttcccg	aagtcttctg	tggagtgtct	ttatttctct	ttccatgtcg	tgcttttggg	180
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tttctgtttc	tttttcatcc	aggtctgata	ttaatTTTTc	taacgtcata	ttcaaactct	360
caatttgttt	cttagcttct	tcttggaagg	ctcggtattc	atcctctacc	ttagcaatgg	420
catcctgtaa	togattggca	tcatttccgg	tatgagccag	atcttctctg	aagctactag	480
ccaaagtctc	tgctttttct	ttgtccagcc	tgacactctc	caggaggtcc	tgaatatcag	540
atttgnctcc	agagttatgg	atagaatata	gctctgccac	tttctgcttt	tcattctcca	600
gctgagcctt	caggcgattc	atctctatct	ggtcactggc	cactgnggct	ttgnattcct	660
ctaaagtggc	tgncaaaggct	gcttttccct	tctgctcnac	tcaaataaat	tcgctccata	720
tggngggact	ggcggttcct	tggagtgcgc	cctatcattt	cttggngett	tccttantgg	780
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<210> 349

<211> 832

<212> DNA

<213> Homo Sapiens

<400> 349

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aacaaaatta	ttttttaaaa	aagcaaaaaga	ataaagaata	tatacaaaaag	ggacctggaa	180
tctgtaagct	gattccaaaa	acgaaataag	tagaaaatcc	atggtgaaac	ctgaacattc	240
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gaggtgtgtc	tatacataaa	cttcagtcac	ttttgcttgt	gcagaatcat	cccaatcttc	360
ccaagactga	atgggagctc	ctgtggcttt	cttccctttc	catattccca	acaaggctac	420
gtgaagttca	actcttgatg	agccgcttac	aacagcagtt	ccttaggagc	caacatgaca	480
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ggtaagtcct	tccttccctc	tcctcctgat	tatatacaac	atatctcctt	tcaagactat	600
tatttccatc	atgcttattc	cttcacaaat	ctaaaccttg	aggtgatatg	aaggaaacca	660
acatcangaa	aagaaaactc	aattcagaaa	tgaagaaaac	tggcaggtat	acaatacacc	720
cccagaacat	ctcaatatcc	ctggccagta	caattcaagt	gnactgggta	caggcccata	780
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<210> 350
 <211> 782
 <212> DNA
 <213> Homo Sapiens

<400> 350
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 tnaaanaaang cgnancacna ancatngact aatncaagggt cttnaaatat gaancaaaat 120
 natttttttaa aaaagcaaaa naataaanaa tatatncaaa ngggaccngn aatcngnaag 180
 cngatnccaa aaccnaaata agtaaaaaan ccanggggaa nccngancat tcnacctnng 240
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 caactntnga nganccgttt acaacagcag ttccttagga nccancatga caggggggnc 480
 aaatttccct atgagaanac aaacnggcca cctacagcaa aatatcaaaa ggggnaagnc 540
 ctctcttctt ctctctccng attatatnca ccatatctcc tttcangact atnatttcca 600
 tcagggtat tctttcacaa atntaaacct tgaggggata tgaaggaacc caacttcngg 660
 aaangaaaaac tcaattcana aattgaagaa acctggcagg tatacaatac cccccagggn 720
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 aa 782

<210> 351
 <211> 775
 <212> DNA
 <213> Homo Sapiens

<400> 351
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 gggtaaaagt aaaccctaaag tgaacgtgaa gccatctgtg gttaaagttg tgtcatcccc 480
 caaattggcc ccaaaacgta aggcagtgga gatgcacgtc gctgtcattg ccgctgtgaa 540
 gccactcagc tccagcagtg tccacagga acccccagcc aaaaaggcag ctgtggctgt 600
 tgtcccgctt gtctctgagg acaaatcagt cactgtgcct gaagcagaaa atcctagaga 660
 cagtctttgt gcttgncttc aaccagtcct ttnttcagat tccctacccc cagagggtgtc 720
 ttggnccttt ctcatncca aatggagcct tgaaaaactt cgcccgactt agctt 775

<210> 352
 <211> 865
 <212> DNA
 <213> Homo Sapiens

<400> 352
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 tatttttttaa aaaagcaaaa gaataaagaa tatatacaaa agggacctgg aatctgtaag 180
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 ctttgagaa gggctatcat acaacattca gtcagctgaa gatggattgg tagagggtgtg 300
 tctatacata aacttcagtc atttttgctt gtgcagaatc atcccaatct tcccaagact 360
 gaatgggcag tccctgtggct ttcttctctt tccatattcc caacaaggct acgtgaagtt 420
 caactcttga tgagccgctt acaacagcag ttccttagga gccaacatga cagggtgggtc 480


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agattttccct atgagaaaca aaactggcca cctacagcaa aatatcaaaa tgggtaagtc      540
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tcatgcttaa tntttccaaa tctaaacctt gagngatat tgaanggaaa cccaccttca      660
nggaaaagaa aacctcaatt tcagaaatgg aagaaaaact ggcaggggat accaatacac      720
ccccccagag cattttttaa atatccctgg ncacaagtn caattcaagg gnacctggtt      780
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<210> 353

<211> 875

<212> DNA

<213> Homo Sapiens

<400> 353

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caaaattatt ttttaaaaaa gcaaaagaat aaagaatata tacaaaaggg acctggaatc      180
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atttccatca tgcttattcc ttccaaatct aaacccttga ggtgatatga aggaaaccaa      660
catcaagaaa aagaaaactc aattcagaaa atgaagaaaa ctggcagggg tacaatacac      720
ccccagagca tcttcaatat cccctgggca cagtncccaa ttcaggggact gggtagaggc      780
ccataagaat naaataattg ggcagctttg gaataaagcc tcattttttt ccttcagggn      840
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<210> 354

<211> 705

<212> DNA

<213> Homo Sapiens

<400> 354

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caaaattatt ttttaaaaaa gcaaaagaat aaagaatata tacaaaaggg acctggaatn      180
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tttccatcat gcttattcct tccaaatcta aaccttgagg ngatatgaan ggaaaccaca      660
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<210> 355

<211> 862

<212> DNA

<213> Homo Sapiens

<400> 355

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accgcaatgg	ggcctctatc	cacgagttct	gcatcaacct	gcggcagctc	tacggggaca	180
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<210> 356

<211> 750

<212> DNA

<213> Homo Sapiens

<400> 356

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accgcaatgg	ggcctctatc	cacgagttct	gcatcaacct	gcggcagctc	tacggggaca	180
gccgcaagtt	cctgctgctt	ggtctgaggc	ccttcatccc	tgagaaggac	agccagcact	240
tcgagaactt	cctggagacc	attggcgtga	aggatggccg	cggcatcatc	actgacagct	300
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gatggacagt	ggatgggggg	gcacccacac	cttcgcgcga	gtcgtcatag	gccttcccag	540
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agatggcccc	gggcccggccc	aagtcctcta	ctgtgaagga	acagggagct	tgccgangga	660
cacgaacctc	aatgcccggg	tgggaangctc	tttggcttgt	ccaccaaggc	ttagcccagc	720
ccttgcaatg	nggccccgct	tcggggaagg				750

<210> 357

<211> 725

<212> DNA

<213> Homo Sapiens

<400> 357

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gcccccccat	ccactgtcca	tcactgctgag	tcctgggtcca	tgctgcagcc	cagcgccctca	420
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cggatcatcag	agctgcccgt	ggccctgttc	ccattggtgg	tggaaactgga	tgtggtgctc	540
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atggtctnca	ggaagtcttc	gaantgctgg	ctgncctttt	tcagggatga	anggccttan	660
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acttc						725

<210> 358
 <211> 813
 <212> DNA
 <213> Homo Sapiens

<400> 358
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 gagtttccag tcttttactt cacccttgag ccccgntcca ngctcctgaaa aagaaaatgt 720
 caaggactgt ggtgangaca gtactntttt caccaaccaa ggagaagaac ctttggttag 780
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<210> 359
 <211> 756
 <212> DNA
 <213> Homo Sapiens

<400> 359
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 tagaagagaa aaaacgtgcc atgcaagaga caaagataaa aggggaaaag gtagaacaga 180
 aaatagaagg gaaatgggta aatgaaaaga aagcacaaga agataaactt cagacagctg 240
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 aagaagacaa gcctaccttc aaaaaagaag agatcaaaga tgaaaagatt aaaaaggaca 360
 aagaacccaa agaagaagtt aagagcttca tggatcgaaa gaagggattt acagaagtta 420
 agtcgcagaa tggagaattc atgaccaca aacttaaaca tactgagaat actttcagcc 480
 gccctggagg gagggccagc gtggacacca aggaggctga gggcgcccc cagggtggaag 540
 ccggcaaaaag gctggaggag ctctcgtcgtc gtgcggggga gaccgagagc cgaagagttc 600
 gagaagctca aacagaagca gcaggaggcg gctttggagc tggaggaact caaggaaaaa 660
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 ccgatcggaa aaccttcaag aggaggaaga agaaga 756

<210> 360
 <211> 706
 <212> DNA
 <213> Homo Sapiens

<400> 360
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 gatcttctgt tgacttcana tgnngtttgt atcactgctc aaatacagag ttatgatgat 180
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 tgggtttact gggatattga aaaataaaaag ataataaacc caatttagta aatcaacata 360
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caggtgactt	gtttccatct	gggtttttaa	gttagccatt	cattgatgcy	gctagaaacc	600
cctaccttta	agccagcagt	ttnccttatt	tggggngcc	ctgctgcant	ggggggatga	660
aaacncattt	cctttntcca	catactcttg	aaggttgcyg	tacacc		706

<210> 361

<211> 726

<212> DNA

<213> Homo Sapiens

<400> 361

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gagcgagtga	acatgccggc	cgcggtggac	cctgcggagt	tcttcgtgct	gatggagcgt	180
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gcccgaagg	ccgaagaggt	gcangcctgg	gcgcagcgca	aggagcgnga	antgctgcag	480
ctgcagnaag	aggtgaaaaa	cttcatcacc	cgagagaacc	tggaggcacg	ggtggaagca	540
gcattggact	cccggaagaa	ctacaactgg	gccatcacca	gagaggggct	ggtggtcagg	600
ccacaacgca	nggacttcta	agggcccagt	aaggacagtg	cccggcaggg	accatgtatg	660
tatcatggcg	gaagagttgc	ccttgactgg	aattaaagca	attggtgttg	cttatgagga	720
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<210> 362

<211> 747

<212> DNA

<213> Homo Sapiens

<400> 362

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acatgctagt	cagctngcag	ttttacctcg	taaagatanc	aganaattat	agncaaacca	180
gtaaacangg	aattnaactt	tcaaaaagatt	aatccaaac	tgancaaaat	tntaccctaa	240
aacttactcc	atccaaatat	tggaaataaaa	gtcagcaggg	atncattctn	ttctgaactt	300
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aaagcaangt	taccttacca	taggccttaa	ttcaaacctt	gatccatttc	actccaanga	420
cgggagtcaa	ngctacctgg	gacacttgta	tttgtaaatt	ctgatttagc	ttatngtaaa	480
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gactttgtaa	cgcanatgtc	acttttaaat	ccagccctgc	cctgggttagc	ncttctggag	660
gaatactgca	gataagaaaa	atagttatct	gggaggctcc	ctcagngggg	tanggaattg	720
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<210> 363

<211> 1227

<212> DNA

<213> Homo Sapiens

<400> 363

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gaccacccaaa	tggtgccagc	aaggaaatac	cagaattgga	agaagaaaaa	acaattccta	180
ccaaagagcc	tgagcagata	aaatcagaat	acaaggaaga	aagatgcaca	gagaagaatg	240

aagatcgtca	tgactacac	atggattaca	tacttgtaaa	ccgtgaagaa	aattcacact	300
caaagccaga	gacctgtgaa	gaaagagaaa	gcatagctga	attagaattg	tatgtagggt	360
ccaaagaaac	agggctgcag	ggaactcagt	tagcaagctt	cccagacaca	tgtcagccag	420
cctccttaaa	tgaagaaaa	ggtctctctg	cagagaaaaat	gtcttctaaa	ggcgatacga	480
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gacagtccag	atgaaattga	catcaatgtg	gatgaacttg	ataccccga	tgaagcagat	1140
tcttttgagt	acctggccc	atgaagaatc	ccacagccac	aaagattctg	gcccagaag	1200
tcagagtcta	tttcnnga	ataccgg				1227

<210> 364

<211> 831

<212> DNA

<213> Homo Sapiens

<400> 364

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tctgaggagt	ccgtctcccg	cctcccgag	gagatccgga	gactggagga	agagctccgc	180
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tttgaggcac	tccagcaaaa	gagtcaggga	ctggactcca	ggctccagca	cgtggaggat	300
ggggtgctct	ccatgcaggt	ggcttctgcg	cgccagaccg	agagcctgga	gtccctcctg	360
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gacaagttgg	gtgcataact	cggtcaaaat	tagaaaccaa	cgagnacaat	tttggaaatca	780
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<210> 365

<211> 785

<212> DNA

<213> Homo Sapiens

<400> 365

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caggggctgc	gcttcaggaa	accaaccaa	tgacagaagca	gagaacttaa	atattgtaaa	180
taagttaact	gggcatgaaa	atacaatgcc	ttggtgttca	ggtggtgaca	actgctcttt	240
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tcatgagaaa	ttggacttta	aatccgcgcc	ctgcacacgc	aattcattta	gaccttttcg	360
tgaatcttct	ccactttcac	aaacaacct	tccagatcat	tcctcaggtc	atctagtaaa	420
cccttggtcg	attccagatt	gttctcggtg	gtttctattt	tgaccgagta	tgcaaccaa	480
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gcttgggtcct	gactgagcag	cggtgtgcacc	tgctcctgcc	ctttctggga	gtgattccac	660
ggtgctgggg	agctngccca	cacttctctt	tcagcttctt	ccacgtcacc	cgtaaaagca	720
cccagctggg	tctcgnccaa	gcttcntacc	gtgctggggc	aggcccatcc	tggntctggt	780
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<210> 366

<211> 816

<212> DNA

<213> Homo Sapiens

<400> 366

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atagttaggt	tggtgatcca	tacttgatg	ccagggactc	agggcctggg	tggtctggca	180
agactgtgga	gccgttctct	gaactcggct	tggttgaggg	tccccagctg	cagattctgg	240
aagaaatgaa	gcctctagaa	tcttttagcac	tagaggaagc	ctctgggtcca	gtcagccaat	300
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tgaggcctga	acctccta	tctctggatc	ttaatgacac	tcattcctcg	agaatcaagc	600
tcacagcccc	aaatatcaat	ctttctctgg	accaaagtga	aggatctatt	ctctctgatg	660
ataacttttg	acagtccaga	tgaattgac	atcaatgtgg	atgaacttga	tacccccgat	720
gaagcagatt	cttttgagta	ccctggccca	tgaagaatcc	cacagccaca	aagattctgg	780
ccaagaagt	cagagtctat	ttcnggaata	taccgg			816

<210> 367

<211> 803

<212> DNA

<213> Homo Sapiens

<400> 367

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gttcaagcca	ggtggaccaa	gaaacagggt	ttaataggca	tgaggcgaaa	caaagaagtg	120
ttcaaagatg	gagagaggct	ttggaagtgg	aggaaagtgg	ctcagatgac	ctcttaataa	180
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ttattacaca	aagggaaaca	gaaaataacc	aaatgacatc	agaaagtgga	gccacagcag	300
gaaggcaaga	agtggataac	accttttggg	atggctgtgg	agattattac	caactctatg	360
acaaagatga	agatagtctt	gaatgcagtg	atggggaatg	gtctgcttct	ttgcctcatc	420
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aagtgaagac	ttagatgtgg	attggagcct	atthttgatg	ctttgcaa	gggcctagga	780
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<210> 368

<211> 809

<212> DNA

<213> Homo Sapiens

<400> 368

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tgcattccat	tttaacaatt	cgtatgtatc	taacaaatac	ataaatccag	atcacaaata	180
atcttaagag	tttaacaatt	aagaaacaca	aagaatacca	catagatcta	cctttaaata	240
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<210> 369

<211> 826

<212> DNA

<213> Homo Sapiens

<400> 369

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gaccaccaa	tggtgccagc	aaggaaatac	cagaattgga	agaagaaaaa	acaattccta	180
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aagatcgtca	tgactacac	atggattaca	tacttgtaaa	ccgtgaagaa	aattcacact	300
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acctctagaa	tcttttagcac	tagangaagc	ctntgggtcca	gtcagcccat	cacaggaaga	720
gttagaacc	gaggcanggc	tgggcccggg	tgcagtaccc	cntgacagtg	gaatgggnaa	780
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<210> 370

<211> 783

<212> DNA

<213> Homo Sapiens

<400> 370

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cgagagtgtc	aaacatagta	ccataactga	atatttataa	ttacatctta	acaaaggcta	300
ggagttagtg	cttcctcaca	cacctcagag	aatgtcttag	agagtaaccc	catagaacat	360
tgtatggctt	caacagaaac	ttcaggattt	tcttcacac	tgagctactg	ccctcaaaca	420
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aagagctaga	gagctaaatc	atgtgaatgg	ttacctctgn	ctacctatct	gcttanggat	660
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<210> 371
 <211> 793
 <212> DNA
 <213> Homo Sapiens

<400> 371

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caccaagcat	ccctccagta	atgtcaagac	ctgttagctc	ttcctccatt	tccactccct	180
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catcagcagc	tttgccaact	cacttgcaag	ctgcattgat	gtcaacagtt	gtcacaatgc	300
ccaatgcggg	tagcaagggt	atggttttctg	agggacagtc	agctgctcag	tctaattgcc	360
ggcctcagtt	cattacacct	gtctttatca	attcatcctc	aataattcag	gttatgaaag	420
gatcacagcc	aagcacaatt	cctgcagccc	cactgacaac	caactctggc	ctgatgcctc	480
cctctgttgc	agttgtttggc	cctttacaca	tacctcagaa	cataaaattt	tcttctgctc	540
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tggtccttag	ctcacgagcc	accctgttc	agcttccttc	ccttcttgn	cgtcttctnc	660
agttgccctt	ctnatccctt	gtgcaacaag	tgaaagaatt	gaatncagat	gangctagcc	720
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<210> 372
 <211> 804
 <212> DNA
 <213> Homo Sapiens

<400> 372

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ctctttgggc	tactgtcttt	gtccagagac	tatggcagca	tttacctccg	ctttgggctg	720
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<210> 373
 <211> 792
 <212> DNA
 <213> Homo Sapiens

<400> 373

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gtaagctggt	catcattgag	agcgacctgg	aacgtgcaga	ggagcgggct	gagctctcag	480
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aactaaantt	ggagaaaaag	catttgatga	cttagaagaa	gaaagtggct	tcatgcccaa	720
agaagaaaan	cttatatgca	tcaanatgct	ggatcagact	ttactggagt	taaaccacat	780
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<210> 374

<211> 745

<212> DNA

<213> Homo Sapiens

<400> 374

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taaacacgct	atgctagcca	gagaggagcg	ccatcgtaga	agaatggaag	aagaaagatt	660
gcgtncacca	tnnttaccctc	cagtggtcac	tatttagatc	atgaatgcag	cattggtgct	720
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<210> 375

<211> 734

<212> DNA

<213> Homo Sapiens

<400> 375

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tgtttgtgcg	tgtgtgcccc	cacatgagca	tatttttaatt	cacagaaaaa	ctgaaacatg	660
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<210> 376

<211> 822

<212> DNA

<213> Homo Sapiens

<400> 376

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gaatggggaa	tatgtaggta	aatggattac	ccgaaaaaan	ttatctgntt	aacaaactta	780
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<210> 377

<211> 812

<212> DNA

<213> Homo Sapiens

<400> 377

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tacaattttt	aacattaata	tacacattcc	ataatctcat	ctatttaaca	ttaacacagg	180
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actcaattcc	catttttatga	acacctctgt	gctcactgta	attctgaaaa	cacagacttt	480
gctaactggt	aaatactatt	tacaagaaga	ttcaacctaa	tcaatatcac	ttatcaaaaag	540
cagtggtctga	ctgtaagtat	caacatgttt	ccagaatgaa	taaaccacac	aatcaactca	600
gaatgatata	aattaggggtc	catatcattt	aatttccctt	gaacctgctc	tgctagggtta	660
atctgctaata	atgaaagtta	attaagactg	gttttgaagg	accgaggaca	atagtttctt	720
ttgcacaatt	ttctgaacta	tgagaaaaat	ttaaaggatc	cntaaagcnc	ctggcaaaaaa	780
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<210> 378

<211> 870

<212> DNA

<213> Homo Sapiens

<400> 378

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gttcagctct	caacattgct	ggttgagttt	ggaacaaaaa	cctcttaaca	actggcagat	180
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tttagcaacg	taagtttaac	cagtaagtgt	cacaactgat	caacagtact	taaaaggaaa	360
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aagaactcct	aaattacaaa	ttcatcacat	tacatgcatg	caatgggtcac	ttttggttta	660
cccataaaaag	gatacncagt	attttgctgn	aaataccagg	accacattta	caatatatgc	720
aaaaaattag	aatgcagnng	taagntcctt	anattttaagc	cctcatatgn	gncaacaggg	780
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870

<210> 379

<211> 837

<212> DNA

<213> Homo Sapiens

<400> 379

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accctnttga	gaaagaccat	gaacagcagt	cctatcaaaa	tcttgaaccg	tgaagcactg	780
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<210> 380

<211> 793

<212> DNA

<213> Homo Sapiens

<400> 380

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<210> 381

<211> 807

<212> DNA

<213> Homo Sapiens

<400> 381

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<210> 382

<211> 800

<212> DNA

<213> Homo Sapiens

<400> 382

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<210> 383

<211> 1203

<212> DNA

<213> Homo Sapiens

<400> 383

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<210> 384

<211> 2651

<212> DNA

<213> Homo Sapiens

<400> 384

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<210> 385
 <211> 804
 <212> DNA
 <213> Homo Sapiens

<400> 385

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<210> 386
 <211> 782
 <212> DNA
 <213> Homo Sapiens

<400> 386

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<210> 387
 <211> 865
 <212> DNA
 <213> Homo Sapiens

<400> 387

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actgtgtgaa	caaggaatta	tctgtcacat	cagcgcccttg	gtcagtaata	gaccagcaag	480
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<210> 388

<211> 753

<212> DNA

<213> Homo Sapiens

<400> 388

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ancagtttca	nggttcactt	ccctcccttg	anccaggnc	aggnccattt	gctttggggn	180
aaattaaaa	canaattcta	aaagttganc	anctttgttt	ttttttaatn	gactnanctn	240
tanccacca	ttacaactta	nggacggcat	gactngataa	nganggactt	gngtgaggtt	300
ttgagttttc	aattaanctt	tgnatcacat	gaggnaatng	ncagcattct	tgagncnggt	360
tatggaatag	gcagatanaa	ccctgtagta	ccaanagttg	gaaatnggct	aatngacaac	420
gcactngcct	taaacatctc	angtagagaa	cttttacatt	agngagangt	ncttgaattt	480
cananctcac	caaattttta	ttacttttta	tngaaaactg	cagngaangc	taaaggctta	540
cgtttacaat	aaacaaatcc	agtancagta	actcacactg	aaccaaaan	tacttctgat	600
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<210> 389

<211> 737

<212> DNA

<213> Homo Sapiens

<400> 389

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<210> 390

<211> 775

<212> DNA

<213> Homo Sapiens

<400> 390

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<210> 391

<211> 776

<212> DNA

<213> Homo Sapiens

<400> 391

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tgactgtgg agatgcccct cctgaaggac ctggccactg tggccttctg tgacgcgcag      180
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ttcagcgtca tattttatga cccctacttg caggatggga tcgagccggt ccctgggcgt      660
gcagaaggtc tacaccctgc aggatttget gtatcagaac cgaactgcgtc ttctttcact      720
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<210> 392

<211> 909

<212> DNA

<213> Homo Sapiens

<400> 392

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tttttctgtt tgggacaatt ttaaagtttt tcttttgtca caaaaacagg aatgtacct      180
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agggacctg

909

<210> 393

<211> 769

<212> DNA

<213> Homo Sapiens

<400> 393

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caatcctatg	cgtgcaggng	tttaccaca	ggcaaacagg	ttttctnccc	catttttgga	720
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<210> 394

<211> 813

<212> DNA

<213> Homo Sapiens

<400> 394

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<210> 395

<211> 762

<212> DNA

<213> Homo Sapiens

<400> 395

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<210> 396

<211> 822

<212> DNA

<213> Homo Sapiens

<400> 396

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<210> 397

<211> 812

<212> DNA

<213> Homo Sapiens

<400> 397

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gtgcaggccc	acaagctgac	gggcgatgaa	cctccttcac	cagcttcttc	tccttgagcc	660
cgcacagcct	tcttcaccgc	gatctcacag	gaaggggttc	atggagtgtc	tacaaccatc	720
cggngaccac	accgggccct	gtcaggcttt	aactcggant	ctttacgggg	taatcgnntg	780
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<210> 398

<211> 751

<212> DNA

<213> Homo Sapiens

<400> 398

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ggtcctccac	actgatcaca	gagagcttgg	aggtcaggtc	cacacccagg	tccccaggct	180
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cgaatgtgcc	ctgtggccag	tcaagaaatc	cagctgtcat	ctgccctgtc	tggttacagt	420
catcatcgat	ggcctgtttg	cccagcagca	ccagggtccac	cttctctctc	tctgccagct	480
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ccacgtggat	acctcgggtc	gcacccatgg	ccagggcggt	acnnaatcgn	ctcctggcac	600
tgtgcaggcc	cacaagntga	cggggaatga	cctccttnac	caagcttntt	ntccttgacc	660
cgaaaagctt	cttcaccgng	aacttncaga	angggttcaa	tggantgctt	tacacattcg	720
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<210> 399

<211> 800

<212> DNA

<213> Homo Sapiens

<400> 399

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gggtcctcca	cactgatcac	agagagcttg	gaggtcagg	ccacacccag	gtccccaggc	180
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gcgaatgtgc	cctgtggcca	gtcaagaaat	ccagctgtca	tctgccctgt	ctggttacag	420
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tccgggancac	aaccggncct	gncaaggctt	naacttggac	ntttacggng	taatccgatg	780
aacctttttt	gacagntacc					800

<210> 400

<211> 810

<212> DNA

<213> Homo Sapiens

<400> 400

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ttccagaaga	aagggagaa	tttcttcagc	aattgtacaa	atztatggaa	gatagaggta	180
cacctattaa	caaacgacct	gtacttggat	atcgaaattt	gaatctcttt	aagttattca	240
gacttgtaca	caaacttggg	ggatttggata	atattgaaag	tggagctgtt	tggaaacaag	300
tctaccaaga	tcttgggaatc	cctgtcttaa	attcagctgc	aggatacaat	gttaaagtgtg	360
cttataaaaa	atnctnatnt	ggctntgngg	agtactgtac	atcagccaac	attgaatttc	420
agatggcatt	gccagagaaa	gttggttaaca	agcaatgtaa	ggagtgtgaa	aatgtaaaag	480
aaataaaagt	taaggaggaa	aatgaaacag	agatcaaaga	aataaagatg	gaggaggaga	540
ggaatataat	accaagagaa	gaaaagccta	ttgaggatga	aattgaaaga	aaagaaaata	600
ttaagccctc	tctgggaagt	aaaaagaatt	tattagaatc	tatacctaca	cattctgatc	660
aggaaaaaga	agttacatta	aaaaaccnga	agacaatgaa	aatctgggcc	gaccaagatg	720
atgacncaac	tagggtagat	gaatccctca	accttaaggt	agaactgagg	aagaaaaagc	780

caaatctgga tncnatgaat gggattaagc

810

<210> 401

<211> 860

<212> DNA

<213> Homo Sapiens

<400> 401

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cccagctaga	gctagcagat	ataaagtcca	agcttgagaa	ggtaggcccag	cagaaacaag	180
aaaagacctc	tgaccgatca	tcagtgtctg	agatggagaa	acgggagagg	cgagccttgg	240
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accagaggct	gaaagatgaa	aatggtgccc	tcatcagagt	catcagcaaa	ctgtccaagt	360
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attcgagcca	tctggagaat	gctctgggga	gtacaccagg	ctcagctgtg	gacccctcaa	660
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gtccttgnng	gtagccactt	tcaggatcct	ggaatggggg	gccaagaga	aacngccagg	840
atggttgaat	tggatcattc					860

<210> 402

<211> 779

<212> DNA

<213> Homo Sapiens

<400> 402

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tacaggcgcc	cgccaccacg	cctggctaata	tttttgtatt	tttagtagag	attgggtttc	180
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tgaagtgtctg	ggattacagg	catgagccac	tgcacctggt	ggaattggga	tcttgaatta	300
cagcttctag	tttaaacagc	atgtggtgtt	tcagagggag	gaccatggag	agctacatgt	360
catgttagga	aagaattaac	agacagaggt	agtatatatt	aagggaatga	accactctaa	420
acactgaata	tcactggcaa	ccctaaaatg	atgaggattt	aatgacttgc	acactcaagt	480
gaaccaaggg	ataaaaactcc	tacaaaaaga	aaatactgta	agtattaatg	ctaggttatc	540
atcaaganct	aatgggttaa	ttttgcaactg	gatttgnatt	cttttccagg	cctggacatg	600
atattttaaa	ggctggttnt	ggctagagga	ggatgggcca	anatgtgaca	gggangaaaa	660
gcatgcctta	tgaggaatga	cttaaaggga	ctagaggtaa	cagcagctca	aaagtaagaa	720
ctgaggggga	aaacccccca	ctgnaccata	tntnaagggc	cgttaaagaa	ttgcagaat	779

<210> 403

<211> 1443

<212> DNA

<213> Homo Sapiens

<400> 403

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actgaatctc	aaaaagattt	ggaaataacc	aaagaaaatc	tggtcaagc	agttgaacac	180
cgcaaaaagg	cacaagcaga	attagctagc	ttcaaagtcc	tgctagatga	cactcaaagt	240
gaagcagcaa	gggtcctagc	agacaatctc	aagttgaaaa	aggaacttca	gtcaaataaa	300

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gaatcagtta aaagccagat gaaacaaaag gatgaagatc ttgagcgaag actggaacag      360
gcagaagaga agcacctgaa agagaagaag aatatgcaag agaaactgga tgctttgcgc      420
agagaaaaag tccacttgga agagacaatt ggagagattc aggttacttt gaacaagaaa      480
gacaagggaag ttcagcaact tcaggaaaac ttggacagta ctgtgaccca gcttgcagcc      540
tttactaaga gcatgtcttc ccttcaggat gatcgtgaca gggatgata tgaagctaag      600
aaatgggaga ggaagttag tgatgcgatt caaagcaaag aagaagaaat tagactcaaa      660
gaagataatt gcagtgttct aaaggatcaa cttagacaga tgtccatcca tatggaagaa      720
ttaaagatta acatttccag gcttgaacat gacaagcaga tttgggagtc caaggcccag      780
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aaaanggaag catttagnca aaaggcncag ttggattcct tggtnaaatc ctgncttctn     1380
ttccaaatgg atccgagaac cgcntagtgg ggggactatt caccagctgg gaanagccga     1440
ctt

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<210> 404

<211> 819

<212> DNA

<213> Homo Sapiens

<400> 404

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gaacatgaca agcagatttg ggagtccaag gccagacag aggtccagct tcagcagaag     180
gtctgtgata ctctacaggg ggaaaacaaa gaacttttgt cccagctaga agagacacgc     240
cacctatacc acagttctca gaatgaatta gctaagttgg aatcagaact taagagtctc     300
aaagaccagt tgactgattt aagtaactct ttagaaaaat gtaagggaaca aaaagggaac     360
ttggaaggga tcataaggca gcaagaggct gatattcaaa attctaagtt cagttatgaa     420
caactggaga ctgatcttca ggctccaga gaactgacca gtaggctgca tgaagaaata     480
aatatgaag agcaaaagat tataagcctg ctttctggca aggaagaggc aatccaagta     540
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tnccaggagg aagaggagaa tattggttta gaagaggaga acaanaangc ttgtggttaa     660
aaccatca gcttatggga acacttgaac accatcaaaa nggaaacatt tagncaaaag     720
gencagttgg attccttggg naaatcctgn cttctnttcc aaatggatcc gagaaccgcn     780
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<210> 405

<211> 761

<212> DNA

<213> Homo Sapiens

<400> 405

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ctgaaaataa ttttattatt ttacagttgt tcaggaaact tcccaggatg ttgtaaccaa      60
natttaatca ccacagtana tttanagcan atcagtcagc ccacttgtct tccctcttct     120
ttaggganag gctaggcagt gaacacatca tgtatgcaat ganaaaataa ccaactggta     180
ggatggggga ggggagggga ggcagggaat aggcncaaat ggaattctat cctggctgtc     240
cttctcaggt ctatctatat ttaattttgt cttctctata ttctccttcc attgccacag     300
agggcanaga caatggggct gaaaaactgt aataactgnc actaacagca aagtanctta     360
gtncctcaag aggtcaggag ttgcagtgtg gtgttanacc agtcanactc ctggctgaaa     420

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gtcaatgcct aatattggct cccagnggcc cctgagcact gtctcagggc ccacattcca 480
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tccctgccct ttgggtgaaag gaaagacttt gggccccttt aataccttan tatcccatgt 600
gatcaagggc caaaagccaa aggggattct tatccttata gcctaagacc ctgaaattct 660
tcccttccca attatatctg gaaattggcc aggggaanaa aaatgctgnc cttcccatgn 720
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<210> 406

<211> 758

<212> DNA

<213> Homo Sapiens

<400> 406

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gatactgaac ttcagattat taggtttatt gaaaccatcc tcttggettgt gctgaaagac 60
attcctcagt atctttttaca ggaccacaaa agatcagggc cctgcaaaat ctcaacaaat 120
attaggctca acaaaccaaa tgtgattctc agattaagca gaagcgttca ggctcagggc 180
agtagaagaa agcagactcg ccagtcctcg cagtcccaac ctgtcctcgt atcacctctg 240
tttttgcagg cactttccgt gaagagttgg agagaagacc tgtaaattggg aagactgttc 300
cactggaatt gatgttctga tgtagaggt gagagaattc caagttttga ggggagtggg 360
ccaaagagta acaactaagt ctatagatgg cccgtaaaac acagaatgag caggacatga 420
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<210> 407

<211> 778

<212> DNA

<213> Homo Sapiens

<400> 407

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cttcaggaac tgttaaaaga aaaacaacaa gaagtaaagc agctacagaa ggactgcatc 60
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cgcaaaaagg cacaagcaga ctatagtagc ttcaaagtc tgctagatga cactcaaagt 240
gaagcagcaa gggtcctagc agacaatctc aagttgaaaa aggaacttca gtcaaataaa 300
gaatcagtta aaagccagat gaaacaaaag gatgaagatc ttgagcgaag actggaacag 360
gcagaagaga agcacctgaa agagaagaag aatatgcaag agaaactgga tgctttgcgc 420
agagaaaaag tccacttgga agagacaatt ggagagattc aggttacttt gaacaagaaa 480
gacaaggaag ttcagcaact tcaggaaaac ttggacagta ctgtgacca gcttcagacc 540
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gaagataatt gcagtgtcta aaggacactt agacagatgt ccttcntatg gaagaattaa 720
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<210> 408

<211> 752

<212> DNA

<213> Homo Sapiens

<400> 408

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canattatta ggttnatnga anccatcctn tnggntnggn tgaaanacnt tectnagtnt 60
nttttacngg accncaaaan atcagggnc tgcaaaatct cancaaatnt taggctcanc 120

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aaaccaaang	ngattntnaa	attaancaaa	ancgttcagg	ctcagggcag	taaaaaaaag	180
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aactaagtnt	ntananggcc	cgtaaaacnc	anantganca	ggacntgaat	cnttaaaaag	420
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ncnttttggg	ccccgttntt	ttttccagca	ngcttccctt	taattcattc	ncttcccggg	720
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<210> 409

<211> 736

<212> DNA

<213> Homo Sapiens

<400> 409

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gctcagccaa	gatcaagtta	aagagcagtg	agctgcaggc	catcaagacg	gagctgacac	120
agatcaagtc	caatatcgat	gccctgctga	gccgcttgga	gcagatcgct	gcggagcaaa	180
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cacccccccag	cgggtaccag	aggaaaagctg	cagcaggccg	cctcctcccc	caacgcattc	600
cagccagtgc	catgtcctct	gcagggtggg	ttactggcct	actccttccc	atgaaccctt	660
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<210> 410

<211> 766

<212> DNA

<213> Homo Sapiens

<400> 410

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ctaccctctg	gcctgggcag	tgcanacagg	gagggctcat	ggggaaggag	taggccagta	180
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cgggttaanc	agggcatcna	tatttggact	tgaactgggn	caantctccg	ncttgaangg	720
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<210> 411

<211> 812

<212> DNA

<213> Homo Sapiens

<400> 411

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tcctgtctctg	cactgcccag	gccagagggg	agagcacagg	ggtttcccca	tactacctcc	720
cctccccagg	acactcccag	gcttggggtt	tttctatagg	tttggcgggg	ggcncaggg	780
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<210> 412

<211> 857

<212> DNA

<213> Homo Sapiens

<400> 412

aaccatctta	gcccccaaaa	tgatgatgct	ctggagacac	gagctaagaa	gtctgcatgc	60
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gaagaagatg	aggagaagat	tcagaatgaa	gattatcatc	acgagctttc	agatggagat	180
ctggatctgg	atcttgttta	tgaggatgaa	gtaaatcagc	tcgatggcag	cagttcctct	240
gctagtcca	cagcaacaag	taatacagaa	gaaaatgata	ttgatgaaga	aactatgtct	300
ggagaaaatg	atgtggaata	taacaacatg	gaattagaag	agggagaact	catggaagat	360
gcagctgctg	caggaccgcg	aggtagtagc	catggttatg	tgggttccag	tagtagaata	420
tcaagaagaa	cacatttatg	ctcgcgtgct	accagtagtt	tactagacat	tgatccatta	480
attttaatac	atttggttga	ccttaaggac	oggagcagta	tagaaaattt	gtggggctta	540
cagcctcgcc	cacctgcttc	actctgcag	cccacagcat	catattctcg	aaaagataaa	600
gaccaaagga	agcaacaggc	aatgtggcga	agtgcctct	gatttaaaga	tgctaaaaag	660
actcaaaact	caaatggccc	gaagtccgat	gtatgaaaac	tgatgtaaag	gaatacactt	720
tcagaaataa	aaagcacagt	gctgcttctg	gagacatgcn	gacaagnctt	ttttgctga	780
nccagcagnt	ntggctgatg	tggactgaaa	cttttggcag	aatgcaggat	ttggatggac	840
tcctggcnaa	agtctta					857

<210> 413

<211> 790

<212> DNA

<213> Homo Sapiens

<400> 413

ctcaagtnga	ttttattanc	aaaaagngca	aactattttg	ancaaaaagta	aactatgagt	60
cacagcnttc	agcaagacat	canacncgga	anagnganca	atattcacta	agtaaaatnc	120
agcanatgan	atgtctntca	catgtatatt	naattattca	tgttttttca	atagtctntt	180
agtcaacttt	cagnptaatt	tcacaaaata	tatagcagnt	caaacncaaa	tgagganncn	240
caanggcaaa	gttnggcaac	tgtttngggc	taattatgag	tntgaaagaa	anccttatat	300
cacagtttca	cgttcagtga	anccactgng	caacatgaat	gaatntttta	angngttgac	360
nctgaaatca	angtncaact	aangaaanta	aagaanaaaa	gggggcttta	aaatatnngt	420
ngcnctacag	tcgtatagta	agaggcagaa	aaaaatgaan	gaatttttaa	taatcttaca	480
cgtgtntaca	gggccaggaa	cgtaatgaat	ccatgttaac	ttaatttcat	ttaaaattnc	540

attttagtaa	gtcnncnaac	agaaaagatcc	atgcgggttga	acagtgtgcc	tgtnccttgac	600
aagttagaga	agatccttct	ccaaaaggga	gattcagtct	agggntactt	cagttnttcc	660
catagnngct	acagggcana	atctttttca	aaagcaatct	tctgggtccct	aaatctacag	720
gcnctantgg	gacctgtaat	taaaancccc	caattttaag	gangattttt	aaacccact	780
taagctttta						790

<210> 414

<211> 1063

<212> DNA

<213> Homo Sapiens

<400> 414

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nggcnttgac	tctgnnnngc	gacntnttgc	tagtcttcag	gnctcctact	acaggctttg	120
taatganctn	nacttgnctt	gagacagcct	angggagacc	acggatgntc	tattannngn	180
gcangctggn	ctatngcaan	ntgggnctna	nnctgnanaa	tcannngcng	ccatgnnaga	240
tnaatagaag	ctcatnntgt	cataaatggn	ccatgactta	taaatnaagt	ggactggata	300
tcttatgaca	gnagcnatnt	angcttngtg	ngnagttaan	gcttccacct	nnggangata	360
agaggncnac	cttgtntnan	ctnntgcngc	tgnaagancc	agaganannt	gccttgggag	420
attcatggcc	natgatagta	tatnatctct	tacaccanct	atgccttget	gnatcncaaa	480
tctggacata	cacgntttcc	ccatctcaga	cttctnttgc	gcagctgctt	nccnacnnta	540
cccatgaacg	acanntgctt	acgntanagc	ntgaacnatn	tgatgagctt	cntcagccca	600
gacctcatca	tttcgagaag	cacatgtccc	tgcgtttcaa	cctatggatg	aggaaaagnc	660
ctngngctta	aagctcttga	aaatccttta	cacnngaanc	nttctgcata	gcttnaatca	720
ctctgagntg	cccacatngn	gtntctggaag	gcttccggnt	annatgggtc	cgggacctnc	780
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gaacttaacc	ntcacaattn	ggntgngant	tcttggtaac	ggcntaatct	ccccaggaa	900
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ggngccentt	tttcaatttt	cngactcccg	gagcttttaa	aaaccggggg	ccttaggttn	1020
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<210> 415

<211> 824

<212> DNA

<213> Homo Sapiens

<400> 415

gtttgattnt	aacaaaaant	attatgcaca	aatnacnnag	gntanagact	ctnnatctn	60
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taaatatcac	aggaaataca	ntgcattttc	aagntgnana	gacnaatact	tnctcattca	180
cagngnttga	catanganag	cctattttaca	tancnatctg	tataaagtca	tgctctnant	240
ancaggntat	ncagngctgn	gccancacaa	tgnttttnaga	angtgaagaa	ccggncaaac	300
cactnntggn	gctggggatc	tganaaagcc	acctgnanaa	gcttccactct	gagcangact	360
cannaatgnc	ttnggccctt	taggtggcac	tggtcttgga	agtgggttaag	ctgctgctga	420
actcaattcg	tggaactgnag	aattaggaat	ggganccagg	cggttnggat	gaccattgcc	480
cactcnanca	natnccaaag	nnctnagaan	gggaacnctc	caancctgct	tnatggngat	540
taancatnct	tcttcttttg	cttaacccat	ggattananc	acancagcna	gtacngactt	600
ggntttaccc	ncttcngttg	gaaataagga	ttcttgatng	actaaannnc	agctggtnaa	660
aacntaactn	tcctcaatt	tagcnttatt	ntatgaancc	ggggcctant	ntcntgttca	720
aaaangngnt	tttaagttcc	ggtaatccta	ccggnaatta	nttgggggct	ntgaattcan	780
cnccttana	anatttnggn	ttaccatttn	aatccaaagg	ccac		824

<210> 416

<211> 838

<212> DNA

<213> Homo Sapiens

<400> 416

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aaatacacaa	ttttactagc	aaatgcctct	actgtaatcg	ctattttacc	acagatactc	180
tgctcaacca	tatgttaatt	catggtctgt	cttgctccata	ttgccgttca	acttttcaatg	240
atgtggaaaa	gatggcgcga	cacatgcgga	tggttcacat	tgatgaagag	atgggaccta	300
aaacagattc	tacttttgagt	tttgatttga	cattgcagca	gggtagtcac	actaacatcc	360
atctcctggg	aactacatac	aatctgaggg	atgccccagc	tgaatctggt	gcttaccatg	420
cccaaaaata	tcttccagtt	cctccaaagc	cacagccaaa	gggttcaggaa	aaggcagata	480
tccctgtaaa	aagttcacct	caagctgcag	tgccctataa	aaaagatggt	gggaaaaccc	540
tttgtcctct	ttgcttttca	atcctaaaag	gacccatata	tgatgcactt	gcacatcact	600
tacgagagag	gcaccaagtt	attcagacgg	tcatccagtt	tgagaaaaag	ctnacctaca	660
aatgnatcca	ttggcttggt	gngnatacca	gcaacatgga	ncggctnaac	tatcacttct	720
gnatctagnt	cactggangg	gccgtttggg	aagganccca	aatggggccag	gataagacaa	780
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<210> 417

<211> 880

<212> DNA

<213> Homo Sapiens

<400> 417

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acaaaattat	acatactaca	acagtgtgtc	atatattaga	tggtataaat	gaatccacca	120
tgatggtggt	gaactaaaga	taaaactaaa	tatccaaaat	gcagcactca	ttggtttgct	180
gcttcaacac	aacacacttt	tatacagatc	taaaagggtg	caaaattagt	agctgcaaag	240
tcaattcttg	catgtgattt	tagcttaaaa	gatttcagaa	aacagatctg	aaataccagt	300
ttttgttttt	gacagctgta	atgtcaagga	tattcagaac	aagaaaaatc	ctataatata	360
agagagtcca	gatatatata	ttacgtgggt	ggcctctggt	gcaagattgt	acaaggttat	420
gtgcaaaaac	taagtctgtc	caaaaagtc	atactagcgc	agttttgagc	ttttgctagg	480
taaactagat	agagcgttta	ttacacagca	agggcaacac	taaaaaaaga	aatctatgat	540
gggcacacag	taacaggatc	atgagcatca	cttgaatagg	tctaaaagac	tgtcaaata	600
acatttcaac	tattcagaat	gaatacatga	aaaaaaatcg	cttttcccaa	aggtctacta	660
tacncattan	actgggagct	tgnatgttgg	gcctacact	accatgggga	attangttta	720
acacttntta	aaaacatttg	gccaatcatt	tcncagangg	gaaagaaatg	ttgaaaaggc	780
cgataaaata	aacccttggg	ttttcctcgg	gggattcatg	gagtcacccg	ccttaattggg	840
ttttcacatt	taagttaccc	gggcttggca	aaaaaaggtt			880

<210> 418

<211> 763

<212> DNA

<213> Homo Sapiens

<400> 418

agaagatggc	ggaagcggaa	tttaaggacc	atagtacagc	tatggatact	gaaccaaac	60
cgggaacatc	ttctgtgtca	acaacaacca	gcagtaccac	caccaccacc	atcaccactt	120
cctcctctcg	aatgcagcag	ccacagatct	ctgtctacag	tggttcagac	cgacatgctg	180
tacaggtaat	tcaacaggca	ttgcatcggc	ccccagctc	agctgctcag	taccttcagc	240
aatgtatgc	agcccaacaa	cagcacttga	tgtgtcatac	tgcatgctct	cagcagcagc	300
atttaagcag	ctcccagctt	cagagccttg	ctgtgtttca	ggcaagtttg	tccagtggaa	360
gaccatctac	atctcccaca	ggaagtgtca	cacagcagtc	aagtatgtcc	caaacgtctg	420
tagaaaattct	tatggactgg	aatcttcttc	aaggcttact	ttgttctctg	gatgcagtgg	480
tgcatagaag	atagggcatt	gactcactca	gacctggctt	gcccagcatg	cattgcaaca	540

ataatgtgca	agttattataa	gacatgagtg	aattcgtgac	agattgtcag	aaaagaaaca	600
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gttggggctg	agtgtaaaga	aatgcaagct	gcaaactctg	cttacatgtg	gaaccaaagc	720
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<210> 419

<211> 753

<212> DNA

<213> Homo Sapiens

<400> 419

ggactatttta	cttttaaatgt	aattatcaat	acagtcgggt	taaatctacc	atthttgttgt	60
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tggattcact	acttttttta	nagngtcgtt	ttaccactac	tattggccta	ttacctgtat	180
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ttgaaatagt	agngtaacac	ttcacaataa	gagtaaaaaa	cttataatct	tccattttttc	300
ccttcctttct	tttgtgctat	tgatgacnca	tatttactcc	tacagatatt	ataaacaat	360
tgatatacnc	acattatcat	ttttgcttta	catactcaat	tatcttttaa	ataaaaataa	420
aattgaggag	aaaatccgtt	atattatcta	cacatttact	gtttccagca	cttttcattt	480
ctttgngtag	attcaaatth	ctgncatctt	ccctttgccc	aaagaacttc	ttttcatctt	540
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catatattat	cttgattttc	aaatggnatt	taagctctat	ataggaattc	ttaggtgact	660
ttaattcctt	catcattggg	aagangtcac	aaagggcttg	caaaggacta	gaaatctgct	720
tacatttttt	natttggtta	tctttcttac	cca			753

<210> 420

<211> 799

<212> DNA

<213> Homo Sapiens

<400> 420

gaaaaacgct	ttgatacca	gaattaaaaa	tgcttgtcta	caaacatctt	cccttgccgt	60
tcgtgtaaat	tcattagtgt	gcttaggaaa	gattttggaa	tacttggtata	agtggtttgt	120
acttgatgat	atcctaccct	tcttacaaca	aattccatcc	aaggaaacctg	cggctctcat	180
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gcagctggcc	ggaaaagtgt	tgccctcatct	tattcccctg	agtattgaaa	acaatcttaa	300
tcttaatcag	ttcaattctt	tcattttccgt	cataaaagaa	atgcttaata	gattggagtc	360
tgaacataag	actaaactgg	agcaacttca	tataatgcaa	gaacagcaga	aatctttgga	420
tataggaaat	caaatgaatg	tttctgagga	gatgaaagt	acaaatattg	ggaatcagca	480
aattgacaaa	gtttttaaca	acattggagc	agaccttctg	actggcagtg	agtcggaaaa	540
taaagaggac	gggttacaga	ataaacataa	aagagcatca	cttacacttg	aagaaaaaca	600
aaaattagca	aaagaacaag	agcaggcaca	gaagctgaaa	agccagcagc	ctcttaaacc	660
ccaagtgcac	acacctgttg	ctactgttaa	acagactaag	gacttgacag	acacactgat	720
ggataaatatg	tcatccttga	ccagccnttc	tggtagtacc	cctaaatctt	ctgcttcaag	780
tctttcactt	ctggctcctt					799

<210> 421

<211> 770

<212> DNA

<213> Homo Sapiens

<400> 421

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tttagattht	gctgaatttg	aagacacctt	gaaaacattt	tcaaaagaat	gcaaaaataa	120
aggaaaacca	ttgtgtaaaa	cagtaggcgg	atctttcaga	gactccaaat	cattgacaat	180

tcagaaggat	cttgtcgtctg	catttgacaa	cgagagaccag	aagggtgttct	tcgatctgtg	240
ggaggagcac	atttcaagtt	ccatccgaga	tggggactcc	tttgcccaga	agctggaatt	300
ctatctccac	atccattttg	ccatctatct	tttgaagtac	tctgtgggga	gaccggacaa	360
agaggagctg	gatgaaaaga	tttccactt	caaaacctac	ctggagacca	aaggggcagc	420
cttgagccag	accacagagt	ttcttccttt	ctatgccctt	ccttttgttc	ccaaccttat	480
ggtgcacccc	tcattttaaag	aactcttcca	ggattcctgg	actccagagt	taaagttgaa	540
gttggaagaa	tttctagctt	taatatctaa	agccagcaac	acgccaagc	ttttaacaat	600
atataaggag	aatgggacan	agtaacaaag	aaatcttgca	gcagcttcac	cagcagctgg	660
ntgaagcttg	aaccgtagg	caatgacata	cctcaaaccg	naccataaga	tccaggcccc	720
actaccacaa	tctcantgga	gtcacagcan	aactgggtggg	attctcttga		770

<210> 422

<211> 733

<212> DNA

<213> Homo Sapiens

<400> 422

caaaangaan	gctttatttt	gaatttttaa	aatacatata	tcttacactg	taatcaaaac	60
aaagcttaag	aaagtcaatt	cccgcttct	ttagccctga	cttacactgg	gtacccgttt	120
ctgtggccgc	cgggggtgac	ggncccttgc	aggggctcat	ccccgctcca	ctgcacatta	180
gccagccct	tccgccttgt	cttccccgng	ttggctcatga	tccccaggta	ctccgnggtc	240
anaagcttct	ctcctgagag	ttctccgagc	tggggctgga	tcagttcgtc	tttgtccana	300
tcggcttcca	tgatgtcatg	gncctcttca	tcatcttcat	cttcatcatc	atcagattca	360
agaacaccat	ctggtagctc	ttcggaattt	agctgcttga	tgatgaattc	tatctggcgg	420
atcatttcag	cattgccttc	tttgatgaag	cagcgtagga	tgtcttccat	tccattgct	480
cttgcttct	caogaatgga	tggancagaa	aggatgctgt	acagagctcc	attcacatac	540
ggctgtatct	catgggtttc	atggccaaga	agatccgaaa	ggactttgag	caccgaggcc	600
tgccaccttg	gcacacatgg	tcttccctgn	gctgcgagg	gcagagggtc	atggagcaaa	660
agccaccgag	tactccaacg	gggnagccag	acagggcagn	cagggtcctt	tcanaacatc	720
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<210> 423

<211> 862

<212> DNA

<213> Homo Sapiens

<400> 423

catctgtcca	gggtgcacgc	agccgggagg	gctcaccagc	caggagcagc	acgccactcc	60
actccccctc	gcccatccgt	gtgcacaccg	tggtcgacag	gcctcagcag	cccatgaccg	120
atcgagaaac	tgcacctgtt	tcccagcctg	aaaacaaacc	agaaagtaag	ccaggcccag	180
ttggaccaga	actccctcct	ggacacatcc	caattcaagt	gatccgcaaa	gaggtggatt	240
ctaaacctgt	ttcccagaag	ccccacctc	cctctgagaa	ggtagagggtg	aaagttcccc	300
ctgctccagt	tccttgtcct	cctcccagcc	ctggcccttc	tgctgtcccc	tcttccccca	360
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caaaaccagg	agaagccgag	gctcccccaa	aacatccagg	agtgtctgaa	gtggaagcca	480
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acaaaaagta	cctgatgata	gaagagtatt	tgaccaaaga	gctgctggcc	ctggattcag	600
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atgaacttca	agccaagcaa	ccnttgaagc	agatcaagcc	cctggaggca	atcatggaaa	780
aggggtgcgt	ggcagcaaga	caagggcaag	aaaaatgctt	ggaaatggcn	gaagatcccc	840
acacnggaaa	ccagcaggcc	cg				862

<210> 424

<211> 859

<212> DNA

<213> Homo Sapiens

<400> 424

gagttatatt	attacttttat	tttctttttt	taaaatgtag	cattaaagtc	atccaacata	60
cagatattcc	tatggctcct	ggcacatttt	actctctcta	aagtcaggta	ttttaattat	120
gagatgaaga	aatcatctc	attaaaaatgg	caacatttct	gataaatgtt	tcatatttat	180
gtgatgggta	attgactccc	catctacccc	tccagtccag	agctacaaaa	gacagtgcac	240
aaccacagct	aacaggtggt	gggggtgccc	aagtagacag	ggctgcagaa	caagcaacgg	300
ggttaaactt	ctcaaacaac	aagcaacttc	tttatttgta	cagagtaaga	atatagaaga	360
aaagcatcat	tttccttttt	agccctttta	ttagtgtttt	gcctccaccc	aagttactgc	420
ataccaagca	gctaataaaa	accaactgac	ttaaagtctc	tgaaatgcat	gcaacttaaa	480
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gctgggttac	caggggtgtc	tggcatgctg	ctggggtttg	aagtcgctgc	tgtgnggct	600
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gttgctgggg	ctggagttca	ttagacctgg	accttggccc	tgggacatca	aagggctttc	780
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tggacgcnc	attgggggtt					859

<210> 425

<211> 837

<212> DNA

<213> Homo Sapiens

<400> 425

cagaatggag	gtggagtccc	taaacaaaat	gcttgaggag	ctaagacttg	aacggaagaa	60
actaattgag	gattatgaag	gcaagttgaa	taaagctcag	tccttttatg	aacgtgagct	120
tgatactttg	aaaaggctac	agctttttac	agcagaaagc	ctacaggcca	gcaaagaaaa	180
ggaagctgat	cttagaaaaag	aatttcaggg	acaagaagca	attttacgaa	aaactatagg	240
aaaattaaag	acagagttac	agatggtaca	ggatgaagct	ggaagtcttc	ttgacaaatg	300
ccaaaagctt	cagacggcac	ttgccatagc	agagaacaat	gttcaggttc	ttcaaaaaca	360
gcttgatgat	gccaaaggag	gagaaatggc	cctattaagc	aagcacaaag	aagtggaaag	420
tgagctagca	gctgccagag	aacgtttaca	acagcaagct	tcagatcttg	tcctcaaagc	480
tagtcatatt	ggaatgcttc	aagcaactca	aatgaccag	gaagttacaa	ttaaagattt	540
agaatcagaa	aaatcgagag	tcaatgagag	attatctcaa	cttgaagagg	aaagagcttt	600
tttgcgaaag	caaaacccaa	agtctggatg	aagagcagaa	gcnacagatt	ctaagaactg	660
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anctgcaagt	agaatggaag	aagaggggct	taattaacga	nggccattct	aagacttttg	780
gaagaattag	cttggaacnc	cttttggcaa	ttgaacttgt	cncaggtaat	gccattt	837

<210> 426

<211> 724

<212> DNA

<213> Homo Sapiens

<400> 426

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atcacaggaa	atacagtga	ttttcaagtt	ggagagacaa	atactttctc	attcacagtg	180
tttgacatag	gaaagcctat	ttacataaca	atctgtataa	agtcatgctc	ttagtaacag	240
tctatacaga	gctgtgccaa	cacaattctt	tcagaatgtg	aagtaccggg	caaaccactc	300
ctggcgctgg	ggatctggag	aagccactgg	agaagcttca	ctctgagcag	gactcaaaaa	360
tgtcttgggc	cccttaggtg	gcaactggctg	tggagtggt	ttgctgctgt	tgaactcaat	420
atcgtggact	ggagaattag	gaatgggatc	caggcggtta	ggatgtccat	tgcccactcc	480

accagattcc	agagcactta	nattgggaac	actcacaaac	ctgtttgttg	gtgatttatac	540
attcttcttc	ttttgcttag	ccaatggatt	aataacacca	acagtaggac	ttgagttaaa	600
cactttggtg	aaagttagtt	tctcgaattg	actaatccca	gotgataaaa	cttattatcc	660
tcaattagtt	tctttatgan	ctgggcctct	ttctgtaagc	atggccttta	attctggaat	720
catc						724

<210> 427

<211> 981

<212> DNA

<213> Homo Sapiens

<400> 427

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acacacacac	acacaactca	aagagttana	atcattacnt	ncaaatgaaa	gtcgtaatga	120
tagatgatga	tagntncaat	gaanctgnga	ncatanatta	angaaacana	naacantncn	180
aaagggtccac	aaatctgggtc	ctatgaaaag	agtaaaatta	ccaagactng	gtgaaaganc	240
ccannaaaaan	ncanagagag	anagagagag	agagaganac	anagagagag	aganaaaagg	300
aaggcacacn	taancnatat	cagcaataaa	anggggnact	ttantacana	ttctgcaanc	360
attannnnna	taatganagg	atattatgaa	cagttgtatg	gcnatatgtt	tgaaaactta	420
gatgccgata	tgtttgaaaa	cttaaatgaa	acggaaaaat	tccttgaaga	accacaantt	480
aaatttgaca	caggtagaaa	atntgaatgc	agttngncct	tcagtatctg	tggggaaatc	540
ggttnccagaa	ccactcccc	antaccnaaa	tttataattg	ctcaagttcc	tgatataaaa	600
tgggcaaagta	tttgcatata	ncctatccct	acccttttac	atactttaaa	taacctntga	660
gttncttnat	tatacctaac	ataatgtaca	tttctgtggc	aaatcgntnn	taatattgga	720
ttttnaaaat	tatnttantt	ttggaatagg	nngtantatt	tcctggggct	ttttttttcc	780
ccaaatattt	tntaattccc	caattnggtt	ggaatcttgg	gaaccccatg	gnggggancc	840
catangattt	tggggaanggn	ccaacttggg	gccttngtaa	cttttttaaag	aaatngggaa	900
ttctttgntn	aanaattcct	ncncccaaag	aaaaccctt	tgggcccaaa	agttntttna	960
aatggggaaa	tttncccaaa	c				981

<210> 428

<211> 655

<212> DNA

<213> Homo Sapiens

<400> 428

ataggacaac	atgaacattg	ttgagtcact	gaagctaaac	caaacttgct	tttctgtaat	60
aaacccaatt	tggtcatgat	ttaatatattt	ttggatcgct	ctggatttgg	tttgctaata	120
ttttattcat	ccaagaaata	ttcattagag	aaattggcat	gggatttttt	tttcattgta	180
atgtccttgt	caggtatcaa	ggctttttca	gcctgataaa	gcatattaag	aaatgcttcc	240
tcttttctta	ttctctggaa	aagatttgtg	aatattgctg	ttactacttc	ctgtaatgtt	300
tggtgaaatt	cacaattgaa	gacatctggg	cctagcgtgt	tccttgtagg	agaatatta	360
agaaagaatt	ccatttcttt	aaaagttacg	agcacagtgt	gccttcacga	tctatggatc	420
ccacatgagt	tccagattca	accaattgtg	tattaaaaat	atttgggaaa	aaaagccaca	480
agaaataata	caactataca	aaataatata	atttttaaaa	tacaatataa	caacgattta	540
cacagaatgt	nccattatgt	taggnattat	aagtaactca	gaggntattt	aaagnatgtg	600
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<210> 429

<211> 788

<212> DNA

<213> Homo Sapiens

<400> 429

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ttctggetca	tgaatctgaa	ttacttggac	tagtgaaaga	gtatttagat	tttgctgaat	120
ttgaagacac	cttgaaaaaca	ttttcaaaag	aatgcaaaat	aaaaggaaaa	ccactgtgta	180
aaacagtagg	cggatctttc	agagactcca	aatcattgac	aattcagaag	gatcttgtcg	240
ctgcatttga	caacggagac	cagaaggtgt	tcttcgatct	gtgggaggag	cacatttcaa	300
gttccatccg	agatggggac	tcctttgccc	agaagctgga	attctatctc	cacatccatt	360
ttgccatcta	tcttttgaag	tactctgtgg	ggagaccgga	caaagaggag	ctggatgaaa	420
agatttcta	cttcaaaacc	tacctggaga	ccaaaggggc	agccttgagc	cagaccacag	480
agtttcttcc	tttctatgcc	cttccttttg	ttcccaaccc	tatggtgcac	ccctcattta	540
aagaactctt	ccaggattcc	tggactccag	agttaaagtt	gaagttggaa	aagtttctag	600
ctttaatatc	taaagccagc	aacacgccna	agcttttaac	aatatataag	gagaatggac	660
aaagtaccaa	gaaatcttgc	agcagcttca	ccacagctgg	ttgaagctga	acgtagggtca	720
gngccttcc	taaacggggc	aattaagaat	ccaggccgac	taccacaatc	ttantggggg	780
tcccagca						788

<210> 430

<211> 655

<212> DNA

<213> Homo Sapiens

<400> 430

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aaagcttaan	aaagtcaatt	cccgnttcc	ttanccctga	cttacnctgg	gtncccgttt	120
ntggggccnc	cggggngac	gggcctttgc	aggggctcat	ccccgntcca	ctggacatta	180
nccagcccct	tccgccttgg	cttccccgng	ttggctcatga	necccaggtn	ctccgnggtc	240
aaaagcttnt	ntcctgaaag	ttctccganc	tggggctgga	tcanttcgtc	tttgnccaaa	300
ncggnttcca	tgatgncatg	ggcctnttca	tcattctcat	tttcatcatc	atcanattca	360
anaacnccat	ntggnanctt	ttcggaattt	aactgcttga	tgangaattc	tatntggngg	420
ancatttcag	cattgccttn	tttgaagaac	cancgtagga	nggtttccat	tcccattgggt	480
nttgnttcc	cacgaatgga	tgggaacana	aggatgctnt	acanantcc	attcacatac	540
ggntgnatnt	catggntttc	atggccaana	anaatcccaa	aggctttgag	cccaggntctg	600
gcccttggca	caaatgttnt	tcctggcttc	cgaaggccaa	ggttcattga	ccaaa	655

<210> 431

<211> 844

<212> DNA

<213> Homo Sapiens

<400> 431

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aaattgaaga	gtactgttac	aaaagtaaca	gctgatgtca	ctagtgtgt	aatgggaaat	120
cctgtcacta	gagaatttga	tgttggtcga	cacattgccca	gtggtggcaa	tgggctagct	180
tgggaagattt	ttaatggcac	aaaaaagtca	acaaagcagg	aagtggcagt	ttttgtcttt	240
gataaaaaac	tgattgacaa	gtatcaaaaa	tttgaaaagg	atcaaatacat	tgattctcta	300
aaacgaggag	tccaacagtt	aactcggctt	cgacaccctc	gacttcttac	tgtccagcat	360
cctttagaag	aatccaggga	ttgcttggca	ttttgtacag	aaccagtttt	tgccagttaa	420
gccaatgttc	ttggtaactg	ggaaaatcta	ccttccccta	tatctccaga	cattaaggat	480
tataaacttt	atgatgtaga	aaccaaatat	ggtttgcttc	aggtttctga	aggattgtca	540
ttcttgcata	gcagtgtgaa	aatgggtgca	tggaaatata	actcctgaaa	atataatttt	600
gaataaaaagt	ggagcctgga	aaataatggg	ttttgatttt	tgngtatcat	caaccaatcc	660
ttctgaacaa	gagcctaaat	ttccttgtaa	agaatgggac	ccaaatttac	cttcattgng	720
tcttncaaat	cctgaatatt	tggcttctga	atcctacttt	ctgngaactt	gtgaaaccag	780
ccagtggata	tgggattcnt	ttaggaactg	gtatggaatg	cgggattttt	aataaaaggg	840
gaaa						844

<210> 432

<211> 807
 <212> DNA
 <213> Homo Sapiens

<400> 432
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 ctttttcttt catgtgtaaa aacaaccatg tgaggtat ttt tacaggtcaa aagaaaacaa 120
 aaactacttc cttattcagt gtaaaggagg cttataagca ttccaaaata aaaacaaaca 180
 aaaaccagac aagtacatag tctattttcca tttcctttta tacatcctct ctatatatca 240
 cacatttagc aataggagaa tagagaacta attcaaatgc aaggggaatct tttttgtaga 300
 ttctgttgac agatgctctt taacctaaac attttctact ctaaacataa cggacttaat 360
 tgtcttcagt acgtgaaata attttaaggt gatctagtag tttgaaaatt tcattcactt 420
 aagaacactt aagctgaaaa atagcactat ttttcagagg caattttctca acagaaaaag 480
 gcaatggtaa cagttcaatt gatggaaatg gttgaaataa aatacctgaa gtagaaaaaa 540
 ggtgtaggaa caattttgtg aaaacatagc accattacct caacgaatga acaaatttta 600
 catactggat ttttttcaaa tgactttatt tcatatttag tagttcaagg tctataagct 660
 ggtatattaa gctttctttc tgggttaagag ntcaacactt acatcatggt attttacnaa 720
 attaaaaacc aattttcttaa ataaaccgng gctcctaaaa tggtagcaag gaaaaattct 780
 tcaataccta atttaattcc ataagga 807

<210> 433
 <211> 866
 <212> DNA
 <213> Homo Sapiens

<400> 433
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 acacctcttt ggcaactagt cagaatggtg atgtgtcggc cccctctgcc atactcagaa 180
 caccagaaa gacaaaaacc ggtcctggtt gtcagccacc agtgagtcag agccgctccc 240
 tgttttcttc tgtcccgctc aagccaccaa tgtctctgga gcctcaaaat gggacgtatg 300
 caggaccagc gccagcattc cagccatttt tcttacttgg agcattttcca tttaatatgc 360
 aagagctggt actcaagggt agaattcaga acccatctct tcgagaaaaat gatttcattg 420
 aaattgaact ggaccgacag gagctcacct accaagagtt gctcagagtg tgttgctgtg 480
 agctgggtgt taatccagat cangtggaga ngatcagaaa gttacccaat actctgttaa 540
 ggaaggacaa ggatgttgct cgactccaag atttcagga gctggaactg gttctgatga 600
 taagtgaaaa taattttctg ttcanaaatg ctgcatccac actgactgaa aggccttgct 660
 ataacaggag agcttcaaaa actgacttac taatgcacag ggacttttat cactggagta 720
 ttatgacagt gngcatcacc ttntgggccc aaggaccaag ccattggtct aaaaggcctc 780
 aaaatgcccc ggganggcct ctggtggcca tggcattagt atatactaac catcattctg 840
 gccaggtaag gaagccctg gacccc 866

<210> 434
 <211> 764
 <212> DNA
 <213> Homo Sapiens

<400> 434
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 gaaaatgaaa gtggagaaca tgggaacagca atatttgn gc tcttctcata ggatgcagtt 180
 acacacacat atgactggaa tcacttcaga gtaaaaaaaa agtgggctgg gtgcagtggc 240
 tcacacctgt aatcccagca ctttgggagg ccaaggacag gagcatcact taaggccaga 300
 agtttgagac cagcctgggc cacatagtga gacctgtct ctatgggagg ggtgggggtg 360
 gggggcattg taaaaaagca gttgttcttt tanaaggcat cagagagccc tntagtgacc 420

acgaagggga	gttaatgcag	agatgactcg	agacagagaa	gcagtcacga	gtgtttacaa	480
aggaaaaagt	gagggaggga	aagctctttt	ggttaacagc	atattttacaa	ttagttaact	540
gnattcttaa	atacttttaa	cctgagtaac	atattataaat	atgttatagg	aaacctcaca	600
gtcacaagtc	acactagaat	ccatctgtcc	agtatctggg	ctttccccac	accagaatcc	660
atctgtccag	tatctgggct	ttcccgagtc	ttcctcttct	cataagttcc	caanggcagc	720
anaagtgtga	agcatgcaca	ccaaggaaaa	acgcattcca	gccc		764

<210> 435

<211> 834

<212> DNA

<213> Homo Sapiens

<400> 435

agattttgtt	aatttttcta	caaaaaatgg	atttgctact	aacccaaaacc	cctcctgatg	60
agataaagaa	cagtgttcta	cccatgggtt	acagagcact	agaagctcct	tccattcaga	120
tccaggagct	ctgtctaaac	atcattccaa	cctttgcaaa	tcttatagac	tacctatcca	180
tgaaaaacgc	tttgatacca	agaattaaaa	atgcttgtct	acaaacatct	tcccttgagg	240
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tacttgatga	tatcctaccc	ttcttacaac	aaattccatc	caaggaacct	gcggctcctca	360
tgggaatttt	aggtattttac	aaatgtactt	ttactcataa	gaagttggga	atcaccaaag	420
agcagctggc	cggaaaagt	ttgcctcatc	ttattcccct	gagtattgaa	aacaatctta	480
atcttaatac	gttcaattct	ttcatttccg	tcataaaaaga	aatgcttaat	agattggagt	540
ctgaacataa	gactaaactg	gagcaacttc	atataatgca	agaacagcag	aaatctttgg	600
atataggaaa	tcaaataaat	gtttctgagg	agatgaaagt	tcaaataattg	ggaatcagca	660
aattggcaaa	gtttttaaca	acattggagc	agaccttntg	actggcagtg	agtcggaaaa	720
taaagangac	gggttacaga	ataaccttaa	aagagcatcc	ttaccaattg	gaggaaaaaac	780
caaaattttgc	caaaaagaacc	aggaccggcn	ccgaagctgg	aaaagccgca	ggct	834

<210> 436

<211> 812

<212> DNA

<213> Homo Sapiens

<400> 436

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aaatatagtt	taattcttac	aaatcttctt	ttgaaaatgc	aattcatata	tgctgcaacc	120
tcagaagttt	gaatttgaaa	tgaatatga	aggtagtagt	cagggagagc	acatcagagt	180
gccttgtcaa	atatccaaac	aaatcagcac	atacctcttc	cttgatacag	gaggaaaaaa	240
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caatgaaatg	aagggttaagt	tgaattttgt	agtatttggc	cagtctctgt	actaaacaat	420
agttcatctg	aaaagtttgg	aaaaagcaaa	taacctgata	cttctcttta	tgcttatcat	480
tttctcactg	tcattcttaa	tgcaaacaaa	tcaatacagc	atcaagattt	tttacaatatt	540
aaaatgaaga	ctaatagactc	atagactgng	taccatatag	tacttaatag	atgagcttgc	600
aatgaccatc	acctcaattt	tttaaataac	accaagatcc	acaagccaaa	ataaacattt	660
gattaaaaag	ttatgggtatt	caagataact	cagtttccct	tttctctttg	agattgggna	720
anggctgggt	ctttaaaaaa	ccctggaaaa	gggagttggg	taaagagggg	aaaaaatcct	780
tcaangcttt	taaaaaaact	tcnactgggt	ta			812

<210> 437

<211> 842

<212> DNA

<213> Homo Sapiens

<400> 437

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agagcaaagc	cccaacttgc	cctccactgg	tgatgtcaca	cccacccatg	aagagcctgc	120
ctctaggggt	gttgaatgtt	gggtcacgaa	gatctcaacc	tggccaaaga	agagaaccca	180
gaaagatcat	cacagtttct	gtaaaagaag	atgtacacct	gaaaaaggca	gaaaatgcct	240
ggaagccaag	ccaaaaacga	gacagccaag	ccgatgatcc	cgaaaacatt	aaaacccagg	300
agcttttttag	aaaagttcga	agtatcttaa	ataaattgac	accacagatg	ttcaatcaac	360
tgatgaagca	agtgtcagga	cttactgttg	acacagagga	gctggctgaaa	ggagtatttg	420
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gtcgatgtct	agtaacgctg	aaagtaccca	tggcagacaa	gcctggtaac	acagtgaatt	540
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atgtctttga	gaagaagcag	aaagaacttg	aggctgccag	tgctccagag	gagaggacaa	660
ggcttcatga	tgaactggaa	gaagccaagg	acaaaagccc	ggcggagatc	cattggcaac	720
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tgactgtgtg	gtgaagctgc	ttaagaaccn	ttgatgaaga	atccctggaa	tggcctgtgt	840
cg						842

<210> 438

<211> 678

<212> DNA

<213> Homo Sapiens

<400> 438

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nngctctaaa	gatntcaaga	gnattaanag	nacttttntc	agggnagcac	tnnttttttt	180
ttaaacantt	nttggngttc	tgtggncac	annatttctt	tntgtntcaa	ngtnatgtat	240
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gatntgangc	cnnaaaaaaa	aaaatctttt	ttacctgtgn	caccccaaac	tttttcaa	360
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ctggnatattg	cngaccttaa	aataaattaa	aagtnctcaa	ctnttttttt	ttttgntaaa	540
cnttttttta	agnatgannc	cntggttaaa	aagaaaagnt	ttaaaccgaa	aatattttct	600
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ntccnangac	ctttttcc					678

<210> 439

<211> 826

<212> DNA

<213> Homo Sapiens

<400> 439

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gaaaaattat	cagccacgga	gagcattgtg	gaaatagtaa	aacaggaagt	attgccattg	180
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gtcccatca	ccccttccac	agttccttcc	tttctccaa	ctcctccaac	tcctccagct	300
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gctgccatca	cagtccagag	agtcctagag	gaggacgaga	gcataagaac	ttgccttagt	420
gaagatgcaa	aagagattca	gaacaaaata	gaggtagaag	cagatgggca	aacagaagag	480
attttggaat	ctcaaaactt	aaattcaaga	aggagccctg	tcccagctca	aatagctata	540
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gaccaggata	aaatgagcca	ggggtttcat	cctgaaagag	acccctntgg	cctaaaaaaa	720
gtgaaaagct	gtggaagaaa	atggagaaga	actgagccag	accgtaatgg	ggcctgaaag	780
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<210> 440
 <211> 689
 <212> DNA
 <213> Homo Sapiens

<400> 440
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 ccacagcatt tccttctgtt tcaatgttat gtatgttttg attactattg tgatttttta 180
 aattttctga agcaagctga gaggcaggca gaaagatttg atgccaaaaa aaaaaaaatc 240
 tttcttacct tgttcacccc aaactttctc aaatctggac taaatgctat accttaaaac 300
 aaacatgagg tgcattctga aggggaggga aattttatttc tctgcttttc tattatacaa 360
 gttgtttaca gaaactgcaa attaaaaaat tacactggca tttgcagtcc ttaaaaaataa 420
 ttaaaagttc tcaacttttt ttttttgcta aacatttttt taagtatgag tccttgttta 480
 aaaagaaaag attaaaacag aaaatatttt ctataaataa tacatgtatt ttggtttttag 540
 tgctcccgcc ctaaggtttg aagtttactt ttatccagta cctttttcct ccatgatcac 600
 ctttttttct ctttccctn ttccactcgg gcacacgtgg ggggtttctg cnanaattgg 660
 ccttgctgca ctgngaattg gcnaaaacc 689

<210> 441
 <211> 883
 <212> DNA
 <213> Homo Sapiens

<400> 441
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 gcgaccagaa gcaagctcaa atagctataa ctgtaccaa gacatggaag aaaccaaaaag 420
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 agctttccat tgacaaagta cttgaatctg aacaagataa aatgagccag gggtttcatc 540
 ctgaaagaga cccctctgac ctaaaaaaag tgaaagctgt ggaagaaaat ggagaagaag 600
 ctgagccagt acgtaatggt gcttgagagt gtttcttgag ggtgaaggaa tagatgctaa 660
 ttcaggcttc acagatagtt ctgggtgatgg gggtaacatt ccatttaaac cagaatnctg 720
 gaagcctact ggtacttgaa ggtaagaaca gtatgaccag ggagtttctg gtggactttc 780
 cagttcatgc ctggctgnat tccaaaancc naagggcctg gcttctatta anggatgnngg 840
 ttnttgacag gatcaaccaa ncccaaattg ccaatgggga act 883

<210> 442
 <211> 777
 <212> DNA
 <213> Homo Sapiens

<400> 442
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 gtgaaacttt ttaaaaaaat acttaaatg tttcttttgt ttcattttgt gtattttgaag 300
 ttttagttat cctcagactc ctcttctgct tcccgagcc acgtgaagaa tgccgtgaca 360
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 tagaaggcat cctcgagat cacctctcgt tcatatagac aatcaaaaaa catccgcagc 480

aaattggcag	ggtgatcaag	ttttactatc	gatgcttgta	gtgcataaag	tgcttgagct	540
tccttctctg	natctgagtc	taggtacttg	agtaagatcg	gcactctctg	cttgaaacag	600
cagtgtccac	ttcttgaang	tagaagaagt	cggctattaa	tagctgggtt	acaaacagca	660
gtcattttaa	gctctaagga	atggtaggtg	aactcntctg	ggatttcggc	taagaataag	720
ccctttancc	aggccaaaga	acctgggtcan	tcaattcgct	tttggccctc	caataaa	777

<210> 443

<211> 875

<212> DNA

<213> Homo Sapiens

<400> 443

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agaggagagg	acaaggcttc	atgatgaact	ggaagaagcc	aaggacaaag	cccggcggag	180
atccattggc	aacatcaagt	ttattggaga	actctttaa	ctcaaaatgc	tgactgaagc	240
catcatgcat	gactgtgtgg	tgaagctgct	aaagaacct	gatgaagaat	ccctggagt	300
cctgtgtcgc	ctgctcacca	ccattggcaa	agacttggac	tttgaaaaag	caaagccacg	360
tatggaccag	tactttaatc	agatggagaa	aattgtgaaa	gaaagaaaaa	cctcatctag	420
gattcgggtc	atgcttcaag	atgttataga	cctaaggctg	tgcaattggg	tatctcgaag	480
agcagatcaa	gggcctaaaa	ctatcgaaac	gattcacaaa	gaggctaaaa	tagaagaaca	540
agaagagcaa	aggaaggtcc	agcaactcat	gaccaaagag	aagagaagac	caggtgtcca	600
gagagtggac	gaaggtgggt	ggaacactgt	acaaggggac	caagaacagt	cgggtactgg	660
acccctcaaa	antcctaaaa	atcactaagc	ctacaattga	tgaaaaaant	cactggacct	720
aaagccagct	aggcagctgg	ggaaaaggca	gcagtgggtg	accaangcaa	gtgaaactga	780
gccttacggc	aagtgtctnc	agttaaacag	atctntgncc	tgaaccttca	gaaccttang	840
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<210> 444

<211> 756

<212> DNA

<213> Homo Sapiens

<400> 444

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taaagtgtgt	ctaaagattt	caagagtatt	aagagtactt	ttctcagggg	agcacttttt	180
ttttttttaa	caattcttgg	agttctgngg	nccacagcat	ttccttctgn	ttcaatgnta	240
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ngaaagattt	gatgccnaaa	aaaaaaaaaa	aatctttntt	accttgggtc	ccccaaactt	360
tntcaaactt	ggactaaatg	ctatacctta	aaacaaacnt	gaggggcatn	ttgaagggga	420
gggaaattta	tttctctgnt	tttctattat	acnagttgnt	taccgaaact	gnaaattaaa	480
aaattaccct	ggcntttgca	ggccttaaaa	taaattaaaa	gntctcaact	tttttttttt	540
gccaaacatt	tttttaagta	tgagnccttg	nttaaaaaga	aaagattnaa	nccgaaaata	600
ttttctataa	ataatacntg	nattttgggt	ttaaggctcc	cgccctaang	nttgaagggt	660
acttttatcc	nagnnccctt	tttccctcca	tgaanacccc	tttttttcnc	ctttcccttt	720
ttcccaactn	ggggcccccc	tngggggggt	tttgcg			756

<210> 445

<211> 783

<212> DNA

<213> Homo Sapiens

<400> 445

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tttatatcag	ataatgaaag	ttttaaccct	tcattgtggg	aggaacagag	gaaacagcgg	120
gctcaagtgt	catttgaatg	tgatgaagac	aaagatgaaa	gggaggcacc	tcccagggag	180
ggaaatttaa	aaagatatcc	aacaccatac	ccagatgagc	ttaagaatat	ggcctaaaact	240
gttcaaacca	ttgtacatag	attaaaagat	gaagagacca	atgaagactc	aggaagagat	300
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agtactacta	cagtaaaaag	caaagttgat	gaaagagaaa	aatatatgat	aggaaactct	420
gtacagaaga	tcagtgaacc	tgaagctgag	attagtctctg	ggagtttacc	agtgactgca	480
aatatgaaag	cctctgagaa	cttgaagcat	attgttaacc	atgatgatgt	ttttgaggaa	540
tctgaagaac	tttcttctga	tgaagagatg	aaaatggcgg	agatgcgacc	accattaatt	600
gaaacctcta	ttaaccagcc	aaaagtcgta	gcacttagta	ataacaaaaa	agatgatata	660
aaggaaacag	attcttttatc	agatgaagtt	acacacaata	gcaatcagaa	taccagcaat	720
tgggtctctc	catctcggat	gtctgattca	gttctcttaa	tactgatagt	agtcaagaca	780
cct						783

<210> 446

<211> 866

<212> DNA

<213> Homo Sapiens

<400> 446

agattacaac	acacatacaa	taagtgaatt	ttatcaaaat	acagcacatt	tcttctacta	60
tatccataaa	aatcaattcc	tatgtaaata	gtactgaaaa	tcaactaaaa	tgagttaaaa	120
tttacaaga	gttggttaaag	ggtttcaatc	aaaattatta	aaactataca	gtacaataac	180
caattgataa	catcttgaaa	gaagtgcatt	atttgagttc	acatattttt	aaaagtgtctg	240
cctacttact	ctgactagca	agaatggaaa	gtgagtccaa	ctcacttttg	caaaaaataat	300
gttggttggg	gttttaagct	agtcttataa	aagtcttaat	taaaatcaag	gttgataaac	360
aaagcataac	agattaaaaa	ttcccaaatt	gcattttctta	gtaaataaaa	atgaagtgc	420
ataaccaa	attgctctaa	tgaaagggtc	cagactagcc	tcaactaaac	agttattggg	480
cttctatggc	acttttttct	gggtccaaata	accatgcatt	aatccttacc	attacatgtt	540
actcaaattt	tatttgatta	catagaacaa	aaacaaataa	aattaatggg	ctggataaac	600
aaaattaata	aacctctatc	atcaaataat	tgttacagta	actaggaaca	aagaaaggca	660
gtttggtggg	taaaacacta	ttacactgat	ccccatagga	aaccccttta	aagactctgg	720
aagtgttgag	ttcacattta	atggtacctg	tagaaacagn	cctttatttg	gacaccttta	780
cccactggca	ngccctaang	gacccatccc	tttgccttat	aacttttcac	aagcaattct	840
ctaactcctg	gccagtttnc	aaaagc				866

<210> 447

<211> 789

<212> DNA

<213> Homo Sapiens

<400> 447

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aatcggctgc	acttcccac	ttttcctcgt	ttgtcagcaa	ttgggatgaa	gccacaaaaa	180
gatctttgct	taataagaag	aaaaaaagag	caaggagaaa	acgaagagaa	agaaattttg	240
aaaaacaaaa	ggagaggaag	aagaagagcc	agcaggctag	gaagactgca	tcagttctta	300
gtaaagatga	tgtggcacct	gaaagtgggt	atactacagt	gaagaaacct	gaatcaaaga	360
aggaacagac	ccagagcat	gggaagaaaa	aacgtggcag	aggaaaagcc	caagttaaag	420
caacaaatga	atccgaagac	gaaatccac	agctgggtacc	aataggaaag	aagactccag	480
ctaataaaaa	agtagagatt	caaaaacatg	ccacaggaaa	gaagtctcca	gcaaagagtc	540
ctaactccag	cacacctcgt	gggaagaaaa	gaaaggcttt	gccagcatct	gagaccccaa	600
aagctgcaga	gtctgagacc	ccagggaaaa	gccagagaaa	gaagccaaaa	atcaaagaag	660
agcagtgaag	gaaaaaagtc	cttcgctggg	gaaaaaagat	gccgaagaca	gacttcaaaa	720
aagccagang	ccaggttttc	ccactcctag	taaatctgtg	agaaagcttt	ccacaccccc	780

aaaaaatgg

789

<210> 448

<211> 820

<212> DNA

<213> Homo Sapiens

<400> 448

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cctgcctcag	cctccctagt	agctgggatt	acagggtgtcc	accaccatgc	ccaattaatt	180
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gcccctggac	tacttatgga	ggtttttaaa	aatcttttaa	gtccaggcct	gacgttttaga	360
gaaggttaca	aaggcggcca	ggatctgagt	atttccaaaa	agctctggag	gcagcattga	420
ggtttccttc	cagttgaatc	actgacttta	ggtcgactgg	ggtacttttg	gttttttggg	480
ccattttttg	ggggtgtggg	aagcttttct	cacagattta	ctaggagtgg	tgaaaaactt	540
ggcctctggc	ttttttggag	tctgtctcgc	atcttttttc	cccagcgaag	gacttttttc	600
cttcaactgc	tcttctttga	tttttggtct	cttctcttgg	gcttttccct	ggggtctcag	660
actctgcagc	tttttggggg	tcttcaanat	gctggcaaaa	gccttttctt	ttcttccac	720
gagggggngc	ctgggggatta	ggactctttt	gctggggana	cttcttttct	tgngggngang	780
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<210> 449

<211> 936

<212> DNA

<213> Homo Sapiens

<400> 449

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aaaaaaatat	taatagtttg	caggaagagc	ttttacagtt	gaaagctata	caccaagaag	120
aggtgaaaaga	gttgatgtgc	cagattgaag	catcagctaa	ggaacatgaa	gcagagataa	180
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tccagaagaa	atatgaatgt	gagttagaaa	atttaaggaa	agccacctca	aatgcaaacc	300
aagacaatca	gatatgttct	attctcttgc	aagaaaatac	atttgtagaa	caagtagtaa	360
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tactagctaa	agaagaacag	ggctgtgtaa	ttgaaaaatt	aaaatctgag	ctagcagggt	600
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aacaccatca	aaaagaaata	tcagaactaa	atgagacatt	tttgtcagat	tcagaaaaag	720
gaaaaattaa	cattaatggt	tgaaattcaa	ggtcttaang	gacagtgtga	aaacctaccg	780
ccaggaaaag	caagaagcca	ttttaaantt	ntgagagntt	acctcagagga	ttttggaaat	840
ttccaanncn	gaactggggg	gaatctgctg	ggaaaaatag	gtcaggaggt	cgaatcatgg	900
aaccaccagc	aggcctttga	ngtcatgacc	tgagca			936

<210> 450

<211> 806

<212> DNA

<213> Homo Sapiens

<400> 450

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agaatagttg	ggcattttaa	taaaatttgc	taaatgaatg	aaaaatccaa	aataaatcat	180

gaagccat	ataaatcaca	ccaatcttgc	ttgggttaaa	caatagaaa	taacactttt	240
gaaagagaag	gcaaacaggt	gttagagggg	caagaatgtg	agctcgagga	aaagacagct	300
acgaactgtg	tttttaacaa	ctcattat	ggctactata	tttcccaatc	tattctaaca	360
ctaacaagaa	tctgtcta	taattgtgac	aacatctgca	aaaccatagt	tacctat	420
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ggaatccttt	aatagtatca	actctgctct	cctatctcgt	aattcttttt	gntctagtag	540
tggtcttagg	ttttcatggt	cctttataaa	acatttttct	ttttcattat	ggatttcact	600
tttgctacat	gtttgagata	cttctttcaa	cttgaattaa	aagaatctga	ttttcaagcc	660
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ggactggaat	tcttctaact	cttttccttt	aagaagaacc	tttttcttgg	ntcataggcc	780
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<210> 451

<211> 909

<212> DNA

<213> Homo Sapiens

<400> 451

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tgagagagag	agtattaaga	gggaaataca	gaattccctt	ctacatgtct	acagactgtg	180
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aaccagagct	agacatctca	gacccaaaaa	gaatagatat	tatggtggga	atgggatatt	360
cacaagaaga	aattcaagaa	tctcttagta	agatgaaata	cgatgaaatc	acagctacat	420
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<210> 452

<211> 672

<212> DNA

<213> Homo Sapiens

<400> 452

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aaaccacagg	cntgaactgn	aaacctgtct	taactatgaa	ctggncctta	ggttaattct	180
tannngccat	tcantatttc	nntccttggn	aactgtaatg	ttntagcacc	ggatgatctc	240
cognanaggt	nctagaanng	acngnctgcc	agngnangga	gatncttccn	tatacaccac	300
ttnanacnca	taccgtcnan	tttcanaccn	accagacgg	nangcacatg	gngatggggc	360
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gactttaatn	ncatgattta	naanatncag	nacgntattg	cctaaatntt	attctataca	540
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ggaatgnccc	cc					672

<210> 453

<211> 834
 <212> DNA
 <213> Homo Sapiens

<400> 453
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 tcaagtacca catgaccaa cacaaggtg agactgagct ggactttgcc tgtgaccagt 480
 gtggccggcg gtttgagaag gccacaaacc tcaatgtaca catgtccatg gtgcaccgcg 540
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 gtgcaccgcg atgggagggg cggagggttg cttgccgncc ttggtgctgg angcgggctt 780
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<210> 454
 <211> 703
 <212> DNA
 <213> Homo Sapiens

<400> 454
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 gnttggtcca attnggtaca agatatagtt cccacacctt ggg 703

<210> 455
 <211> 825
 <212> DNA
 <213> Homo Sapiens

<400> 455
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 atccttttga gataaaagaa aaaccagaag aagcaggtca tgaagctgag gaaagaggag 180
 agaccgagac cgaccagaac gaaagtcaga gtccacagga gcctgaggaa ggccccagt 240
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ctgcagatgc	aaaccaggca	gaaggccatg	aatcgaat	cattgcccag	ttggccttcc	660
agaacacacc	aggaaaaaca	cacagagttt	taagaggaaa	cctgggcagg	cttgacaatt	720
gaacgttnca	tgggtgatca	caattgaacg	tgtgcacaag	aagctganga	cttgtggaat	780
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<210> 456

<211> 740

<212> DNA

<213> Homo Sapiens

<400> 456

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ctgtgtcttt	gatgaccacc	tcaaaaagggt	cgcagacttc	acagtgtaac	ttggaaacag	180
acaaggagat	agatgattac	atcatgacat	actgcctaca	aaagaacatt	ctgacagaac	240
attaagtaga	acagagcaca	cagtttcaag	tattcagcac	tgctttctgg	ccaagtaaaa	300
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cacagcgttt	ctttcccaga	atgagactgg	ctcagttccag	cttgaaagca	gtgtgaggaa	420
tcactctttc	ccttgactgt	taagaaaaaa	aaaaatgaac	taaacaaata	aattactaca	480
acaacaggga	ccatggcact	gaatgaaata	aaggggcaat	caccttccca	tcattgcata	540
gtctcccga	gcagcaagt	tgaaagagga	tactgaaaaag	ccacttcatt	tttacacagc	600
ccaagggatc	gtttttatng	atgacctggg	cacctataat	gnccagttgc	tttatgagaa	660
ccacacacac	accacattct	tcctacctn	taagagaagg	taggttcctt	tcacaataag	720
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<210> 457

<211> 726

<212> DNA

<213> Homo Sapiens

<400> 457

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cagaactcct	gtgggggtctc	tttaaaatgc	taacacccag	gttaaaagac	ttggggcaag	180
ggtggtgctg	gagctggcag	ggccccacc	ccaagtctgg	gggaggtgcc	tgctccteta	240
ggagggcaca	gggcccaggc	cacggcgccc	aggccttacg	gggcggcggc	tgctgcacag	300
tgccacatct	tcaggggccca	cagcgccggg	tgagggcctg	ccagaagca	ccagagccac	360
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cggacttcgg	caaggggaca	nggcacgctt	cgggtgccgg	tggcttccgg	actttggaog	720
ccgcaa						726

<210> 458

<211> 870

<212> DNA

<213> Homo Sapiens

<400> 458

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ataaaagaaa	aaggcaagcc	acttatgctg	aacccaagaa	caaacaaggg	aatggcattt	180
actttacaag	aacgacaaat	gcttgggtctt	caaggacttc	tacctcccaa	aatagagaca	240

caagatat	tc aagccttacg	atttcataga	aacttgaaga	aaatgactag	ccctttggaa	300
aaatatat	ct acataatggg	aatacaagaa	agaaatgaga	aattgtttta	tagaataactg	360
caagatgac	a ttgagagttt	aatgccaat	gtatatacac	cgacggttgg	tcttgccctgc	420
tcccagtat	g gacacatctt	tagaagacct	aagggattat	ttatttcgat	ctcagacaga	480
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gtaggaaaac	tttgttgnat	cagcttggtc	aggaatacgg	cctgatagat	gcctgccagt	660
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<210> 459

<211> 761

<212> DNA

<213> Homo Sapiens

<400> 459

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caatgacttt	tatttactta	aagccagcag	tagttcccat	tactctcata	atgttatagt	120
taaggcttga	tttagttcca	gaaaataaat	agggtaaatt	tttaatattt	ccctagctct	180
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gtactttctat	ccataaaaagt	aaattttctat	tttagtagct	ctgtaagaac	taggccagag	360
aagagtatta	cccataatag	taaatagcaa	atactttggc	aagtctgaat	tagagtacaa	420
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gagaacaaaa	ccccagaaaa	cacccttaaa	actgaagaca	ttatctcttc	ttggctgaaa	660
aaaggggttc	cctggagcac	angaaagggt	ttatcaaggg	aggcttctat	tcngtaatca	720
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<210> 460

<211> 876

<212> DNA

<213> Homo Sapiens

<400> 460

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cactcagccc	tccagtgtctg	ggtctgcatg	gtgtgacatt	cggctaccag	ggacagaaac	120
cactctttta	gaacttggat	tttggcatcg	acatggattc	aaggatttgc	attgtgggcc	180
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cccgactcat	cacagaaacc	aattgccagc	ttgtgggtgg	tggaggaaca	gagtggtagc	660
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catgggcagc	cnggccccga	naagtgaagc	tttnttttcc	agaagnttcc	gagagaacat	780
aattgggggg	gcctaaaann	cctctggggg	cttcccttct	tttgaanaat	gctntggnc	840
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<210> 461

<211> 689
 <212> DNA
 <213> Homo Sapiens

<400> 461
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 ggcagcaact cttttccttt atttcttccc cttgtaaagg gaaattcaag ttcagcagca 180
 ttcctttcct gccccaagtc ctcaaccaga caagaggctg caggcaccaa atcttgggct 240
 ggataatggc aaaggcctca gaagctcacc tccagctctg agcttcaaca gctgtttgta 300
 ccagtgaatc agcattaaat ccaccagaaa agaacagcac cacccaaaga ctgggggggca 360
 gctgggcctg aagctgtagg gtaaatacaga ggcaggcttc tgagtgatga gagtcctgag 420
 acaataggcc acataaaactt ggctggatgg aacctcacia taagggtggc acctcttggt 480
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 aaagtctttc agagaaatgg atgcaatcag aagtgggagc cccggncaca tcaaggctac 600
 actccacctt catgtgcctg aaatggttgc caggctcagct gcaggcccan aggcagtcct 660
 canaaggaag gggagaccac agaggactt 689

<210> 462
 <211> 840
 <212> DNA
 <213> Homo Sapiens

<400> 462
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 tgttacggct cggaggcacc aagcaagatt accttatgct ggctactttg gatgagaatg 180
 aggaagtgat agatggaggc aaaaaaggag caatcgatga ccttcagcaa ggtgaattgg 240
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 atgaaccagc tgaaaaagaa aattccagca aaaaagaagt aaaaatacct aaaataaata 360
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 cagaaccaca ttctgatgag aatggcagta ccacaccgaa agtaaagaaa gataaacaga 480
 acatctttga attttttgag agacagactt tgttacttag gcctggaggc aaatgggtatg 540
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 acaaaaccct tgctcagaag ctgtatcagc atgaaatcaa cttattcaaa agtaagacga 660
 atagtcaaaa gggagcctct tctacctgga tgaaaggcaa ttgtgtcatc ggggaccact 720
 aggtgacagg atggcagcca ttgattcttc ttattcagga tgatgcccg tccacaccact 780
 ttcagnntgt agnaaactct tggggaaccc ttggtaaaaa ggaanggcna caaacagca 840

<210> 463
 <211> 784
 <212> DNA
 <213> Homo Sapiens

<400> 463
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 tttgcatctc tgttgtgtag ccagtcacat cggttcagcct cccatctaag ctgtttgaga 180
 cttgcattat ctttgttagc catggcattc atgccaatgt tatcaaactt ggatcccata 240
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 tttctcttgc ttttcttagt actgactttg gagtggactt caagttcttg aacactctca 420
 ctttcatcat ctaacacatc catgaatgtt cctccatctt catcaacttc agcaaattct 480
 tcatcatcca tacttcttaa agaaacttca tcgtcatcca ggttaccaag ttcacatca 540
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tttccagcaa	aaatccatat	catcctttnc	agagctgaaa	cagttatcat	cttcaaatgt	660
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catccccgtt	tttggnttct	cttttaanca	gcaacttttt	ttatnaaacc	ctgggggaaa	780
aaac						784

<210> 464

<211> 850

<212> DNA

<213> Homo Sapiens

<400> 464

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ccacagaagc	cgcaggtcgg	ggtctgcagc	ccctgaagct	ggactaccgc	gccctggccg	180
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caccctgggc	cagcccagagc	cccacttaag	gcagaaccgc	gcgtccccc	ggccctggaa	720
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canagtnccg	gacccaccgg	gaccccaneg	tgccctggte	ccttgcccaa	cttccgggcc	840
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<210> 465

<211> 759

<212> DNA

<213> Homo Sapiens

<400> 465

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cagaactcct	gtgggggtctc	tttaaaatgc	taacacccag	gttaaaagac	ttggggcaag	180
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ggagctttgg	canggggaca	aggcaacgct	tcgggtgccc	ggtgggttcc	ggacttttga	720
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<210> 466

<211> 1240

<212> DNA

<213> Homo Sapiens

<400> 466

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<210> 467

<211> 885

<212> DNA

<213> Homo Sapiens

<400> 467

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<210> 468

<211> 748

<212> DNA

<213> Homo Sapiens

<400> 468

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atgctgtggt	cagaaggaat	gccagggtgg	gaccgtgata	cctttaatga	caataggaac	180
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<210> 469

<211> 770

<212> DNA

<213> Homo Sapiens

<400> 469

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tgggagctcn	gctattttgc	ttgcccttgt	ggangcaggc	caaaanaagc	caacgaatgg	720
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<210> 470

<211> 892

<212> DNA

<213> Homo Sapiens

<400> 470

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<210> 471

<211> 759

<212> DNA

<213> Homo Sapiens

<400> 471

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gctcgtctat	ttgctgcctt	gtggaggcag	gcgananagg	caacgagtgg	gccctgaaaa	720
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<210> 472

<211> 852

<212> DNA

<213> Homo Sapiens

<400> 472

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<210> 473

<211> 804

<212> DNA

<213> Homo Sapiens

<400> 473

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naagctgagt	tttgcggaag	gatgtctcca	cgcccgctgt	cgcagacact	gtcactgtct	660
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804

<210> 474

<211> 819

<212> DNA

<213> Homo Sapiens

<400> 474

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gagcccatTTg	aaataccatc	ggaagacgat	gggacgggtc	tgctctccac	ggttacagcc	180
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aaaacaaccg	aacaggacct	gaaagagtat	tttagtacct	ttggagaagt	tcttatgggtg	480
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<210> 475

<211> 721

<212> DNA

<213> Homo Sapiens

<400> 475

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ttccaccctt	ctttgagaca	cctgagctca	ctgggtgaact	ctgcttcaag	tcctcctgca	180
aagcacacca	caagctcagt	ccatgtttctc	agcccatcag	cttcagttca	cattgccaca	240
cttacatata	agtaacagaa	gagaacacac	accatacagc	attcacagca	gttgacaaag	300
gggtaggggg	agtacaagta	tcattttact	taacacattc	atctaattgtg	ggttatctaa	360
gaacaaaaac	tcacttaaaa	gtcttccaac	agatgtggat	gtcctttgaa	tgcaaaaaac	420
attcgtacat	tatttgcctat	cttggtcttc	tcacactctc	ctcaccaaag	ccacaggatt	480
gagagacaca	tctcgccaag	ttaaaaaata	tccattatgc	accaccaagt	ctctgcacgc	540
gctctctcct	tttctcgtct	atactagcct	ttcatgcctc	ggcaccacca	tcaatcccac	600
acaagggtttc	aaaagtccag	acagccttct	ggttccatat	cacaggcctt	gcgttcatag	660
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<210> 476

<211> 442

<212> DNA

<213> Homo Sapiens

<400> 476

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nttncntatc	agtaccagaa	gagaccncnc	ncntncagc	nttncagca	gtngncaaag	300
gggtaggggg	agtcangta	tcatttnant	taccacattc	atctaagggg	ggttatctaa	360

nacccaaaanc tcanttaaan gtnttccanc anangnggan gnccttngaa ngcaaaaaanc 420
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<210> 477

<211> 878

<212> DNA

<213> Homo Sapiens

<400> 477

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gatgagccca	ttgaaatacc	atcggaagac	gatgggacgg	tgctgctctc	cacgggttaca	180
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agtaccgggg	atgtgatgga	tgtctttatt	ccccaagccc	nttcaggggc	ttttggcttt	780
ggtacatttg	ccagatgatc	agaatgccc	gtctcttttg	tggaaaagga	ctttgatcat	840
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<210> 478

<211> 768

<212> DNA

<213> Homo Sapiens

<400> 478

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gacgccggcc	tgnggatgcc	gtgatgacca	attcttgaat	gagaaagcat	gtagaccgna	720
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<210> 479

<211> 815

<212> DNA

<213> Homo Sapiens

<400> 479

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tcttttttta	ataccgggat	gtgatggatg	cttcatttcc	caaccatttc	agggcctttg	780
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<210> 480

<211> 812

<212> DNA

<213> Homo Sapiens

<400> 480

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cttcaaaatc	ttcttagggg	aaaataaata	ccggtatcta	tgcagtacca	taaacatggt	180
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<210> 481

<211> 1127

<212> DNA

<213> Homo Sapiens

<400> 481

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<210> 482

<211> 773

<212> DNA

<213> Homo Sapiens

<400> 482

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<210> 483

<211> 794

<212> DNA

<213> Homo Sapiens

<400> 483

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<211> 788

<212> DNA

<213> Homo Sapiens

<400> 484

caagaccaga	aggaaatgca	cagttggata	agatgggggtt	cacaattatc	agaaaatgca	60
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gttcaaaggt	ccagagactt	ctgagtatgt	tgatggatgt	aaaaacatgc	aatgaggtgg	180
acctggagaa	ttctgcagat	tgggaagtga	agacaataac	aagtgccttg	aaacagtatt	240
tgaggagtct	tccagagcct	ctcatgacct	atgagttaca	tggagatttc	attgttccag	300

ccaaaaagcgg	cagcccagaa	tctcgtgtta	atgcgatcca	tttcttggtg	cacaaactgc	360
cagagaagaa	taaagagatg	ttggatat	tggtgaaaca	cttaacaaat	gtttcaaata	420
actccaagca	gaacctgatg	actgtggcaa	acttaggagt	ggtgtttgga	ccaactctga	480
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ggaaatctta	attgaaaacc	atgaaaagat	ttttcggacg	cognccgata	ctacattccc	600
tgagcccacc	tgctgtcag	catcaccccc	aaatgcgcca	ccaangcagt	cnaagagaca	660
aggncagaga	accaagaagg	cccgtggggc	gtctacaata	tttggttgga	gctggaaaga	720
tggtgacaat	ccttaccctt	tccangggagg	acacccctta	ccacagtctg	gactcacttt	780
tcttcccg						788

<210> 485

<211> 430

<212> DNA

<213> Homo Sapiens

<400> 485

agtaaattac	agttttatttc	atttacagag	accttgaggc	aaaaaggtgg	tgtttgga	60
acagcacacg	ggtgaggagc	accggagaag	cctgttacaa	atacgccagt	gcacgctgcc	120
agtgcagtga	gtgtgggggtc	ctgcagggtg	cgtctagga	agggcaggct	tgagacgcgc	180
gtctctgctt	ccctntgact	tgagaccatc	tcccttgnac	caacagcagc	ttntccaagc	240
taggctgcca	ggccaaagca	cacactctgc	aaacctatca	ctgcgagtng	tacagttccc	300
tttanaatcg	nagcagcang	tgctcaggga	ggagagggag	ccnnngtggc	tctggtggcg	360
tgactgccag	tnaggcgga	cacangtggc	ataaggctgc	ccgtcccttc	tcattcttat	420
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<210> 486

<211> 831

<212> DNA

<213> Homo Sapiens

<400> 486

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tttgtacttc	tggaattggt	acttctatac	cgggtgccctt	ggcaggaagt	gcccttctcc	180
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attcaaatgg	tgattctgcc	caagtgcata	ttgccacaaa	aaacagagaa	gaaaaagcag	300
cttgtctcag	aaatatttgt	ttaccttcag	aacacaatcc	aggtaatcag	aatgatttta	360
aaccaactaa	tgacgatatt	gaaatgcaga	gttccctaaa	attaccaaat	gatcctgcaa	420
ttattagcaa	cttttctgca	gcagtgggtg	atacgatagt	aaatgaaact	ttagagtcaa	480
tgacatcatt	ggaagttaca	aaaatgggtg	atgaacgtac	agattattta	actaaatctt	540
ttaaaggagaa	aaccctcca	ttttccact	gtgatcaggc	agtgtcgcaa	tgacgtgaag	600
ctagtagcaa	taaggacatg	tttgtgacc	ggttatctaa	atctattatt	aaacattcca	660
tagataagag	caaatacagt	atcccaaata	tagataaaaa	tgacgtatac	aaggaaagct	720
tgctgttttc	tgagagaaga	tcacagttga	caccagaaa	agtcttncca	aatttntctga	780
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<210> 487

<211> 728

<212> DNA

<213> Homo Sapiens

<400> 487

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atctctgcct	cccaggttca	agcaattctc	ctgccttagc	ctcccaagta	gctgggatta	120
caggtgcctg	ccaccacgcc	tggctaattt	ttgtattttt	ggtagagaog	gggtttcacc	180

atgttgccca	ggctgggtctt	gaactcctga	cctcaagtga	tccacccccca	ccccattgg	240
cttcccagag	ttctgggatt	acaggcgtga	atcacccgc	ccagcccaaa	tgcgcgaagt	300
ctttatctcc	taccttgatc	tctgtagcag	aaaagaacag	tatagatatc	aattgtcatc	360
aacagatgca	acatatcttg	taaatcaata	tattttcaag	tgaggctctc	gaatcacctg	420
cactgaaatc	atctgtgatg	cttatcaagc	atgcagattc	tcaggaccct	tactgactt	480
cataaatctt	catctctgga	ggtgagaccc	tggacactgt	atatgcaacg	agcacaccac	540
caatcctgga	tgagccccgc	tttttctctg	tgccagaacc	ttaatgccac	gcagcattac	600
attaagtcac	attacaactt	tggccaatgg	aaacacaggg	tctttttctg	acaaaatgcc	660
atcaagccag	gtttggctcc	ccacttaagt	tcaaatnttt	aatcattaat	tttctgagcc	720
taaaatgc						728

<210> 488

<211> 788

<212> DNA

<213> Homo Sapiens

<400> 488

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tggccccgag	gcctccgacc	gccgcgcccc	aggaatcagt	gacattcaaa	gatgtgtctg	120
tggacttcac	ccaggaagaa	tggtagcatg	tcgaccctgc	tcagaggagc	ttatacaggg	180
atgtgatgct	ggagaactat	agccacctgg	tttctcttgg	atatcaagtt	tccaagccag	240
aggtgatctt	caaattggag	caaggagaag	agccatggat	atcagaggga	gaaatccaac	300
gacctttcta	tccagactgg	aagaccaggc	ctgaagtcaa	atcatcacat	ttgcagcagg	360
atgtatcaga	agtatcccac	tgcacacatg	atctcttaca	tgctacatta	gaagactcct	420
gggatgttag	cagccagtta	gacgggcaac	aggaaaactg	gaagagacat	ctgggatcag	480
aggcatccac	ccagaagaaa	ataattacac	cacaagaaaa	ttttgagcaa	aataaatttg	540
gtgaaaattc	tagattgaac	accaatttgg	ttacacaact	gaacattcct	gcaagaataa	600
ggcctagtga	atgtgagacc	cttggaagca	atttgggaca	taatgcagac	ttacttaatg	660
agaataatat	tcttgcaaaa	aagaaaccct	tttagtgnga	taatgtagaa	aagnctttan	720
tcatagatca	tcgnttacta	aaccttgaga	aaaccctta	anggaaaagg	gagctttcct	780
aatgggac						788

<210> 489

<211> 875

<212> DNA

<213> Homo Sapiens

<400> 489

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gttaattttt	ttaatgggtga	aatcttttct	ttgcacataa	aatgagccag	tgcatgttgc	180
ttctctgagt	acaagacaaa	atcttatggca	atgggcaatt	agacttatac	ttttctgcaa	240
gaaaattaac	gggaaaattc	tcctcttagt	tttctgttgt	tttcccattg	atctgatact	300
gtaggcttaa	gaaagtgcct	tttcatgggc	atgccataaa	aagtacaata	aggggactta	360
atagttctgt	gaaactggca	tatgttagct	gaaagtataa	ttgtaactgg	gaaaagggga	420
aaaaagtcac	tagtagttca	accatctaca	gtttctgtta	aattgtgggt	tgtaagcctc	480
caagaagtgg	ctttaaatag	tttgtgataa	atttgcatac	atcttgctcc	cacttatact	540
tttaagaatt	ctcaaagtgt	ccaaccata	ggtgccatt	aatgttttgt	gtatctgac	600
atcttaaaat	ttatttttaa	gccctctgag	tcccaaaaat	aaccttttca	ctggcaaggc	660
catggggccc	caaaccaggg	aaacctggc	atcttttaacc	caacttttac	ccttataggc	720
tggaatcata	ctgngggaaa	cccacttcac	atcttttggc	tttcagtctt	caatctgncc	780
cnaatggaaa	atgggttggg	cctagtggga	actaaattct	tttgaatggg	ggactttcct	840
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<210> 490

<211> 844
 <212> DNA
 <213> Homo Sapiens

<400> 490
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 aaggtgaagg gaaaagcaag aagatttcaa agaaaaatgc cgccatagct gttcttgagg 180
 agctgaagaa gttaccgccc ctgcctgcag ttgaacgagt aaagcctaga atcaaaaaga 240
 aaacaaaacc catagtcaag ccacagacaa gcccagaata tggccagggg atcaatccga 300
 ttagccgact ggcccagatc cagcaggcaa aaaaggagaa ggagccagag tacacgctcc 360
 tcacagagcg aggctccccg cgccgcaggg agtttgtgat gcaggtgaag gttggaaacc 420
 aactgacaga aggaacgggc accaacaaga aggtggccaa gcgcaatgca gccgagaaca 480
 tgctggagat ccttggtttc aaagtcccgc aggcgcagcc caccaaaccg cactcaagt 540
 cagaggagaa gacaccata aagaaaccag gggatggaag aaaagtaacc ttttttgaac 600
 ctgctcttgg ggatgaaaat gggactagta ataaagagga tgagttcagg atgccttacc 660
 taagtcatca gcagctgcct gctggaattc tttccatggt gcccgangtc gcccaagctg 720
 taggaagtta gtcaaggaca tnacacccaa gattttacca ggcagcttcg aatcttgcca 780
 nggcncngta ctgccatgat agcccanagt tggtgtattg gggcancttt gccccaggcc 840
 ggga 844

<210> 491
 <211> 825
 <212> DNA
 <213> Homo Sapiens

<400> 491
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 ggcaagtgtg gaggggacca acctagcagt agtggcattt gagaataaat taacaaaaaa 180
 atttagtatt accattttatt gatgacaaac acttaagttt tacttacatt ccatggggag 240
 aaaaattcca gcgtaaacaa tgaatggaag cagtacttaa ctgcgagggc taccaggctt 300
 tccatacgga ccacacgcag agcctcagtg cacacacttc tgtgtacagt aacacaacat 360
 caaaagcaac acagctgtat acagaaacgt aggtcattct tttcagccct aatggagatg 420
 taattaacag tatcgagcac tctggaaaaat cactctgcag gtttatatgg actacatgga 480
 gatcatatcc tgtagtgtag tgaaagctaa gtccctcaaga gccatatgta tagatacaca 540
 atgtttttta ataattctta aaacagagat caaagtccat ttaaagtctt gtttgcatta 600
 acaaaaaataa aaatganaat aaaaatggac caaatgatca tctaaagttt aaaattccta 660
 aatgggtcaa tttatacaac tgggggagac ttattcaagg tttttgaaag tccaggactg 720
 gtttcagctg aaccagangg cccccaattt gcatcactgg aactgnccct gggttagcca 780
 aggaaattaa aaaagnctta acccccttcc cctgggattt gaacc 825

<210> 492
 <211> 946
 <212> DNA
 <213> Homo Sapiens

<400> 492
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 gagaatccga agaagaaaat ctcaataaat ctgaaataag tcaagtgttt gagattgcac 180
 ttaaaccgaa cttgcctgtg aatttcgagg tggcccgga gagtggccca ccccatga 240
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 ccctgcctgc agttgaacga gtaaagccta gaatcaaaaa gaaaacaaaa cccatagtca 420

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cgcgccgcag	ggagtttgtg	atgcaggtga	aggttggaaa	ccacacttgc	agaaggaacg	600
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attaaggaaa	ccangggatg	gaagaaaagt	ancnttttga	anctggctnt	tgggattaaa	780
atgggcttgt	antaaagagg	atgagttcag	gatgncntat	ctaagtcatn	aacacttgct	840
gctggaaatc	tttccatggg	ggccgaggtc	ncccgacttt	taggagttat	canggccntt	900
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<210> 493

<211> 804

<212> DNA

<213> Homo Sapiens

<400> 493

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ttcctgattt	tgcatgttct	cattcccaaa	gtagtctacc	ttagtttaca	ctcaaaggta	180
gcacttggtg	aaactacatg	acagaaacag	gctgcaaagg	tggacaaggg	gaagcatgtc	240
cctcttgtct	tgataaatca	gtgccacaca	cagaacccac	atTTTctgag	acattatcct	300
cattatagag	ccgtttgatt	ccatcataga	agtcatccac	ttccatttcc	tctactttgc	360
gttttagtaga	ggtctgcttg	cacccactgg	cagctgggag	atgatggtaa	aaggctgctg	420
tacctctgac	tggcacttct	ggcttgctgt	tgtccttgga	gaagtctggg	cctggggacag	480
aggagggatg	taatctgaac	actcctttgt	cacaggtcac	caggggtgtc	ttgaggggac	540
ggtagacata	aacggaattc	agaggcaggg	aagactgcag	agtanaaagg	tgatgtgccc	600
aagcttccga	ccatggatca	actgggagct	atncatctgg	ctttctgaag	cagntcaatt	660
gtaagagaaa	gccaatccn	ggaatggagt	tcntccattt	tcagactaac	cctgggcncn	720
aagcaaggca	tgggatcccc	tgggaattgcc	anaaanttgg	gttgcagggg	ccatacnccg	780
nggnaagtaa	ttngctttgg	gtaa				804

<210> 494

<211> 856

<212> DNA

<213> Homo Sapiens

<400> 494

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gaaaggcaaa	aagggcagct	agctgtagaa	agagctaaac	aagtagaaga	gttctctgcag	300
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cgccaacaga	ttaaagccaa	acttcgtggg	gaaaagaaa	aagctaataca	ttctgaaggga	540
caagaaggaa	gtgaagaggc	tgacatgagg	cgcaaaaaaa	atcgaatcac	tgaaggccca	600
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aaanctggta	nttctggnac	ttcacttttn	aagaanttgg	ccgtggnggt	agtttaactg	840
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<210> 495

<211> 757

<212> DNA

<213> Homo Sapiens

<400> 495

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agataagatt	ttatttttca	aattacatat	tatgccaacc	agcctgcttt	ggactcagag	180
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<210> 496

<211> 1759

<212> DNA

<213> Homo Sapiens

<400> 496

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accaggaaga	gcagctgaca	gtgaattcaa	aggcattaga	gattcttgac	aagatttctc	180
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<210> 497
 <211> 842
 <212> DNA
 <213> Homo Sapiens

<400> 497
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 tgagagaggg aatcattgtc actggaaagc ggctggggac tctgggtggtg acttatgtag 180
 atgccatcaa cagtggagca gtaccttgtc tggagaatgc agtgacagca ctggcccagc 240
 ttgagaaccc agcggctgtg cagagggcag ccgaccacta tagccagcag atggcccagc 300
 aactgagggt cccacagac acgctccagg agctgctgga cgtgcatgca gcctgtgaga 360
 ggggaagccat tgcagtcttc atggagcact ccttcaagga tgaaaacccat gaattccaga 420
 agaagcttgt ggacaccata gagaaaaaga agggagactt tgtgctgcag aatgaagagg 480
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<211> 787

<212> DNA

<213> Homo Sapiens

<400> 500

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<210> 501

<211> 886

<212> DNA

<213> Homo Sapiens

<400> 501

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<210> 502

<211> 626

<212> DNA

<213> Homo Sapiens

<400> 502

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<210> 503

<211> 884

<212> DNA

<213> Homo Sapiens

<400> 503

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<210> 504

<211> 612

<212> DNA

<213> Homo Sapiens

<400> 504

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<210> 505

<211> 2215

<212> DNA

<213> Homo Sapiens

<400> 505

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<211> 742

<212> DNA

<213> Homo Sapiens

<400> 506

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<211> 735

<212> DNA

<213> Homo Sapiens

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<210> 508

<211> 666

<212> DNA

<213> Homo Sapiens

<400> 508

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<210> 509

<211> 818

<212> DNA

<213> Homo Sapiens

<400> 509

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<210> 510

<211> 651

<212> DNA

<213> Homo Sapiens

<400> 510

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<210> 511

<211> 712

<212> DNA

<213> Homo Sapiens

<400> 511

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<210> 512

<211> 850

<212> DNA

<213> Homo Sapiens

<400> 512

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<210> 513

<211> 727

<212> DNA

<213> Homo Sapiens

<400> 513

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<210> 514

<211> 877

<212> DNA

<213> Homo Sapiens

<400> 514

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877

<210> 515

<211> 685

<212> DNA

<213> Homo Sapiens

<400> 515

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<210> 516

<211> 790

<212> DNA

<213> Homo Sapiens

<400> 516

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aacagagact	catcagttaa	atagagtaca	ggctagaaag	gtctcctgtg	gatgaatcag	180
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<210> 517

<211> 747

<212> DNA

<213> Homo Sapiens

<400> 517

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agtgctgtga	gtgagtgatt	catttttcttt	cttccaaaat	atctgaggtg	gtggcactcc	480
caatacacga	cattccagcc	gcactgggta	cccacagca	actcctgtgt	tttggagctt	540
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gactggctct	atgatcagag	agtgcacccc	gttcttttac	caccagcatc	ttgggagccc	720
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<210> 518

<211> 926

<212> DNA

<213> Homo Sapiens

<400> 518

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ctgtggaaca	aaaagaaggc	gctttctcta	atctgaagaa	actattaaac		420
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<210> 519

<211> 789

<212> DNA

<213> Homo Sapiens

<400> 519

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cacctttcaa	aanggaaaaa	ctggatgaag	taacnnttaa	agntataaat	ggataatgga	720
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<210> 520

<211> 827

<212> DNA

<213> Homo Sapiens

<400> 520

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<210> 521

<211> 710

<212> DNA

<213> Homo Sapiens

<400> 521

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<210> 522

<211> 638

<212> DNA

<213> Homo Sapiens

<400> 522

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<210> 523

<211> 833

<212> DNA

<213> Homo Sapiens

<400> 523

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<210> 524

<211> 766

<212> DNA

<213> Homo Sapiens

<400> 524

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<210> 525

<211> 847

<212> DNA

<213> Homo Sapiens

<400> 525

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<210> 526

<211> 746

<212> DNA

<213> Homo Sapiens

<400> 526

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<211> 837

<212> DNA

<213> Homo Sapiens

<400> 527

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<211> 822

<212> DNA

<213> Homo Sapiens

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<210> 529

<211> 842

<212> DNA

<213> Homo Sapiens

<400> 529

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<210> 530

<211> 815

<212> DNA

<213> Homo Sapiens

<400> 530

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 <213> Homo Sapiens

<400> 531
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 <212> DNA
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<210> 533
 <211> 678
 <212> DNA
 <213> Homo Sapiens

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 ttttaaaaaa aaatcgaagt ttacattatt catacanatt gggcattgtt aaaaaatatg 300
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<210> 534

<211> 789

<212> DNA

<213> Homo Sapiens

<400> 534

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<211> 802

<212> DNA

<213> Homo Sapiens

<400> 535

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<210> 536

<211> 901

<212> DNA

<213> Homo Sapiens

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<210> 537

<211> 761

<212> DNA

<213> Homo Sapiens

<400> 537

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<210> 538

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<212> DNA

<213> Homo Sapiens

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<211> 760
<212> DNA
<213> Homo Sapiens

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<211> 729
<212> DNA
<213> Homo Sapiens

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gcatgaatca ggtttttaga aggaaggtag gagaggaaaa ctactcacta gcagaactga 180
actgctgtaa aataggttaa attctttgaa aagtgaaaaa tgatagtagc aaaatcatga 240

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agttgtatct gaaccagagc cgtgatgtaa ccaagtaaga tggaggtttc catccagagg 300
agttaattcc gaacaagtca cagaaagggtg agagctgccg gttccggcac gctgtcttct 360
ggagtgccag tgaccgggca agaaatttga ttctttcctt tgattctctt gggaaagaac 420
acatttccca agcccttggg gaccacagag gtttggcact gtccgtgagg ctgtgctcct 480
gaggacggac gttcaggagg ccgtggagga gcagcgctgc aggagcaggg tgtggcagct 540
gtcgcacact cgcaccggct tggggtagga gggcagggcc cagctcgttg ctgggagcag 600
gtgtttgcan aagatgtggc ccacagttcc ggcagtnggt gctttctccg gggaaaatgg 660
agaacttcct ttntcacacn tggctaccag tggggtcgnt ttccgcatct tttcaagcca 720
ggccgtggg 729

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<210> 542

<211> 830

<212> DNA

<213> Homo Sapiens

<400> 542

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tgggcccgcag cctggatgcg gaccatgccc ccttgcagca gttcttttga gtgatggagc 180
actgctctcaa acatgggctg aaagttaaga agagttttat tggccaaaat aaatcattct 240
ttggtccttt ggagctgggtg gagaaacttt gtccagaagc atcagatata gcgactagtg 300
tcagaaatct tccagaatta aagacagctg tgggaagagg ccgagcgtgg ctttatcttg 360
cactcatgca aaagaaactg gcagattatc tgaaagtgtt tatagacaat aaacatctct 420
taagcgagtt ctatgagcct gaggttttaa tgatggagga agaagggatg gtgattgttg 480
gtctgctggt gggactcaat gttctcgatg ccaatctctg cttgaaagga gaagacttgg 540
attctcaggt tggagtaata gatttttccc tctaccttaa ggatgtgcag gatcttgatg 600
gtggcaagga gcatgaaaga attactgatg tccttgatca aaaaaattat gtggaagaac 660
ttaaccgggc acttgagctg caccagttgg ggatctttca acccaagata gatggctttg 720
gaaaagacta actcaaagct tcagaagagc ntttagctgc accagaccga attttgctcc 780
tttcaagaaa nacagcaccn gttaagaaaa ccaaatggaa ttaatttcag 830

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<210> 543

<211> 733

<212> DNA

<213> Homo Sapiens

<400> 543

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gaaaaataaa tgatttttatt gcaggggccaa tgataggtag tcacaagggc atgaaatggc 60
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gcatgaatca ggttttttaga aggaaggtag gagaggaaaa ctactacta gcagaactga 180
actgctgtaa aataggttaa attctttgaa aagtgaaaaa tgatagtagc aaatcatga 240
agttgtatct gaaccagagc cgtgatgtaa ccaagtaaga tggaggtttc catccagagg 300
agttaattcc gaacaagtca cagaaagggtg anagctgccg gttccggcac gctgtcttct 360
ggagtgccag tgaccgggca agaaatttga ttctttcctt tgattctctt gggaaagaac 420
acatttccca agcccttggg gaccacagag gtttggcact gtccgtgagg ctgtgctcct 480
gaggacggac gttcaggagg ccctggagg agcagcgctg caggagcagg gtgtggcagc 540
tgtcgcacac tcgcaccggc ttggggtagg anggcagggc tagctcgttg ctggancang 600
tgttgcaaaa naatgtggcc acagntnccg cagtgggtgc tttntccggg aaaagggaga 660
acttcttnt cacacttggc tacagnngng gncgctttcg ncatcttttt ancccaggcg 720
nnggcccttt caa 733

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<210> 544

<211> 852

<212> DNA

<213> Homo Sapiens

<400> 544

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gtggagaaat gcgctatcag ctgaataaaa ccaacatgga gaaggatgag gcagaaaagg      60
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agaaattgag aatagaactg gatgaaagca aacaacactt ggaacaggag cagcagaagg      180
cagccctggc cagagaggag tgcctgagac taacagaact gctgggcgaa tctgagcacc      240
aactgcacct caccagatct gaaatagctc aactcagtca agaaaaaagg tatacatatg      300
ataaattggg aaagttacag agaagaaatg aagaattgga ggaacagtgt gtccagcatg      360
ggagagtaca tgagacgatg aagcaaaggc taaggcagct ggataagcac agccaggcca      420
cagcccagca gctggtgcag ctccctcagca agcagaacca gcttctcctg gagaggcaga      480
gcctgtcgga agaggtggac cggctgcgga cccagttacc cagcatgcca caatctgatt      540
gctgacctgg atggaacaga gtgaaataaa tgaattacaa agagatatatt acattcatct      600
ggtttagact taatatgcc aacgcacca cgaccttccc aggttgacac cgcctcagcc      660
tgcagtgggg ctggtcctca tcaacgcggg cgctgtcccc gcacgcagtc gggctggagc      720
tgaggtctga ctctagctga gcagactcct ggtgtatgtt ttcagaaatg gcttgaagtt      780
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<210> 545

<211> 414

<212> PRT

<213> Homo Sapiens

<400> 545

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Leu Leu Asp Ala Ser Glu Lys Leu Lys Leu Thr Tyr Glu Glu Lys Cys
 1          5          10          15
Glu Ile Glu Glu Ser Gln Leu Lys Phe Leu Arg Asn Asp Leu Ala Glu
          20          25          30
Tyr Gln Arg Thr Cys Glu Asp Leu Lys Glu Gln Leu Lys His Lys Glu
          35          40          45
Phe Leu Leu Ala Ala Asn Thr Cys Asn Arg Val Gly Gly Leu Cys Leu
          50          55          60
Lys Cys Ala Gln His Glu Ala Val Leu Ser Gln Thr His Thr Asn Val
          65          70          75          80
His Met Gln Thr Ile Glu Arg Leu Val Lys Glu Arg Asp Asp Leu Met
          85          90          95
Ser Ala Leu Val Ser Val Arg Ser Ser Leu Ala Asp Thr Gln Gln Arg
          100          105          110
Glu Ala Ser Ala Tyr Glu Gln Val Lys Gln Val Leu Gln Ile Ser Glu
          115          120          125
Glu Ala Asn Phe Glu Lys Thr Lys Ala Leu Ile Gln Cys Asp Gln Leu
          130          135          140
Arg Lys Glu Leu Glu Arg Gln Ala Glu Arg Leu Glu Lys Glu Leu Ala
          145          150          155          160
Ser Gln Gln Glu Lys Arg Ala Ile Glu Lys Asp Met Met Lys Lys Glu
          165          170          175
Ile Thr Lys Glu Arg Glu Tyr Met Gly Ser Lys Met Leu Ile Leu Ser
          180          185          190
Gln Asn Ile Ala Gln Leu Glu Ala Gln Val Glu Lys Val Thr Lys Glu
          195          200          205
Lys Ile Ser Ala Ile Asn Gln Leu Glu Glu Ile Gln Ser Gln Leu Ala
          210          215          220
Ser Arg Glu Met Asp Val Thr Lys Val Cys Gly Glu Met Arg Tyr Gln
          225          230          235          240
Leu Asn Lys Thr Asn Met Glu Lys Asp Glu Ala Glu Lys Glu His Arg
          245          250          255

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Glu Phe Arg Ala Lys Thr Asn Arg Asp Leu Glu Ile Lys Asp Gln Glu
 260 265 270
 Ile Glu Lys Leu Arg Ile Glu Leu Asp Glu Ser Lys Gln His Leu Glu
 275 280 285
 Gln Glu Gln Gln Lys Ala Ala Leu Ala Arg Glu Glu Cys Leu Arg Leu
 290 295 300
 Thr Glu Leu Leu Gly Glu Ser Glu His Gln Leu His Leu Thr Arg Ser
 305 310 315 320
 Glu Ile Ala Gln Leu Ser Gln Glu Lys Arg Tyr Thr Tyr Asp Lys Leu
 325 330 335
 Gly Lys Leu Gln Arg Arg Asn Glu Glu Leu Glu Glu Gln Cys Val Gln
 340 345 350
 His Gly Arg Val His Glu Thr Met Lys Gln Arg Leu Arg Gln Leu Asp
 355 360 365
 Lys His Ser Gln Ala Thr Ala Gln Gln Leu Val Gln Leu Leu Ser Lys
 370 375 380
 Gln Asn Gln Leu Leu Leu Glu Arg Gln Ser Leu Ser Glu Glu Val Asp
 385 390 395 400
 Arg Leu Arg Thr Gln Leu Pro Ser Met Pro Gln Ser Asp Cys
 405 410

<210> 546

<211> 2885

<212> DNA

<213> Homo Sapiens

<400> 546

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gagcggcccc cctgggagcg ctccctccta caaactgcct ttgcttgggc cctacgacag      180
tcgagacgac ttccccctcc gcaaaacagc ctctgaaccc aacttgaaag tgcgttcaag      240
gctaaaacag aaggtggctg agcggagaag cagtcccttc ctgcgtcgca aggatgggac      300
tggtatttagc acctttaaga agagagctgt tgagatcaca ggtgccgggc ctggggcgtc      360
gtcogtgtgt aacagcgcac ccggctccgg cccagctct cccaacagct cccacagcac      420
catogctgag aatggcttta ctggctcagt cccaacatc cccactgaga tgctccctca      480
gcaccgagcc ctccctctgg acagctcccc caaccagttc agcctctaca cgtctccttc      540
tctgcccac atctccctag ggctgcaggc caggtcact gtcaccaact cacacctcac      600
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gcaggggtgg acgtgaccg gcaagttcat gagcacatcc tctattcctg gctgctgct      720
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gctgttgctg gagcaggccc ggcagcagag caccctcatt gctgtgccac tccacgggca      840
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gcggcacatg cccctgagcc gactcagtc ctcaccgctg ccgacagagtc cccaggccct      960
gcagcagctg gtcatgcaac aacagcacca gcagttcctg gagaagcaga agcagcagca     1020
gctacagctg ggcaagatcc tcaccaagac aggggagctg cccaggcagc ccaccaccca     1080
ccctgaggag acagaggagg agctgacgga gcagcaggag gtcttgctgg gggagggagc     1140
cctgaccatg ccccgaggag gctccacaga gagtgaagac acacaggaag acctggagga     1200
ggaggacgag gaagaggatg gggaggagga ggaggattgc atccagggtta aggacgagga     1260
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actgttctca gatgcccac cgtgcaacc ttgacaggtg taccaagcgc ccctcagcct     1380
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catgaagaac ccccagacc aaccogtcaa gcacctcttc accacaagtg tggctctacga     1500
cacgttcatg ctaaagcacc agtgcattgt cgggaacaca cacgtgcacc ctgagcatgc     1560
tggccggatc cagagcatct ggtccgggct gcaggagaca ggctgctta gcaagtgcga     1620
gcgatccga ggtcgcaaag ccacgctaga tgagatccag acagtgcact ctgaatacca     1680

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cccaggccgg cagaggagcc catggagcag gaggctgcc tgtgacgcc cggcccccat 2820
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aattt

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<210> 547

<211> 897

<212> PRT

<213> Homo Sapiens

<400> 547

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Glu Phe Leu Leu Ser Lys Ser Lys Glu Pro Thr Pro Gly Gly Leu Asn
1           5           10          15
His Ser Leu Pro Gln His Pro Lys Cys Trp Gly Ala His His Ala Ser
20          25          30
Leu Asp Gln Ser Ser Pro Pro Gln Ser Gly Pro Pro Gly Thr Pro Pro
35          40          45
Ser Tyr Lys Leu Pro Leu Pro Gly Pro Tyr Asp Ser Arg Asp Asp Phe
50          55          60
Pro Leu Arg Lys Thr Ala Ser Glu Pro Asn Leu Lys Val Arg Ser Arg
65          70          75          80
Leu Lys Gln Lys Val Ala Glu Arg Arg Ser Ser Pro Leu Leu Arg Arg
85          90          95
Lys Asp Gly Thr Val Ile Ser Thr Phe Lys Lys Arg Ala Val Glu Ile
100         105         110
Thr Gly Ala Gly Pro Gly Ala Ser Ser Val Cys Asn Ser Ala Pro Gly
115         120         125
Ser Gly Pro Ser Ser Pro Asn Ser Ser His Ser Thr Ile Ala Glu Asn
130         135         140
Gly Phe Thr Gly Ser Val Pro Asn Ile Pro Thr Glu Met Leu Pro Gln
145         150         155         160
His Arg Ala Leu Pro Leu Asp Ser Ser Pro Asn Gln Phe Ser Leu Tyr
165         170         175
Thr Ser Pro Ser Leu Pro Asn Ile Ser Leu Gly Leu Gln Ala Thr Val
180         185         190
Thr Val Thr Asn Ser His Leu Thr Ala Ser Pro Lys Leu Ser Thr Gln
195         200         205
Gln Glu Ala Glu Arg Gln Ala Leu Gln Ser Leu Arg Gln Gly Gly Thr

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210 215 220
 Leu Thr Gly Lys Phe Met Ser Thr Ser Ser Ile Pro Gly Cys Leu Leu
 225 230 235 240
 Gly Val Ala Leu Glu Gly Asp Gly Ser Pro His Gly His Ala Ser Leu
 245 250 255
 Leu Gln His Val Leu Leu Leu Glu Gln Ala Arg Gln Gln Ser Thr Leu
 260 265 270
 Ile Ala Val Pro Leu His Gly Gln Ser Pro Leu Val Thr Gly Glu Arg
 275 280 285
 Val Ala Thr Ser Met Arg Thr Val Gly Lys Leu Pro Arg His Arg Pro
 290 295 300
 Leu Ser Arg Thr Gln Ser Ser Pro Leu Pro Gln Ser Pro Gln Ala Leu
 305 310 315 320
 Gln Gln Leu Val Met Gln Gln Gln His Gln Gln Phe Leu Glu Lys Gln
 325 330 335
 Lys Gln Gln Gln Leu Gln Leu Gly Lys Ile Leu Thr Lys Thr Gly Glu
 340 345 350
 Leu Pro Arg Gln Pro Thr Thr His Pro Glu Glu Thr Glu Glu Leu
 355 360 365
 Thr Glu Gln Gln Glu Val Leu Leu Gly Glu Gly Ala Leu Thr Met Pro
 370 375 380
 Arg Glu Gly Ser Thr Glu Ser Glu Ser Thr Gln Glu Asp Leu Glu Glu
 385 390 395 400
 Glu Asp Glu Glu Glu Asp Gly Glu Glu Glu Glu Asp Cys Ile Gln Val
 405 410 415
 Lys Asp Glu Glu Gly Glu Ser Gly Ala Glu Glu Gly Pro Asp Leu Glu
 420 425 430
 Glu Pro Gly Ala Gly Tyr Lys Lys Leu Phe Ser Asp Ala Gln Pro Leu
 435 440 445
 Gln Pro Leu Gln Val Tyr Gln Ala Pro Leu Ser Leu Ala Thr Val Pro
 450 455 460
 His Gln Ala Leu Gly Arg Thr Gln Ser Ser Pro Ala Ala Pro Gly Gly
 465 470 475 480
 Met Lys Asn Pro Pro Asp Gln Pro Val Lys His Leu Phe Thr Thr Ser
 485 490 495
 Val Val Tyr Asp Thr Phe Met Leu Lys His Gln Cys Met Cys Gly Asn
 500 505 510
 Thr His Val His Pro Glu His Ala Gly Arg Ile Gln Ser Ile Trp Ser
 515 520 525
 Arg Leu Gln Glu Thr Gly Leu Leu Ser Lys Cys Glu Arg Ile Arg Gly
 530 535 540
 Arg Lys Ala Thr Leu Asp Glu Ile Gln Thr Val His Ser Glu Tyr His
 545 550 555 560
 Thr Leu Leu Tyr Gly Thr Ser Pro Leu Asn Arg Gln Lys Leu Asp Ser
 565 570 575
 Lys Lys Leu Leu Gly Pro Ile Ser Gln Lys Met Tyr Ala Val Leu Pro
 580 585 590
 Cys Gly Gly Ile Gly Val Asp Ser Asp Thr Val Trp Asn Glu Met His
 595 600 605
 Ser Ser Ser Ala Val Arg Met Ala Val Gly Cys Leu Leu Glu Leu Ala
 610 615 620
 Phe Lys Val Ala Ala Gly Glu Leu Lys Asn Gly Phe Ala Ile Ile Arg
 625 630 635 640
 Pro Pro Gly His His Ala Glu Glu Ser Thr Ala Met Gly Phe Cys Phe
 645 650 655

Phe Asn Ser Val Ala Ile Thr Ala Lys Leu Leu Gln Gln Lys Leu Asn
 660 665 670
 Val Gly Lys Val Leu Ile Val Asp Trp Asp Ile His His Gly Asn Gly
 675 680 685
 Thr Gln Gln Ala Phe Tyr Asn Asp Pro Ser Val Leu Tyr Ile Ser Leu
 690 695 700
 His Arg Tyr Asp Asn Gly Asn Phe Phe Pro Gly Ser Gly Ala Pro Glu
 705 710 715 720
 Glu Val Gly Gly Gly Pro Gly Val Gly Tyr Asn Val Asn Val Ala Trp
 725 730 735
 Thr Gly Gly Val Asp Pro Pro Ile Gly Asp Val Glu Tyr Leu Thr Ala
 740 745 750
 Phe Arg Thr Val Val Met Pro Ile Ala His Glu Phe Ser Pro Asp Val
 755 760 765
 Val Leu Val Ser Ala Gly Phe Asp Ala Val Glu Gly His Leu Ser Pro
 770 775 780
 Leu Gly Gly Tyr Ser Val Thr Ala Arg Cys Phe Gly His Leu Thr Arg
 785 790 795 800
 Gln Leu Met Thr Leu Ala Gly Gly Arg Val Val Leu Ala Leu Glu Gly
 805 810 815
 Gly His Asp Leu Thr Ala Ile Cys Asp Ala Ser Glu Ala Cys Val Ser
 820 825 830
 Ala Leu Leu Ser Val Lys Leu Gln Pro Leu Asp Glu Ala Val Leu Gln
 835 840 845
 Gln Lys Pro Asn Ile Asn Ala Val Ala Thr Leu Glu Lys Val Ile Glu
 850 855 860
 Ile Gln Ser Lys His Trp Ser Cys Val Gln Lys Phe Ala Ala Gly Leu
 865 870 875 880
 Gly Arg Ser Leu Arg Gly Ala Gln Ala Gly Glu Thr Glu Glu Ala Glu
 885 890 895
 Met

<210> 548
 <211> 1298
 <212> DNA
 <213> Homo Sapiens

<400> 548
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 tgatggagag agaaagcatc naaagcttct ggaagcaatc agttcccttg atggaaagaa 180
 taggcggaaa ttggctgana ggtctgaggc tagtctgaag gtgtcagagt tcaatgtcag 240
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 atcttctttg gccactgtga aaaagcaact gagtagagtc anatcaaaga anacagtggg 360
 gttacctctg aacaaagaag agattgaacg gatccacaga gaatagcatt caataaaacg 420
 cacaagtcct ctccaaatgg gaccctgtcg tcctgaagaa ccggcaggca gagcagctgg 480
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 cagtgcacaga cctttacttg acccctgtgg aaaaggcctc tctccgagcc atgagcctag 660
 aagaggcaaa gatgacgacga gcagagcttc agagggtctg ggctctgcag tctactatg 720
 angccaaggc tcgaagagag aagaaaatcn aaagttaaaa gtatcacaaa gtcgtgaaga 780
 aaggaaaggc caagaaagcc ctaaaagagt ttgagcagct gcggaagggt aatccagctg 840
 ccgcactaga agaacgaaga aaagaggaaa gaaggaggag gagaaagaag aagaacaagg 900
 agaagaagaa agaagaaggg agaaggagaa gaaaagaagg agaagaggaa aaggaagaag 960

gagaaagaaa aggagaagga aaaggaaaag aaggagaaga aagaagaact aagaagaagg 1020
 agaggaagaa taagaaggaa agaagaaaga aaaaagtnaa agaagaagaa agaaggaaga 1080
 aggaaagaag aggaagaact nagaagaaga aagaggagga aagaagaaag aagaataagg 1140
 aacnagaaag aaggagaaga aagaataaga agaggaagaa gaaaaagaag aaaagaagaa 1200
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<210> 549

<211> 236

<212> PRT

<213> Homo Sapiens

<400> 549

Ala Ala Glu Met Thr Ala Asn Arg Leu Ala Glu Ser Leu Leu Ala Leu
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 20 25 30
 Ser Glu Asp Glu Gly Asp Asn Asp Gly Glu Arg Lys His Lys Leu Leu
 35 40 45
 Glu Ala Ile Ser Ser Leu Asp Gly Lys Asn Arg Arg Lys Leu Ala Arg
 50 55 60
 Ser Glu Ala Ser Leu Lys Val Ser Glu Phe Asn Val Ser Ser Glu Gly
 65 70 75 80
 Ser Gly Glu Lys Leu Val Leu Ala Asp Leu Leu Glu Pro Val Lys Thr
 85 90 95
 Ser Ser Ser Leu Ala Thr Val Lys Lys Gln Leu Ser Arg Val Ser Lys
 100 105 110
 Thr Val Glu Leu Pro Leu Asn Lys Glu Glu Ile Glu Arg Ile His Arg
 115 120 125
 Glu Ile Ala Phe Asn Lys Thr His Lys Ser Ser Pro Asn Gly Thr Leu
 130 135 140
 Ser Ser Val Leu Lys Asn Arg Gln Ala Glu Gln Leu Val Phe Pro Leu
 145 150 155 160
 Glu Lys Glu Glu Pro Ala Ile Ala Pro Ile Glu His Val Leu Ser Gly
 165 170 175
 Trp Lys Ala Arg Thr Pro Leu Glu Gln Glu Ile Phe Asn Leu Leu His
 180 185 190
 Lys Asn Lys Gln Pro Val Thr Asp Pro Leu Leu Thr Pro Val Glu Lys
 195 200 205
 Ala Ser Leu Arg Ala Met Ser Leu Glu Glu Ala Lys Met Arg Arg Ala
 210 215 220
 Glu Leu Gln Arg Ala Arg Ala Leu Gln Ser Tyr Tyr
 225 230 235

<210> 550

<211> 2236

<212> DNA

<213> Homo Sapiens

<400> 550

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 gtgctgcgaa tgtaccacca gaccatggac gtggccgtgc tcgtgggaga cctgaagctg 240
 gtcacatgat aaccagccg tctgcctctg tttgatgcca ttcggccgct gatccactg 300


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aagcaccagg tggaaataga tcagctgacc ccccgggcgt ccaggaagct gaaggaggtg 360
cgtctggacc gtctgcaccc cgaaggcctc ggctgagtg tgcgtggtgg cctggagttt 420
ggctgtgggc tcttcacatc ccacctcatc aaaggcggtc aggcagacag cgtcgggctc 480
caggtagggg acgagatcgt ccggatcaat ggatattcca tctcctcctg taccatgag 540
gaggtcatca acctcattcg aaccaagaaa actgtgtcca tcaaagttag acacatcggc 600
ctgatccccg tgaaaagctc tctgatgag cccctcactt ggcagtatgt ggatcagttt 660
gtgtcggaat ctgggggctg gcgaggcagc ctgggctccc ctggaaatcg ggaaaacaag 720
gagaagaagg tcttcacatc cctggtaggc tcccagggcc ttggctgcag catttccagc 780
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<210> 551

<211> 652

<212> PRT

<213> Homo Sapiens

<400> 551

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Tyr His Gln Thr Met Asp Val Ala Val Leu Val Gly Asp Leu Lys Leu
          35          40          45
Val Ile Asn Glu Pro Ser Arg Leu Pro Leu Phe Asp Ala Ile Arg Pro
          50          55          60
Leu Ile Pro Leu Lys His Gln Val Glu Tyr Asp Gln Leu Thr Pro Arg
65          70          75          80
Arg Ser Arg Lys Leu Lys Glu Val Arg Leu Asp Arg Leu His Pro Glu
          85          90          95
Gly Leu Gly Leu Ser Val Arg Gly Gly Leu Glu Phe Gly Cys Gly Leu
          100         105         110
Phe Ile Ser His Leu Ile Lys Gly Gly Gln Ala Asp Ser Val Gly Leu

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115 120 125
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 Cys Thr His Glu Glu Val Ile Asn Leu Ile Arg Thr Lys Lys Thr Val
 145 150 155 160
 Ser Ile Lys Val Arg His Ile Gly Leu Ile Pro Val Lys Ser Ser Pro
 165 170 175
 Asp Glu Pro Leu Thr Trp Gln Tyr Val Asp Gln Phe Val Ser Glu Ser
 180 185 190
 Gly Gly Val Arg Gly Ser Leu Gly Ser Pro Gly Asn Arg Glu Asn Lys
 195 200 205
 Glu Lys Lys Val Phe Ile Ser Leu Val Gly Ser Arg Gly Leu Gly Cys
 210 215 220
 Ser Ile Ser Ser Gly Pro Ile Gln Lys Pro Gly Ile Phe Ile Ser His
 225 230 235 240
 Val Lys Pro Gly Ser Leu Ser Ala Glu Val Gly Leu Glu Ile Gly Asp
 245 250 255
 Gln Ile Val Glu Val Asn Gly Val Asp Phe Ser Asn Leu Asp His Lys
 260 265 270
 Glu Ala Val Asn Val Leu Lys Asn Ser Arg Ser Leu Thr Ile Ser Ile
 275 280 285
 Val Ala Ala Ala Gly Arg Glu Leu Phe Met Thr Asp Arg Glu Arg Leu
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 Asn Glu Arg Tyr Arg Lys Glu Met Glu Gln Ile Val Glu Glu Glu Glu
 355 360 365
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 370 375 380
 Leu Leu Pro Lys Thr Ile Thr Ala Glu Val His Pro Val Pro Leu Arg
 385 390 395 400
 Lys Pro Lys Tyr Asp Gln Gly Val Glu Pro Glu Leu Glu Pro Ala Asp
 405 410 415
 Asp Leu Asp Gly Gly Thr Glu Glu Gln Gly Glu Gln Asp Phe Arg Lys
 420 425 430
 Tyr Glu Glu Gly Phe Asp Pro Tyr Ser Met Phe Thr Pro Glu Gln Ile
 435 440 445
 Met Gly Lys Asp Val Arg Leu Leu Arg Ile Lys Lys Glu Gly Ser Leu
 450 455 460
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 465 470 475 480
 Val Ser Ala Val Tyr Glu Arg Gly Ala Ala Glu Arg His Gly Gly Ile
 485 490 495
 Val Lys Gly Asp Glu Ile Met Ala Ile Asn Gly Lys Ile Val Thr Asp
 500 505 510
 Tyr Thr Leu Ala Glu Ala Asp Ala Ala Leu Gln Lys Ala Trp Asn Gln
 515 520 525
 Gly Gly Asp Trp Ile Asp Leu Val Val Ala Val Cys Pro Pro Lys Glu
 530 535 540
 Tyr Asp Asp Glu Leu Thr Phe Leu Leu Lys Ser Lys Arg Gly Asn Gln
 545 550 555 560

Ile His Ala Leu Gly Asn Ser Glu Leu Arg Pro His Leu Val Asn Thr
 565 570 575
 Lys Pro Arg Thr Ser Leu Glu Arg Gly His Met Thr His Thr Arg Trp
 580 585 590
 His Pro Trp Asp Leu Asn Leu Ser Pro Arg Asn Leu Lys Leu Pro Leu
 595 600 605
 Ala Leu Asn Gln Gly Gln Ile Arg Asn Ser Ser Gly His Phe Phe Glu
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 Gly Gln Cys Gly Gly Lys Gly Ala Ala Ser Arg Leu Gly Glu Asp Leu
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<210> 552

<211> 2162

<212> DNA

<213> Homo Sapiens

<400> 552

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2162

<210> 553
 <211> 403
 <212> PRT
 <213> Homo Sapiens

<400> 553
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 Tyr His Gln Thr Met Asp Val Ala Val Leu Val Gly Asp Leu Lys Leu
 35 40 45
 Val Ile Asn Glu Pro Ser Arg Leu Pro Leu Phe Asp Ala Ile Arg Pro
 50 55 60
 Leu Ile Pro Leu Lys His Gln Val Glu Tyr Asp Gln Leu Thr Pro Arg
 65 70 75 80
 Arg Ser Arg Lys Leu Lys Glu Val Arg Leu Asp Arg Leu His Pro Glu
 85 90 95
 Gly Leu Gly Leu Ser Val Arg Gly Gly Leu Glu Phe Gly Cys Gly Leu
 100 105 110
 Phe Ile Ser His Leu Ile Lys Gly Gly Gln Ala Asp Ser Val Gly Leu
 115 120 125
 Gln Val Gly Asp Glu Ile Val Arg Ile Asn Gly Tyr Ser Ile Ser Ser
 130 135 140
 Cys Thr His Glu Glu Val Ile Asn Leu Ile Arg Thr Lys Lys Thr Val
 145 150 155 160
 Ser Ile Lys Val Arg His Ile Gly Leu Ile Pro Val Lys Ser Ser Pro
 165 170 175
 Asp Glu Pro Leu Thr Trp Gln Tyr Val Asp Gln Phe Val Ser Glu Ser
 180 185 190
 Gly Gly Val Arg Gly Ser Leu Gly Ser Pro Gly Asn Arg Glu Asn Lys
 195 200 205
 Glu Lys Lys Val Phe Ile Ser Leu Val Gly Ser Arg Gly Leu Gly Cys
 210 215 220
 Ser Ile Ser Ser Gly Pro Ile Gln Lys Pro Gly Ile Phe Ile Ser His
 225 230 235 240
 Val Lys Pro Gly Ser Leu Ser Ala Glu Val Gly Leu Glu Ile Gly Asp
 245 250 255
 Gln Ile Val Glu Val Asn Gly Val Asp Phe Ser Asn Leu Asp His Lys
 260 265 270
 Glu Ala Val Asn Val Leu Lys Asn Ser Arg Ser Leu Thr Ile Ser Ile
 275 280 285
 Val Ala Ala Ala Gly Arg Glu Leu Phe Met Thr Asp Arg Glu Arg Leu
 290 295 300
 Ala Glu Ala Arg Gln Arg Glu Leu Gln Arg Gln Glu Leu Leu Met Gln
 305 310 315 320
 Lys Arg Leu Ala Met Glu Ser Asn Lys Ile Leu Gln Glu Gln Gln Glu
 325 330 335
 Met Glu Arg Gln Arg Arg Lys Glu Ile Ala Gln Lys Ala Ala Glu Glu
 340 345 350
 Asn Glu Arg Tyr Arg Lys Glu Met Glu Gln Ile Val Glu Glu Glu Glu
 355 360 365
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<210> 554
 <211> 1789
 <212> DNA
 <213> Homo Sapiens

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<210> 555
 <211> 493
 <212> PRT
 <213> Homo Sapiens

<400> 555
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 Tyr Gln Arg Thr Cys Glu Asp Leu Lys Glu Gln Leu Lys His Lys Glu
 35 40 45

Phe Leu Leu Ala Ala Asn Thr Cys Asn Arg Val Gly Gly Leu Cys Leu
 50 55 60
 Lys Cys Ala Gln His Glu Ala Val Leu Ser Gln Thr His Thr Asn Val
 65 70 75 80
 His Met Gln Thr Ile Glu Arg Leu Val Lys Glu Arg Asp Asp Leu Met
 85 90 95
 Ser Ala Leu Val Ser Val Arg Ser Ser Leu Ala Asp Thr Gln Gln Arg
 100 105 110
 Glu Ala Ser Ala Tyr Glu Gln Val Lys Gln Val Leu Gln Ile Ser Glu
 115 120 125
 Glu Ala Asn Phe Glu Lys Thr Lys Ala Leu Ile Gln Cys Asp Gln Leu
 130 135 140
 Arg Lys Glu Leu Glu Arg Gln Ala Glu Arg Leu Glu Lys Glu Leu Ala
 145 150 155 160
 Ser Gln Gln Glu Lys Arg Ala Ile Glu Lys Asp Met Met Lys Lys Glu
 165 170 175
 Ile Thr Lys Glu Arg Glu Tyr Met Gly Ser Lys Met Leu Ile Leu Ser
 180 185 190
 Gln Asn Ile Ala Gln Leu Glu Ala Gln Val Glu Lys Val Thr Lys Glu
 195 200 205
 Lys Ile Ser Ala Ile Asn Gln Leu Glu Glu Ile Gln Ser Gln Leu Ala
 210 215 220
 Ser Arg Glu Met Asp Val Thr Lys Val Cys Gly Glu Met Arg Tyr Gln
 225 230 235 240
 Leu Asn Lys Thr Asn Met Glu Lys Asp Glu Ala Glu Lys Glu His Arg
 245 250 255
 Glu Phe Arg Ala Lys Thr Asn Arg Asp Leu Glu Ile Lys Asp Gln Glu
 260 265 270
 Ile Glu Lys Leu Arg Ile Glu Leu Asp Glu Ser Lys Gln His Leu Glu
 275 280 285
 Gln Glu Gln Gln Lys Ala Ala Leu Ala Arg Glu Glu Cys Leu Arg Leu
 290 295 300
 Thr Glu Leu Leu Gly Glu Ser Glu His Gln Leu His Leu Thr Arg Gln
 305 310 315 320
 Glu Lys Asp Ser Ile Gln Gln Ser Phe Ser Lys Glu Ala Lys Ala Gln
 325 330 335
 Ala Leu Gln Ala Gln Gln Arg Glu Gln Leu Thr Gln Lys Ile Gln
 340 345 350
 Gln Met Glu Ala Gln His Asp Lys Thr Glu Asn Glu Gln Tyr Leu Leu
 355 360 365
 Leu Thr Ser Gln Asn Thr Phe Leu Thr Lys Leu Lys Glu Glu Cys Cys
 370 375 380
 Thr Leu Ala Lys Lys Leu Glu Gln Ile Ser Gln Lys Thr Arg Ser Glu
 385 390 395 400
 Ile Ala Gln Leu Ser Gln Glu Lys Arg Tyr Thr Tyr Asp Lys Leu Gly
 405 410 415
 Lys Leu Gln Arg Arg Asn Glu Glu Leu Glu Glu Gln Cys Val Gln His
 420 425 430
 Gly Arg Val His Glu Thr Met Lys Gln Arg Leu Arg Gln Leu Asp Lys
 435 440 445
 His Ser Gln Ala Thr Ala Gln Gln Leu Val Gln Leu Leu Ser Lys Gln
 450 455 460
 Asn Gln Leu Leu Leu Glu Arg Gln Ser Leu Ser Glu Glu Val Asp Arg
 465 470 475 480
 Leu Arg Thr Gln Leu Pro Ser Met Pro Gln Ser Asp Cys

485

490

<210> 556
 <211> 1306
 <212> DNA
 <213> Homo Sapiens

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<210> 557
 <211> 328
 <212> PRT
 <213> Homo Sapiens

<400> 557
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 35 40 45
 Gln Trp Glu Glu Asp Trp Gly Ser Lys Glu Gln Leu Leu Leu Pro Lys
 50 55 60
 Thr Ile Thr Ala Glu Val His Pro Val Pro Leu Arg Lys Pro Lys Tyr
 65 70 75 80
 Asp Gln Gly Val Glu Pro Glu Leu Glu Pro Ala Asp Asp Leu Asp Gly
 85 90 95
 Gly Thr Glu Glu Gln Gly Glu Gln Asp Phe Arg Lys Tyr Glu Glu Gly
 100 105 110
 Phe Asp Pro Tyr Ser Met Phe Thr Pro Glu Gln Ile Met Gly Lys Asp
 115 120 125
 Val Arg Leu Leu Arg Ile Lys Lys Glu Gly Ser Leu Asp Leu Ala Leu
 130 135 140

Glu Gly Gly Val Asp Ser Pro Ile Gly Lys Val Val Val Ser Ala Val
 145 150 155 160
 Tyr Glu Arg Gly Ala Ala Glu Arg His Gly Gly Ile Val Lys Gly Asp
 165 170 175
 Glu Ile Met Ala Ile Asn Gly Lys Ile Val Thr Asp Tyr Thr Leu Ala
 180 185 190
 Glu Ala Asp Ala Ala Leu Gln Lys Ala Trp Asn Gln Gly Gly Asp Trp
 195 200 205
 Ile Asp Leu Val Val Ala Val Cys Pro Pro Lys Glu Tyr Asp Asp Glu
 210 215 220
 Leu Thr Phe Leu Leu Lys Ser Lys Arg Gly Asn Gln Ile His Ala Leu
 225 230 235 240
 Gly Asn Ser Glu Leu Arg Pro His Leu Val Asn Thr Lys Pro Arg Thr
 245 250 255
 Ser Leu Glu Arg Gly His Met Thr His Thr Arg Trp His Pro Trp Asp
 260 265 270
 Leu Asn Leu Ser Pro Arg Asn Leu Lys Leu Pro Leu Ala Leu Asn Gln
 275 280 285
 Gly Gln Ile Arg Asn Ser Ser Gly His Phe Phe Glu Gly Gln Cys Gly
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 Gly Lys Gly Ala Ala Ser Arg Leu Gly Glu Asp Leu Lys Asp Pro Asp
 305 310 315 320
 Ser His Ser Phe Pro Leu Ala Gln
 325

<210> 558
 <211> 2289
 <212> DNA
 <213> Homo Sapiens

<400> 558

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ccactggagt ctctctctct ccacccctct cctctgccct ctgctcta at tgctgccagg 2220
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<210> 559

<211> 481

<212> PRT

<213> Homo Sapiens

<400> 559

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Met Asp Arg Lys Val Ala Arg Glu Phe Arg His Lys Val Asp Phe Leu
 1          5          10         15
Ile Glu Asn Asp Ala Glu Lys Asp Tyr Leu Tyr Asp Val Leu Arg Met
          20          25          30
Tyr His Gln Thr Met Asp Val Ala Val Leu Val Gly Asp Leu Lys Leu
          35          40          45
Val Ile Asn Glu Pro Ser Arg Leu Pro Leu Phe Asp Ala Ile Arg Pro
          50          55          60
Leu Ile Pro Leu Lys His Gln Val Glu Tyr Asp Gln Leu Thr Pro Arg
65          70          75          80
Arg Ser Arg Lys Leu Lys Glu Val Arg Leu Asp Arg Leu His Pro Glu
          85          90          95
Gly Leu Gly Leu Ser Val Arg Gly Gly Leu Glu Phe Gly Cys Gly Leu
          100         105         110
Phe Ile Ser His Leu Ile Lys Gly Gly Gln Ala Asp Ser Val Gly Leu
          115         120         125
Gln Val Gly Asp Glu Ile Val Arg Ile Asn Gly Tyr Ser Ile Ser Ser
          130         135         140
Cys Thr His Glu Glu Val Ile Asn Leu Ile Arg Thr Lys Lys Thr Val
145         150         155         160
Ser Ile Lys Val Arg His Ile Gly Leu Ile Pro Val Lys Ser Ser Pro
          165         170         175
Asp Glu Pro Leu Thr Trp Gln Tyr Val Asp Gln Phe Val Ser Glu Ser
          180         185         190
Gly Gly Val Arg Gly Ser Leu Gly Ser Pro Gly Asn Arg Glu Asn Lys
          195         200         205
Glu Lys Lys Val Phe Ile Ser Leu Val Gly Ser Arg Gly Leu Gly Cys
          210         215         220
Ser Ile Ser Ser Gly Pro Ile Gln Lys Pro Gly Ile Phe Ile Ser His
225         230         235         240
Val Lys Pro Gly Ser Leu Ser Ala Glu Val Gly Leu Glu Ile Gly Asp
          245         250         255
Gln Ile Val Glu Val Asn Gly Val Asp Phe Ser Asn Leu Asp His Lys

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260 265 270
 Glu Ala Val Asn Val Leu Lys Asn Ser Arg Ser Leu Thr Ile Ser Ile
 275 280 285
 Val Ala Ala Ala Gly Arg Glu Leu Phe Met Thr Asp Arg Glu Arg Leu
 290 295 300
 Ala Glu Ala Arg Gln Arg Glu Leu Gln Arg Gln Glu Leu Leu Met Gln
 305 310 315 320
 Lys Arg Leu Ala Met Glu Ser Asn Lys Ile Leu Gln Glu Gln Gln Glu
 325 330 335
 Met Glu Arg Gln Arg Arg Lys Glu Ile Ala Gln Lys Ala Ala Glu Glu
 340 345 350
 Asn Glu Arg Tyr Arg Lys Glu Met Glu Gln Ile Val Glu Glu Glu Glu
 355 360 365
 Lys Phe Lys Lys Gln Trp Glu Asp Trp Gly Ser Lys Glu Gln Leu
 370 375 380
 Leu Leu Pro Lys Thr Ile Thr Ala Glu Val His Pro Val Pro Leu Arg
 385 390 395 400
 Lys Pro Lys Tyr Asp Gln Gly Val Glu Pro Glu Leu Glu Pro Ala Asp
 405 410 415
 Asp Leu Asp Gly Gly Thr Glu Glu Gln Gly Glu Gln Pro Gln Glu Met
 420 425 430
 Leu Lys Arg Met Val Val Tyr Gln Asp Ser Ile Gln Asp Lys Ile Ser
 435 440 445
 Gly Asn Met Arg Lys Ala Leu Thr Pro Thr Leu Cys Ser Pro Gln Ser
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 Arg Ser Trp Gly Arg Met Ser Gly Ser Tyr Ala Ser Arg Arg Arg Asp
 465 470 475 480
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<210> 560

<211> 2409

<212> DNA

<213> Homo Sapiens

<400> 560

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 ttccggcata aggtggattt tctgattgaa aatgatgcag agaaggacta tctctatgat 180
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 gtcacatcatg aacccagccg tctgcctctg tttgatgcca ttcggccgct gatccactg 300
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 cgtctggacc gtctgcaccc cgaaggcctc ggccctgagtg tgcgtggtgg cctggagttt 420
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 caggtagggg acgagatcgt ccggatcaat ggatattcca tctcctcctg taccatgatg 540
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 ctgatccccg tgaaaagctc tcctgatgag cccctcactt ggcagtatgt ggatcagttt 660
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 gagaagaagg tcttcatcag cctggtaggc tcccagggcc ttggctgcag catttccagc 780
 ggcccatcc agaagcctgg catctttatc agccatgtga aacctggctc cctgtctgct 840
 gagtggggat tggagatagg ggaccagatt gtcgaagtca atggcgtcga cttctctaac 900
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 aagatcctcc aggagcagca ggagatggag cggcaagga gaaaagaaat tgcccagaag 1140

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aagttttaaga agcaatggga agaagactgg ggctcaaagg aacagctact cttgcctaaa 1260
accatcactg ctgaggtaca ccagtagccc cttcgcaagc caaagtatga tcagggagtg 1320
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ggaaatatga ggaaggcttt gaccctact ctatgttcac ccagagcag atcatgggga 1620
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ccactggagt ctctctctct ccatccctct cctctgcctt ctgctctaata tgctgccagg 2340
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<210> 561

<211> 521

<212> PRT

<213> Homo Sapiens

<400> 561

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Met Asp Arg Lys Val Ala Arg Glu Phe Arg His Lys Val Asp Phe Leu
1          5          10          15
Ile Glu Asn Asp Ala Glu Lys Asp Tyr Leu Tyr Asp Val Leu Arg Met
          20          25          30
Tyr His Gln Thr Met Asp Val Ala Val Leu Val Gly Asp Leu Lys Leu
          35          40          45
Val Ile Asn Glu Pro Ser Arg Leu Pro Leu Phe Asp Ala Ile Arg Pro
          50          55          60
Leu Ile Pro Leu Lys His Gln Val Glu Tyr Asp Gln Leu Thr Pro Arg
65          70          75          80
Arg Ser Arg Lys Leu Lys Glu Val Arg Leu Asp Arg Leu His Pro Glu
          85          90          95
Gly Leu Gly Leu Ser Val Arg Gly Gly Leu Glu Phe Gly Cys Gly Leu
          100          105          110
Phe Ile Ser His Leu Ile Lys Gly Gly Gln Ala Asp Ser Val Gly Leu
          115          120          125
Gln Val Gly Asp Glu Ile Val Arg Ile Asn Gly Tyr Ser Ile Ser Ser
          130          135          140
Cys Thr His Glu Glu Val Ile Asn Leu Ile Arg Thr Lys Lys Thr Val
145          150          155          160
Ser Ile Lys Val Arg His Ile Gly Leu Ile Pro Val Lys Ser Ser Pro
          165          170          175
Asp Glu Pro Leu Thr Trp Gln Tyr Val Asp Gln Phe Val Ser Glu Ser
          180          185          190
Gly Gly Val Arg Gly Ser Leu Gly Ser Pro Gly Asn Arg Glu Asn Lys
          195          200          205

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Glu Lys Lys Val Phe Ile Ser Leu Val Gly Ser Arg Gly Leu Gly Cys
 210 215 220
 Ser Ile Ser Ser Gly Pro Ile Gln Lys Pro Gly Ile Phe Ile Ser His
 225 230 235 240
 Val Lys Pro Gly Ser Leu Ser Ala Glu Val Gly Leu Glu Ile Gly Asp
 245 250 255
 Gln Ile Val Glu Val Asn Gly Val Asp Phe Ser Asn Leu Asp His Lys
 260 265 270
 Glu Ala Val Asn Val Leu Lys Asn Ser Arg Ser Leu Thr Ile Ser Ile
 275 280 285
 Val Ala Ala Ala Gly Arg Glu Leu Phe Met Thr Asp Arg Glu Arg Leu
 290 295 300
 Ala Glu Ala Arg Gln Arg Glu Leu Gln Arg Gln Glu Leu Leu Met Gln
 305 310 315 320
 Lys Arg Leu Ala Met Glu Ser Asn Lys Ile Leu Gln Glu Gln Gln Glu
 325 330 335
 Met Glu Arg Gln Arg Arg Lys Glu Ile Ala Gln Lys Ala Ala Glu Glu
 340 345 350
 Asn Glu Arg Tyr Arg Lys Glu Met Glu Gln Ile Val Glu Glu Glu Glu
 355 360 365
 Lys Phe Lys Lys Gln Trp Glu Glu Asp Trp Gly Ser Lys Glu Gln Leu
 370 375 380
 Leu Leu Pro Lys Thr Ile Thr Ala Glu Val His Pro Val Pro Leu Arg
 385 390 395 400
 Lys Pro Lys Tyr Asp Gln Gly Val Glu Pro Glu Leu Glu Pro Ala Asp
 405 410 415
 Asp Leu Asp Gly Gly Thr Glu Glu Gln Gly Glu Gln Thr Phe Cys Pro
 420 425 430
 Ser Pro Gln Pro Pro Arg Gly Pro Gly Val Ser Thr Ile Ser Lys Pro
 435 440 445
 Val Met Val His Gln Glu Pro Asn Phe Ile Tyr Arg Pro Ala Val Lys
 450 455 460
 Ser Glu Val Leu Pro Gln Glu Met Leu Lys Arg Met Val Val Tyr Gln
 465 470 475 480
 Asp Ser Ile Gln Asp Lys Ile Ser Gly Asn Met Arg Lys Ala Leu Thr
 485 490 495
 Pro Thr Leu Cys Ser Pro Gln Ser Arg Ser Trp Gly Arg Met Ser Gly
 500 505 510
 Ser Tyr Ala Ser Arg Arg Arg Asp Pro
 515 520

<210> 562
 <211> 1445
 <212> DNA
 <213> Homo Sapiens

<400> 562

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gaaagctgaa	tgagggttcag	agcttctctg	aagctcaaac	agaaatggtg	aggacgcttg	180
agcggaaagt	agaagcaaaa	atgatcaagg	aggaaagcga	ctaccacgac	ctggagtcgg	240
tggttcagca	ggtggagcag	aacctggagc	tgatgaccaa	acgggctgta	aaggcagaaa	300
accacgtcgt	gaaactaaaa	caggaaatca	gtttgctcca	ggcgcaggtc	tccaacttcc	360
agcgagagaa	tgaagccctg	cgggtcggcc	agggtgccag	cctgaccgtg	gtgaagcaga	420
acgccgacgt	ggccctgcag	aacctccggg	tggtcatgaa	cagtgcacag	gcttccatca	480

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agcaactggt ttccggagct gagacactga atcttgttgc cgaaatcctt aaatctatag      540
acagaatttc tgaagttaaa gacgaggagg aagactcttg aggacctctg ggtgttctca      600
gcatgaagct cctgtgtatac cctgagggtca ccaccgctcg atctaaatgt gcagttgtgt      660
ccttaaatat gcagtcttca cccagagtaa agtgttgatc gcaagagtcc agtgtcgtgc      720
cctcagccag ttcttggcca ccacaatggg agcagccctg gccagagttgt ctctgtgggt      780
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ccagtcccat cccagaacat cagttgtaag ataagtacaa ttggttgtcc ttgatttcat      960
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tccgccgatg ctgagggctc cctctggctc ccgggtcact cttgtggccc cagtgggtgg     1080
tccctgcagt catggcctga gtgcgcaggg gccaccgctg ggctgctgct gtctctctcc     1140
ggggaccacg ggggaacaag gtcacacctt ccgtgctgtg aagctgtcca gatgtgcctc     1200
tttggctggg ggttttggtg gacgtttcaa gtggcatttt gtacaatgca ggtagaatt     1260
caggaatttc aagtatgtgc ccgggtntgt caggtcccgag ttgcctttnt gacggccccc     1320
ctcagaggga cggcgatgag cactaaatgc ttttttgant attttcctat agattttttt     1380
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tcacc                                             1445

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<210> 563
 <211> 192
 <212> PRT
 <213> Homo Sapiens

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<400> 563
Pro Ala Gly Ser Pro Ser Ala Asp Phe Ala Val His Gly Glu Ser Leu
 1          5          10          15
Gly Asp Arg His Leu Arg Thr Leu Gln Ile Ser Tyr Asp Ala Leu Lys
          20          25          30
Asp Glu Asn Ser Lys Leu Arg Arg Lys Leu Asn Glu Val Gln Ser Phe
          35          40          45
Ser Glu Ala Gln Thr Glu Met Val Arg Thr Leu Glu Arg Lys Leu Glu
          50          55          60
Ala Lys Met Ile Lys Glu Ser Asp Tyr His Asp Leu Glu Ser Val
          65          70          75          80
Val Gln Gln Val Glu Gln Asn Leu Glu Leu Met Thr Lys Arg Ala Val
          85          90          95
Lys Ala Glu Asn His Val Val Lys Leu Lys Gln Glu Ile Ser Leu Leu
          100          105          110
Gln Ala Gln Val Ser Asn Phe Gln Arg Glu Asn Glu Ala Leu Arg Cys
          115          120          125
Gly Gln Gly Ala Ser Leu Thr Val Val Lys Gln Asn Ala Asp Val Ala
          130          135          140
Leu Gln Asn Leu Arg Val Val Met Asn Ser Ala Gln Ala Ser Ile Lys
          145          150          155          160
Gln Leu Val Ser Gly Ala Glu Thr Leu Asn Leu Val Ala Glu Ile Leu
          165          170          175
Lys Ser Ile Asp Arg Ile Ser Glu Val Lys Asp Glu Glu Glu Asp Ser
          180          185          190

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<210> 564
 <211> 1226
 <212> DNA
 <213> Homo Sapiens

<400> 564

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agagcccagag cgcgcaggag ctcaaggagc agggcaatcg tctgttcgtg ggccgaaagt      180
acccggaggc ggcggcctgc tacggccgcgc cgatcacccg gaacccgctg gtggccgtgt      240
attacaccaa ccgggccttg tgctacctga agatgcagca gcacgagcag gccctggccg      300
actgccggcg cgccctggag ctggacgggc agtctgtgaa ggcgcacttc ttcctggggc      360
agtgccagct ggagatggag agctatgatg aggccatcgc caatctgcag cgagcttaca      420
gcctggccaa ggagcagcgc ctgaacttcg gggacgacat cccagcgct cttcgaatcg      480
cgaagaagaa gcgctggaac agcattgagg agcggcgcgc ccaccaggag agcgagctgc      540
actcctacct ctccaggctc attgccgcgc agcgtgagag ggagctggaa gagtgccagc      600
gaaaccacga ggggtgatgag gacgacagcc acgtccgggc ccagcaggcc tgcattgagg      660
ccaagcacga caagtacatg gcggacatgg acgagctttt ttctcagggtg gatgagaaga      720
ggaagaagcg agacatcccc gactacctgt gtggcaagat cagctttgag ctgatgcggg      780
agccgtgcat cagccccagt ggcatcacct acgaccgcaa ggacatcgag gagcacctgc      840
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ccaacttggc tatgaaggag gttattgacg cattcatctc tgagaatggc tgggtggagg      960
actactgagg ttccctgccc tacctggcgt cctggtccag gggagccctg ggcagaagcc     1020
cccgccccc aaacatagtt tatgtttttg gccacccga ccgcttcccc caagttctgc     1080
tgttggactc tggactgttt ccctctcag catcgctttt gctgggcccgt gattgtcccc     1140
tttgtgggct ggaagagcag gtgagggtgg gctgggctga ggccattgcc gccactatct     1200
gtgtaataaa atccgtgagc acgaaa                                     1226

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<210> 565

<211> 303

<212> PRT

<213> Homo Sapiens

<400> 565

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Met Lys Gly Lys Glu Glu Lys Glu Gly Gly Ala Arg Leu Gly Ala Gly
  1          5          10          15
Gly Gly Ser Pro Glu Lys Ser Pro Ser Ala Gln Glu Leu Lys Glu Gln
  20          25          30
Gly Asn Arg Leu Phe Val Gly Arg Lys Tyr Pro Glu Ala Ala Ala Cys
  35          40          45
Tyr Gly Arg Ala Ile Thr Arg Asn Pro Leu Val Ala Val Tyr Tyr Thr
  50          55          60
Asn Arg Ala Leu Cys Tyr Leu Lys Met Gln Gln His Glu Gln Ala Leu
  65          70          75          80
Ala Asp Cys Arg Arg Ala Leu Glu Leu Asp Gly Gln Ser Val Lys Ala
  85          90          95
His Phe Phe Leu Gly Gln Cys Gln Leu Glu Met Glu Ser Tyr Asp Glu
  100         105         110
Ala Ile Ala Asn Leu Gln Arg Ala Tyr Ser Leu Ala Lys Glu Gln Arg
  115         120         125
Leu Asn Phe Gly Asp Asp Ile Pro Ser Ala Leu Arg Ile Ala Lys Lys
  130         135         140
Lys Arg Trp Asn Ser Ile Glu Glu Arg Arg Ile His Gln Glu Ser Glu
  145         150         155         160
Leu His Ser Tyr Leu Ser Arg Leu Ile Ala Ala Glu Arg Glu Arg Glu
  165         170         175
Leu Glu Glu Cys Gln Arg Asn His Glu Gly Asp Glu Asp Asp Ser His
  180         185         190
Val Arg Ala Gln Gln Ala Cys Ile Glu Ala Lys His Asp Lys Tyr Met
  195         200         205
Ala Asp Met Asp Glu Leu Phe Ser Gln Val Asp Glu Lys Arg Lys Lys

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210	215	220
Arg Asp Ile Pro Asp Tyr Leu Cys Gly Lys Ile Ser Phe Glu Leu Met		
225	230	235
Arg Glu Pro Cys Ile Thr Pro Ser Gly Ile Thr Tyr Asp Arg Lys Asp		240
	245	250
Ile Glu Glu His Leu Gln Arg Val Gly His Phe Asp Pro Val Thr Gly		255
	260	265
Ser Pro Leu Thr Gln Glu Gln Phe Ile Pro Asn Leu Ala Met Lys Glu		270
	275	280
Val Ile Asp Ala Phe Ile Ser Glu Asn Gly Trp Val Glu Asp Tyr		285
	290	300

<210> 566
 <211> 1857
 <212> DNA
 <213> Homo Sapiens

<400> 566

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tagtggccgg	ccggccgctc	tcatcccccg	taaggagcag	agtcctttgt	actgaccaag	180
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atcccaactt	tgtttggaag	cttattatga	caataccatt	tttcatagag	ttgtgcctgg	360
tttcatagtc	caaggcggag	atcctactgg	cacagggagt	ggtggagagt	ctatctatgg	420
agcgccattc	aaagatgaat	ttcattcacg	gttgcgtttt	aatcggagag	gactggttgc	480
catggcaaat	gctggttctc	atgataatgg	caccactttt	ttcttcacac	tgggtcgagc	540
agatgaactt	aacaataagc	ataccatctt	tggaaagggt	acaggggata	cagtataata	600
catgttgcca	ctgtcagaag	tagacattga	tgatgacgaa	agaccacata	atccacacaa	660
aataaaaagc	tgtgaggttt	tgtttaatcc	ttttgatgac	atcattccaa	gggaaattaa	720
aaggctgaaa	aaagagaaac	cagaggagga	agtaaagaaa	ttgaaacca	aaggcacaaa	780
aaattttagt	ttactttcat	ttggagagga	agctgaggaa	gaagaagagg	aagtaaatacg	840
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tgatggagaa	gatgaaagtg	cagagcatga	tgaatatatt	gatggtgatg	aaaagaacct	1020
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acaagcagaa	aaaagaagtg	aagaggaaga	agccctcca	gatggtgctg	ttgccgaata	1260
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<210> 567
 <211> 372
 <212> PRT
 <213> Homo Sapiens

<400> 567

Met	Ala	Asn	Ala	Gly	Ser	His	Asp	Asn	Gly	Thr	His	Phe	Phe	Phe	Thr
1				5					10					15	
Leu	Gly	Arg	Ala	Asp	Glu	Leu	Asn	Asn	Lys	His	Thr	Ile	Phe	Gly	Lys
			20					25					30		
Val	Thr	Gly	Asp	Thr	Val	Tyr	Asn	Met	Leu	Arg	Leu	Ser	Glu	Val	Asp
		35					40					45			
Ile	Asp	Asp	Asp	Glu	Arg	Pro	His	Asn	Pro	His	Lys	Ile	Lys	Ser	Cys
	50					55					60				
Glu	Val	Leu	Phe	Asn	Pro	Phe	Asp	Asp	Ile	Ile	Pro	Arg	Glu	Ile	Lys
65					70					75					80
Arg	Leu	Lys	Lys	Glu	Lys	Pro	Glu	Glu	Glu	Val	Lys	Lys	Leu	Lys	Pro
			85						90					95	
Lys	Gly	Thr	Lys	Asn	Phe	Ser	Leu	Leu	Ser	Phe	Gly	Glu	Glu	Ala	Glu
			100					105						110	
Glu	Glu	Glu	Glu	Glu	Val	Asn	Arg	Val	Ser	Gln	Ser	Met	Lys	Gly	Lys
		115					120					125			
Ser	Lys	Ser	Ser	His	Asp	Leu	Lys	Asp	Asp	Pro	His	Leu	Ser	Ser	
	130					135					140				
Val	Pro	Val	Val	Glu	Ser	Glu	Lys	Gly	Asp	Ala	Pro	Asp	Leu	Val	Asp
145					150					155					160
Asp	Gly	Glu	Asp	Glu	Ser	Ala	Glu	His	Asp	Glu	Tyr	Ile	Asp	Gly	Asp
			165						170					175	
Glu	Lys	Asn	Leu	Met	Arg	Glu	Arg	Ile	Ala	Lys	Lys	Leu	Lys	Lys	Asp
		180						185					190		
Thr	Ser	Ala	Asn	Val	Lys	Ser	Ala	Gly	Glu	Gly	Glu	Val	Glu	Lys	Lys
		195					200					205			
Ser	Val	Ser	Arg	Ser	Glu	Glu	Leu	Arg	Lys	Glu	Ala	Arg	Gln	Leu	Lys
	210					215					220				
Arg	Glu	Leu	Leu	Ala	Ala	Lys	Gln	Lys	Lys	Val	Glu	Asn	Ala	Ala	Lys
225				230						235					240
Gln	Ala	Glu	Lys	Arg	Ser	Glu	Glu	Glu	Glu	Ala	Pro	Pro	Asp	Gly	Ala
			245						250					255	
Val	Ala	Glu	Tyr	Arg	Arg	Glu	Lys	Gln	Lys	Tyr	Glu	Ala	Leu	Arg	Lys
		260						265					270		
Gln	Gln	Ser	Lys	Lys	Gly	Thr	Ser	Arg	Glu	Asp	Gln	Thr	Leu	Ala	Leu
		275					280					285			
Leu	Asn	Gln	Phe	Lys	Ser	Lys	Leu	Thr	Gln	Ala	Ile	Ala	Glu	Thr	Pro
	290					295					300				
Glu	Asn	Asp	Ile	Pro	Glu	Thr	Glu	Val	Glu	Asp	Asp	Glu	Gly	Trp	Met
305				310						315					320
Ser	His	Val	Leu	Gln	Phe	Glu	Asp	Lys	Ser	Arg	Lys	Val	Lys	Asp	Ala
			325						330					335	
Ser	Met	Gln	Asp	Ser	Asp	Thr	Phe	Glu	Ile	Tyr	Asp	Pro	Arg	Asn	Pro
		340						345					350		
Val	Asn	Lys	Arg	Arg	Arg	Glu	Glu	Ser	Lys	Lys	Leu	Met	Arg	Glu	Lys
		355					360					365			
Lys	Glu	Arg	Arg												
	370														

<210> 568

<211> 1537

<212> DNA

<213> Homo Sapiens

<400> 568

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gccgcgcgcc gatcggtcgt taccgcgagg cgctggtggc cttcaggctg gacggcgcgg      60
gtcagccctg gttcgccggc ttctgggtct ttgaacagcc gcgatgtcga tcttcacccc      120
caccaaccag atccgcctaa ccaatgtggc cgtggtacgg atgaagcgtg ccgggaagcg      180
cttcgaaatc gctgtctaca aaaacaaggt cgtcggctgg cggagcggcg tggaaaaaga      240
cctcgatgaa gttctgcaga ccactcagt gtttgtaaag gtttctaaag gtcaggttgc      300
caaaaaggaa gatctcatca gtgcgtttgg aacagatgac caaactgaaa tctgtaagca      360
gattttgact aaaggagaag ttcaagtatc agataaagaa agacacacac aactggagca      420
gatgtttagg gacattgcaa ctattgtggc agacaaatgt gtgaatcctg aaacaaagag      480
accatacacc gtgatcctta ttgagagagc catgaaggac atccactatt cggtgaaaac      540
caacaagagt acaaaacagc aggcctttgga agtgataaag cagttaaaag agaaaatgaa      600
gatagaacgt gctcacatga agcttcgggt catccttcca gtcaatgaag gcaagaactg      660
aaagaaaagc tcaagccact gatcaaggtc atagaaagtg aagattatgg ccaacagtta      720
gaaatcgtat gtctgattga cccgggctgc ttccgagaaa ttgatgagct aataaaaaag      780
gaaactaaag gcaaaggttc tttggaagta ctcaatctga aagatgtaga agaaggagat      840
gagaaatttg aatgacaccc atcaatctct tcacctctaa aacactaaag tgtttccggt      900
tccgacggca ctgtttcatg tctgtggtct gccaaatact tgcttaaaact atttgacatt      960
ttctatcttt gtgttaacag tggacacagc aaggctttcc tacataagta taataatgtg     1020
ggaatgattt ggttttaatt ataaactggg gtctaaatcc taaagcaaaa ttgaaactcc     1080
aagatgcaaa gtccagagtg gcattttgct actctgtctc atgccttgat agctttccaa     1140
aatgaaagtt acttgangca gctcttggg gtgaaaagtt atttgtacag tagagtaaga     1200
ttattagggg tatgtctata caacaaaagg gggggtcttt cctaaaaaag aaaacatatg     1260
atgcttcatt tctacttaat ggaacttggt ttctgagggt cattatggta tcgtaatgta     1320
aagcttggat gatgttctg attatttgag gaacagatat aggaaaattg tgccggaatt     1380
acctttcatt gaacatgctg ccataaatta gggtattttt ggtaaaaaaa taaaagtcaa     1440
ttatttttaa tttttaaagt ttataatata tattaatata ggtaaaaattg tatgtaatca     1500
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<210> 569

<211> 210

<212> PRT

<213> Homo Sapiens

<400> 569

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Ala Ala Arg Arg Ser Val Val Thr Ala Arg Arg Trp Trp Pro Ser Gly
 1                    5                    10                    15
Trp Thr Ala Arg Val Ser Pro Gly Ser Pro Ala Ser Gly Ser Leu Asn
                20                25                30
Ser Arg Asp Val Asp Leu His Pro His Gln Pro Asp Pro Pro Asn Gln
                35                40                45
Cys Gly Arg Gly Thr Asp Glu Ala Cys Arg Glu Ala Leu Arg Asn Arg
 50                55                60
Leu Leu Gln Lys Gln Val Val Gly Trp Arg Ser Gly Val Glu Lys Asp
65                70                75                80
Leu Asp Glu Val Leu Gln Thr His Ser Val Phe Val Asn Val Ser Lys
                85                90                95
Gly Gln Val Ala Lys Lys Glu Asp Leu Ile Ser Ala Phe Gly Thr Asp
                100                105                110
Asp Gln Thr Glu Ile Cys Lys Gln Ile Leu Thr Lys Gly Glu Val Gln
                115                120                125
Val Ser Asp Lys Glu Arg His Thr Gln Leu Glu Gln Met Phe Arg Asp
                130                135                140
Ile Ala Thr Ile Val Ala Asp Lys Cys Val Asn Pro Glu Thr Lys Arg
145                150                155                160
Pro Tyr Thr Val Ile Leu Ile Glu Arg Ala Met Lys Asp Ile His Tyr

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165 170 175
 Ser Val Lys Thr Asn Lys Ser Thr Lys Gln Gln Ala Leu Glu Val Ile
 180 185 190
 Lys Gln Leu Lys Glu Lys Met Lys Ile Glu Arg Ala His Met Lys Leu
 195 200 205
 Arg Phe
 210

<210> 570
 <211> 1211
 <212> DNA
 <213> Homo Sapiens

<400> 570
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 agacattgat gatgacgaaa gaccacataa tccacacaaa ataaaaagct gtgagggtttt 120
 gtttaatcct tttgatgaca tcattccaag ggaaattaaa aggctgaaaa aagagaaacc 180
 agaggaggaa gtaaagaaat tgaaacccaa aggcacaaaa aatttttagtt tactttcatt 240
 tggagaggaa gctgagggaag aagaggagga agtaaatcga gttagtcaga gcatgaaggg 300
 caaaagcaaa agtagtcatg acttgcttaa ggatgatcca catctcagtt ctgttccagt 360
 tgtagaaaagt gaaaaagggtg atgcagcaga tttagttgat gatggagaag atgaaagtgc 420
 agagcatgat gaatatattg atggtgatga aaagaacctg atgagagaaa gaattgccaa 480
 aaaattaaaa aaggacacaa gtgcgaatgt taaatcagct ggagaaggag aagtggagaa 540
 gaaatcagtc agccgcagtg aagagctcag aaaagaagca agacaattaa aacgggaact 600
 cttagcagca gaacaaaaaa agtagaaaaa tgcagcaaaa caagcagaaa aaagaagtga 660
 agaggaagaa gccctccag atggtgctgt tgccgaatac agaagagaaa agcaaaagta 720
 tgaagctctg aggaagcaac agtcaaagaa gggaacttcc cggaagatc agacccttgc 780
 actgctgaac cagttttaat ctaaactcac tcaagcaatt gctgaaacgc ctgaaaatga 840
 cattcctgaa acagaagtag aagatgatga aggatggatg tcacatgtac ttcagtttga 900
 ggataaaagc agaaaagtga aagatgcaag catgcaagac tcagatacat ttgaaatcta 960
 tgatcctcgg aatccagtga ataaaagaag gaggaagaa agcaaaaagc tgatgagaga 1020
 gaaaaaagaa agaagataaa atgagaataa tgataaccag aacttgctgg aaatgtgcct 1080
 acaatggcct tgtaacagcc attgttccca acagcatcac ttaggggtgt gaaaagaagt 1140
 atttttgaac ctgttgtctg gttttgaaaa acaattatct tgttttgcaa attgtggaat 1200
 gatgtaagca a 1211

<210> 571
 <211> 354
 <212> PRT
 <213> Homo Sapiens

<400> 571
 Pro Ser Leu Glu Arg Leu Gln Gly Tyr Thr Val Tyr Asn Met Leu Arg
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 Leu Ser Glu Val Asp Ile Asp Asp Asp Glu Arg Pro His Asn Pro His
 20 25 30
 Lys Ile Lys Ser Cys Glu Val Leu Phe Asn Pro Phe Asp Asp Ile Ile
 35 40 45
 Pro Arg Glu Ile Lys Arg Leu Lys Lys Glu Lys Pro Glu Glu Glu Val
 50 55 60
 Lys Lys Leu Lys Pro Lys Gly Thr Lys Asn Phe Ser Leu Leu Ser Phe
 65 70 75 80
 Gly Glu Glu Ala Glu Glu Glu Glu Glu Val Asn Arg Val Ser Gln
 85 90 95
 Ser Met Lys Gly Lys Ser Lys Ser Ser His Asp Leu Leu Lys Asp Asp

100 105 110
 Pro His Leu Ser Ser Val Pro Val Val Glu Ser Glu Lys Gly Asp Ala
 115 120 125
 Ala Asp Leu Val Asp Asp Gly Glu Asp Glu Ser Ala Glu His Asp Glu
 130 135 140
 Tyr Ile Asp Gly Asp Glu Lys Asn Leu Met Arg Glu Arg Ile Ala Lys
 145 150 155 160
 Lys Leu Lys Lys Asp Thr Ser Ala Asn Val Lys Ser Ala Gly Glu Gly
 165 170 175
 Glu Val Glu Lys Lys Ser Val Ser Arg Ser Glu Glu Leu Arg Lys Glu
 180 185 190
 Ala Arg Gln Leu Lys Arg Glu Leu Leu Ala Ala Glu Gln Lys Lys Val
 195 200 205
 Glu Asn Ala Ala Lys Gln Ala Glu Lys Arg Ser Glu Glu Glu Glu Ala
 210 215 220
 Pro Pro Asp Gly Ala Val Ala Glu Tyr Arg Arg Glu Lys Gln Lys Tyr
 225 230 235 240
 Glu Ala Leu Arg Lys Gln Gln Ser Lys Lys Gly Thr Ser Arg Glu Asp
 245 250 255
 Gln Thr Leu Ala Leu Leu Asn Gln Phe Lys Ser Lys Leu Thr Gln Ala
 260 265 270
 Ile Ala Glu Thr Pro Glu Asn Asp Ile Pro Glu Thr Glu Val Glu Asp
 275 280 285
 Asp Glu Gly Trp Met Ser His Val Leu Gln Phe Glu Asp Lys Ser Arg
 290 295 300
 Lys Val Lys Asp Ala Ser Met Gln Asp Ser Asp Thr Phe Glu Ile Tyr
 305 310 315 320
 Asp Pro Arg Asn Pro Val Asn Lys Arg Arg Arg Glu Glu Ser Lys Lys
 325 330 335
 Leu Met Arg Glu Lys Lys Glu Arg Arg Ile Leu Pro Val Asn Glu Gly
 340 345 350
 Lys Asn

<210> 572
 <211> 604
 <212> DNA
 <213> Homo Sapiens

<400> 572
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 tcccttttagc aacagggccc ccaagaagct cccgttcatt cacccttacc ttggccccc 120
 gggttggaacc ccaaaggctc ccttaccoca aagtgggttg ttgaataaat cttctcagtt 180
 ccctggctcc caaggcccat tgaagaagat tgtacaaggc gtgcctcaag taccgagat 240
 ggaaacagaa gcacctgcct cacttcaagc cgtggctgca cccggagcag agcccggtgc 300
 cgagcctggc gctgtcggag ctgtcgggtgc agcatgcgga ctactggag aacatcgacg 360
 agagcgcggt ggccgagagc agagaggagc ggatgggagg cgcgggcggc gagggcagcg 420
 acgacgacac cttcacctga gcccgcaccg cttcagggac ggagacagga ccgggcgagc 480
 cctggggcgg cggcgcctcc tgcactttct cccctccccc acccggcacc tgggtggcacc 540
 gggccaggcc caggcgggtg ctgcagcctg gctggacaga gcccaataaa cggatccac 600
 agcc 604

<210> 573
 <211> 195
 <212> PRT

<213> Homo Sapiens

<400> 573

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Leu Arg Gln Lys Ile Leu Val Pro Thr Phe Cys Ser Ile Pro Lys Gly
 1           5           10           15
Leu Thr Phe Ile Pro Phe Ser Asn Arg Ala Pro Lys Lys Leu Pro Phe
          20           25           30
Ile His Pro Tyr Leu Gly Pro Gln Val Gly Pro Pro Lys Ala Pro Leu
          35           40           45
Pro Gln Ser Gly Trp Leu Asn Lys Ser Ser Gln Phe Pro Gly Ser Gln
          50           55           60
Gly Pro Leu Lys Lys Ile Val Gln Gly Val Pro Gln Val Pro Arg Val
65           70           75           80
Glu Thr Glu Ala Pro Ala Ser Leu Gln Ala Val Ala Ala Pro Gly Ala
          85           90           95
Glu Pro Val Ala Glu Pro Gly Ala Val Gly Ala Val Gly Ala Ala Cys
          100          105          110
Gly Leu Thr Gly Glu His Arg Arg Glu Arg Gly Gly Arg Glu Gln Arg
          115          120          125
Gly Ala Asp Gly Arg Arg Gly Arg Arg Gly Gln Arg Arg Arg His Leu
          130          135          140
His Leu Ser Pro His Arg Phe Arg Asp Gly Asp Arg Thr Gly Arg Ala
145          150          155          160
Leu Gly Arg Arg Pro Leu Leu His Phe Leu Pro Ser Pro Thr Arg His
          165          170          175
Leu Val Ala Pro Gly Gln Ala Gln Ala Gly Ala Ala Ala Trp Leu Asp
          180          185          190
Arg Ala Gln
          195

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<210> 574

<211> 742

<212> DNA

<213> Homo Sapiens

<400> 574

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cctaccagga gcagaggccc caggtggagc aagttggcaa agtcgctcct ctctcccag      120
ggctgccggc aatggggggg cctggccccg gccctgtga ggaccccgcg ggtgctgggg      180
gagcaggtgc agggggctcc gagccccctg tgactgtcac cgtgcagtgc gccttcacag      240
tgccctgag ggcaggaaga ggagccgacc tgtccagcct gcgggcactg ctggggccaag      300
ccttccttca ccaggcccag cttgggcaat tcagttacct agccccaggt gaggacgggc      360
actgggtccc catccccgag gaggagtcgc tgcagagggc ctggcaggac gcagctgcct      420
gccccagggg gctgcagctg cagtgcaggg gagccggggg tggccgggtc ctttaccagg      480
tggtggccca gcacagatac tccgcccagg ggccagagga cctgggcttc cgacaggggg      540
acacggtgga cgtcctgtgt gaagtggacc aggcattggc ggagggccac tgtgacggcc      600
gcateggcat cttcccgaag tgcttcgtgg tccccgccgg coctcgatg tcaggagccc      660
cgggcgcct gccccgatcc cagcagggag atcagcccta atgatgctgt gtccatgatg      720
ctttaataa aaacaacccc ca                                742

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<210> 575

<211> 232

<212> PRT

<213> Homo Sapiens

<400> 575
 His Gln Gly Pro Leu Asp Ala Glu Thr Glu Val Gly Ala Asp Arg Cys
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 Thr Ser Thr Ala Tyr Gln Glu Gln Arg Pro Gln Val Glu Gln Val Gly
 20 25 30
 Lys Val Ala Pro Leu Ser Pro Gly Leu Pro Ala Met Gly Gly Pro Gly
 35 40 45
 Pro Gly Pro Cys Glu Asp Pro Ala Gly Ala Gly Gly Ala Gly Ala Gly
 50 55 60
 Gly Ser Glu Pro Leu Val Thr Val Thr Val Gln Cys Ala Phe Thr Val
 65 70 75 80
 Ala Leu Arg Ala Gly Arg Gly Ala Asp Leu Ser Ser Leu Arg Ala Leu
 85 90 95
 Leu Gly Gln Ala Phe Leu His Gln Ala Gln Leu Gly Gln Phe Ser Tyr
 100 105 110
 Leu Ala Pro Gly Glu Asp Gly His Trp Val Pro Ile Pro Glu Glu Glu
 115 120 125
 Ser Leu Gln Arg Ala Trp Gln Asp Ala Ala Ala Cys Pro Arg Gly Leu
 130 135 140
 Gln Leu Gln Cys Arg Gly Ala Gly Gly Arg Pro Val Leu Tyr Gln Val
 145 150 155 160
 Val Ala Gln His Arg Tyr Ser Ala Gln Gly Pro Glu Asp Leu Gly Phe
 165 170 175
 Arg Gln Gly Asp Thr Val Asp Val Leu Cys Glu Val Asp Gln Ala Trp
 180 185 190
 Leu Glu Gly His Cys Asp Gly Arg Ile Gly Ile Phe Pro Lys Cys Phe
 195 200 205
 Val Val Pro Ala Gly Pro Arg Met Ser Gly Ala Pro Gly Arg Leu Pro
 210 215 220
 Arg Ser Gln Gln Gly Asp Gln Pro
 225 230

<210> 576
 <211> 1087
 <212> DNA
 <213> Homo Sapiens

<400> 576
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 caaaataagg gtaaaccaga cttgaatata acattgccaa ttagacaaac agcatcaatt 120
 ttcaaacaac cggtaaccac agtcacaaat catcctagta ataaagtga atcagaccca 180
 caacgaatga atgaacagcc acgtcagctt ttctgggaga agaggctaca aggacttagt 240
 gcatcagatg taacagaaca aattataaaa accatggaac taccacaaagg tcttcaagga 300
 gttggtccag gtagcaatga tgagaccctt ttatctgctg ttgccagtgc tttgcacaca 360
 agctctgctc caatcacagg gcaagtctcc gctgctgtgg aaaagaaccc tgctgtttgg 420
 cttaacacat ctcaaccct ctgcaaagct tttattgtca cagatgaaga catcaggaaa 480
 caggaagagc gagtacagca agtacgcaag aaattggaag aagcactgat ggcagacatc 540
 ttgtcgcgag ctgctgatac agaagagatg gatattgaaa tggacagtgg agatgaagcc 600
 taagaatatg atcaggtaac tttcgaccga ctttcccca gagaaaattc ctagaaattg 660
 aacaaaaatg tttccactgg cttttgctg taagaaaaaa aatgtaccgc agcacataga 720
 gctttttaat agcactaacc aatgcctttt tagatgtatt tttgatgtat atatctatta 780
 ttcaaaaaat catgtttatt ttgagtccta ggacttaaaa ttagtctttt gtaatataca 840
 gcaggacct aagatgaagc tgagcttttg atgccagggt caattttactg gaaatgtagc 900
 acttacgtaa aacatttggt tccccacag ttttaataag aacagatcag gaattctaaa 960
 taaatttccc agttaaagat tattgtgact tcactgtata taaacatatt tttatacttt 1020

attgaaaggg gacacctgta cattcttcca tcgtcactgt aaagacaaat aaatgattat 1080
attcaca 1087

<210> 577
<211> 200
<212> PRT
<213> Homo Sapiens

<400> 577
Lys Met Met Pro Ser Lys Leu Gln Lys Asn Lys Gln Arg Leu Arg Asn
1 5 10 15
Asp Pro Leu Asn Gln Asn Lys Gly Lys Pro Asp Leu Asn Thr Thr Leu
20 25 30
Pro Ile Arg Gln Thr Ala Ser Ile Phe Lys Gln Pro Val Thr Lys Val
35 40 45
Thr Asn His Pro Ser Asn Lys Val Lys Ser Asp Pro Gln Arg Met Asn
50 55 60
Glu Gln Pro Arg Gln Leu Phe Trp Glu Lys Arg Leu Gln Gly Leu Ser
65 70 75 80
Ala Ser Asp Val Thr Glu Gln Ile Ile Lys Thr Met Glu Leu Pro Lys
85 90 95
Gly Leu Gln Gly Val Gly Pro Gly Ser Asn Asp Glu Thr Leu Leu Ser
100 105 110
Ala Val Ala Ser Ala Leu His Thr Ser Ser Ala Pro Ile Thr Gly Gln
115 120 125
Val Ser Ala Ala Val Glu Lys Asn Pro Ala Val Trp Leu Asn Thr Ser
130 135 140
Gln Pro Leu Cys Lys Ala Phe Ile Val Thr Asp Glu Asp Ile Arg Lys
145 150 155 160
Gln Glu Glu Arg Val Gln Gln Val Arg Lys Lys Leu Glu Glu Ala Leu
165 170 175
Met Ala Asp Ile Leu Ser Arg Ala Ala Asp Thr Glu Glu Met Asp Ile
180 185 190
Glu Met Asp Ser Gly Asp Glu Ala
195 200

<210> 578
<211> 2569
<212> DNA
<213> Homo Sapiens

<400> 578
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tgtttctcat ataaatgacc tttcagactt ttatgttcaa ctaatagaag atgaagctga 180
aattagtcac ctttcagaga gattaaacag tgttaaaaca aggcccgat attatgtagg 240
tccacctttg caaagaggag atatgatatg tgctgttttc ccagaagata atttatggta 300
tcgtgctgtg atcaaggagc aacaacccaa tgaccttctc tctgtgcagt ttatagatta 360
tggcaatgtt tctgtggttc atactaacia aataggtagg cttgaccttg ttaatgcaat 420
attgccgggg ttgtgcattc attgctcctt gcagggattt gaggttctctg acaataaaaa 480
ttctaagaaa atgatgcatt acttttccca acggaccagc gaggctgcaa taagatgtga 540
atgtgttaaa tttcaagaca gatgggaagt tattcttgcg gatgaacatg ggatcatagc 600
agatgatatg attagcaggt atgctctcag tgaataatct caagtagaac tttctaccca 660
agtaattaaa agtgccagtt caaagtctgt taacaaatca gacattgaca cttcagattt 720
tcttaactgg tataatccag aaaaaaaat gataagagct tatgccactg tgatagatgg 780

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acctgagtag ttttgggtgc agtttgctga tacggagaaa cttcagtgtt tagaagtaga      840
agtagacagact gctggagaac aggtagcaga caggagaaaat tgtatcccat gtccttatat      900
tgtagatcct tgtatagtaa gatacagaga agatggacat tattataggg cacttatcac      960
taatatattgt gaagattatc ttgtatctgt caggcttgtg gactttggaa acattgaaga     1020
ctgtgtggac ccaaaagcac tctgggccat tccttctgaa cttctgtcgg ttcccatgca     1080
agcctttcca tgttgccctc cagggtttta catttcagaa ggattatgtt ctcaagaggg      1140
aaatgactat ttctatgaaa taataacaga agatgtgttg gaaaataacaa tactagaaat     1200
cagaagggat gtttgtgata tcccttttagc aattgttgac ttgaaaagca aaggtaaaag     1260
tattaatgag aaaatggaga aatattctaa gactggtatt aaaagtgtc ttccctatga     1320
aaatattgac tcagagataa agcagactct tgggtcctac aatcttgatg taggacttaa     1380
gaaattaagt aataaagctg tacaaaataa aatataatg gaacaacaga cagatgagct      1440
tgctgaaata actgaaaaag atgtaaacat tattggaacc aaaccaagta acttccgtga     1500
ccctaaaact gataacattt gtgaaggggt tgaaaaacccc tgcaaagata aaattgatac     1560
tgaggaactg gaaggatgaat tagagtgcc aatgaaacaa aggagatact      1620
atacctgatt acaggattta acacattact accacatgct aatgaaacaa aggagatact     1680
agaactgaat tcacttgagg tgccgctttc tcctgatgat gaatcaaaaag aattcttaga     1740
actggaatct attgagttac agaattctct ggtggtggat gaagaaaaag gggagctaag     1800
cccggtgcca ccgaatgtgc cactctccca agagtgtgtc acaaaaggcg ccatggagct      1860
attacactg cagcttcctc tcagctgtga agctgagaaa cagccagAAC tagaactacc     1920
tacagcccag ctgcctttag atgacaagat ggatcctttg tctttaggag ttagtcagaa     1980
agcacaggaa tccatgtgta ctgaggacat gagaaagtca agttgtgtag aatcttttga     2040
tgaccagcgc aggatgtcat tgcattctaca tggagcagat tgtgatccta aaacacagaa     2100
tgaaatgaat atatgtgaag aagaatttgt agagtataaa aacagggatg ccatttcggc     2160
attgatgctt ttttctctga ggaagaaaagc agtgatggaa gcaagcaca taatggttta     2220
ccagatcata tttcagntca attacagaac acctacactn tgaaagcctt tactgttgga     2280
tctaaatgtg ttgtgtggtc aagtntaaga aacanatggt ctaaatgtga gatttttagaa     2340
acagctgaag aaggnacaag ggttttgaac ctttcaaagt gtatggagga gatagtgaac     2400
cctgagaatg tctggaatgn nanacccaaa ttggataaga gtccacctga gaaaaggggt     2460
ttggaggtga tggagattta accgtggatn tatagctgtg gccaatcagt cagaagctgc     2520
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<210> 579

<211> 752

<212> PRT

<213> Homo Sapiens

<400> 579

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Arg Val Lys Ala Thr Leu Ser Glu Arg Lys Ile Gly Asp Ser Cys Asp
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Lys Asp Leu Pro Leu Lys Phe Cys Glu Phe Pro Gln Lys Thr Ile Met
              20              25              30
Pro Gly Phe Lys Thr Thr Val Tyr Val Ser His Ile Asn Asp Leu Ser
              35              40              45
Asp Phe Tyr Val Gln Leu Ile Glu Asp Glu Ala Glu Ile Ser His Leu
              50              55              60
Ser Glu Arg Leu Asn Ser Val Lys Thr Arg Pro Glu Tyr Tyr Val Gly
65              70              75              80
Pro Pro Leu Gln Arg Gly Asp Met Ile Cys Ala Val Phe Pro Glu Asp
              85              90              95
Asn Leu Trp Tyr Arg Ala Val Ile Lys Glu Gln Gln Pro Asn Asp Leu
              100             105             110
Leu Ser Val Gln Phe Ile Asp Tyr Gly Asn Val Ser Val Val His Thr
              115             120             125
Asn Lys Ile Gly Arg Leu Asp Leu Val Asn Ala Ile Leu Pro Gly Leu
              130             135             140

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Cys Ile His Cys Ser Leu Gln Gly Phe Glu Val Pro Asp Asn Lys Asn
 145 150 155 160
 Ser Lys Lys Met Met His Tyr Phe Ser Gln Arg Thr Ser Glu Ala Ala
 165 170 175
 Ile Arg Cys Glu Phe Val Lys Phe Gln Asp Arg Trp Glu Val Ile Leu
 180 185 190
 Ala Asp Glu His Gly Ile Ile Ala Asp Asp Met Ile Ser Arg Tyr Ala
 195 200 205
 Leu Ser Glu Lys Ser Gln Val Glu Leu Ser Thr Gln Val Ile Lys Ser
 210 215 220
 Ala Ser Ser Lys Ser Val Asn Lys Ser Asp Ile Asp Thr Ser Val Phe
 225 230 235 240
 Leu Asn Trp Tyr Asn Pro Glu Lys Lys Met Ile Arg Ala Tyr Ala Thr
 245 250 255
 Val Ile Asp Gly Pro Glu Tyr Phe Trp Cys Gln Phe Ala Asp Thr Glu
 260 265 270
 Lys Leu Gln Cys Leu Glu Val Glu Val Gln Thr Ala Gly Glu Gln Val
 275 280 285
 Ala Asp Arg Arg Asn Cys Ile Pro Cys Pro Tyr Ile Gly Asp Pro Cys
 290 295 300
 Ile Val Arg Tyr Arg Glu Asp Gly His Tyr Tyr Arg Ala Leu Ile Thr
 305 310 315 320
 Asn Ile Cys Glu Asp Tyr Leu Val Ser Val Arg Leu Val Asp Phe Gly
 325 330 335
 Asn Ile Glu Asp Cys Val Asp Pro Lys Ala Leu Trp Ala Ile Pro Ser
 340 345 350
 Glu Leu Leu Ser Val Pro Met Gln Ala Phe Pro Cys Cys Leu Ser Gly
 355 360 365
 Phe Asn Ile Ser Glu Gly Leu Cys Ser Gln Glu Gly Asn Asp Tyr Phe
 370 375 380
 Tyr Glu Ile Ile Thr Glu Asp Val Leu Glu Ile Thr Ile Leu Glu Ile
 385 390 395 400
 Arg Arg Asp Val Cys Asp Ile Pro Leu Ala Ile Val Asp Leu Lys Ser
 405 410 415
 Lys Gly Lys Ser Ile Asn Glu Lys Met Glu Lys Tyr Ser Lys Thr Gly
 420 425 430
 Ile Lys Ser Ala Leu Pro Tyr Glu Asn Ile Asp Ser Glu Ile Lys Gln
 435 440 445
 Thr Leu Gly Ser Tyr Asn Leu Asp Val Gly Leu Lys Lys Leu Ser Asn
 450 455 460
 Lys Ala Val Gln Asn Lys Ile Tyr Met Glu Gln Gln Thr Asp Glu Leu
 465 470 475 480
 Ala Glu Ile Thr Glu Lys Asp Val Asn Ile Ile Gly Thr Lys Pro Ser
 485 490 495
 Asn Phe Arg Asp Pro Lys Thr Asp Asn Ile Cys Glu Gly Phe Glu Asn
 500 505 510
 Pro Cys Lys Asp Lys Ile Asp Thr Glu Glu Leu Glu Gly Glu Leu Glu
 515 520 525
 Cys His Leu Val Asp Lys Ala Glu Phe Asp Asp Lys Tyr Leu Ile Thr
 530 535 540
 Gly Phe Asn Thr Leu Leu Pro His Ala Asn Glu Thr Lys Glu Ile Leu
 545 550 555 560
 Glu Leu Asn Ser Leu Glu Val Pro Leu Ser Pro Asp Asp Glu Ser Lys
 565 570 575
 Glu Phe Leu Glu Leu Glu Ser Ile Glu Leu Gln Asn Ser Leu Val Val

	580		585		590										
Asp	Glu	Glu	Lys	Gly	Glu	Leu	Ser	Pro	Val	Pro	Pro	Asn	Val	Pro	Leu
	595		600		605										
Ser	Gln	Glu	Cys	Val	Thr	Lys	Gly	Ala	Met	Glu	Leu	Phe	Thr	Leu	Gln
	610		615		620										
Leu	Pro	Leu	Ser	Cys	Glu	Ala	Glu	Lys	Gln	Pro	Glu	Leu	Glu	Leu	Pro
	625		630		635										640
Thr	Ala	Gln	Leu	Pro	Leu	Asp	Asp	Lys	Met	Asp	Pro	Leu	Ser	Leu	Gly
			645		650									655	
Val	Ser	Gln	Lys	Ala	Gln	Glu	Ser	Met	Cys	Thr	Glu	Asp	Met	Arg	Lys
			660		665									670	
Ser	Ser	Cys	Val	Glu	Ser	Phe	Asp	Asp	Gln	Arg	Arg	Met	Ser	Leu	His
			675		680									685	
Leu	His	Gly	Ala	Asp	Cys	Asp	Pro	Lys	Thr	Gln	Asn	Glu	Met	Asn	Ile
			690		695									700	
Cys	Glu	Glu	Glu	Phe	Val	Glu	Tyr	Lys	Asn	Arg	Asp	Ala	Ile	Ser	Ala
					710					715					720
Leu	Met	Pro	Phe	Ser	Leu	Arg	Lys	Lys	Ala	Val	Met	Glu	Ala	Ser	Thr
					725					730					735
Ile	Met	Val	Tyr	Gln	Ile	Ile	Phe	Gln	Asn	Tyr	Arg	Thr	Pro	Thr	Leu
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<210> 580
 <211> 2077
 <212> DNA
 <213> Homo Sapiens

<400> 580

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gaggtgactc	gagcagtgat	gaggataaag	aataacatga	aactcctgtg	gaagtagaac	180
tcatgactca	ggttgaccaa	gaggatatca	ctcttcagag	tggcagagat	gaactaaatg	240
aggagctcat	tcaggaagaa	agctctgaag	acgaaggaga	atatgaagag	gtagaaaaag	300
atcaggattc	tggttggtgaa	atgaaggatg	aagggggaaga	gacttaaatt	atcctgatac	360
taccattgac	ttgtctcacc	ttcaacccca	aagggtccatc	cagaaattgg	cttcaaaaga	420
ggaatcttct	aattctagt	acagtaaata	acagagccgg	agacatttgt	cagccaagga	480
aagaagggaa	atgaaaaaga	aaaaacttcc	aagtgactca	ggagatttag	aagcgtaga	540
gggaaaggat	aaagaaaaag	aaagtactgt	acacattgaa	actcatcaga	acacaagcaa	600
aaatgttgcg	gctgtgcagc	caatgaaacg	aggacaaaag	agtaaaatga	aaaaaatgaa	660
agaaaaatac	aaagaccagg	atgaagaaga	ccgtgaactt	atcatgaagt	tgtctggggtc	720
tgcaggttca	aacaaagaag	aaaaagggaa	gaagggggaag	aaaggaaaaa	caaaggacga	780
acctgtgaag	aaacagcccc	agaaacctag	aggtggacag	aggtctctctg	acaacattaa	840
gaaagaaact	ccgttccttg	aggttataac	tcatgagtta	caagactttg	ctgtagatga	900
tccacatgat	gacaaggaag	agcaagatct	ggatcaacag	ggaaatgagg	aaaacctatt	960
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gaaaaaggga	aaagctgcaa	aaacagcctt	gaatagtttc	atgcattcca	aagaagcaac	1140
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tggcaaagt	aaaagtgtct	gcacccaatc	ttctgaacgt	aaaaaggaaa	tagctgaaat	1260
gaaattctaa	aatatttgag	aagagccaat	tttatagcct	tttggaggtt	caaagatgaa	1320
agcaccatgt	atcaggattt	ccgcattata	aaaatgaact	aaacattgcc	ttgttatatt	1380
caccaaagg	acttaattct	tgtttttttc	ccagttttat	atagaggaaa	cactgtctat	1440
gataggattt	ccaaaagtatt	ttgtggacag	ttaaatgcta	attatataca	tctgtagtta	1500
ttctacattt	tcttgaaatt	tgggaggtta	ataccaagta	ttcatttcat	gatgtaaaga	1560
aactgaacag	tgaagtggct	tgattgctta	aactattgac	ttggttaagtc	tactgtatat	1620

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tcctaaagta tttgtggaca gttaaattgct aattatatac atctgtagtt attctacatt 1800
ttccttgaaat ttgagagggt aataccaagt attcattttca tgatgtaaag aaactgaaca 1860
gtgaagtggc ttgattgctt aaactattga cttggtaagt ctactgtata taacatctaa 1920
tatatatata ttataggcca gctacaagggt gtttaaataat ttaggattgt gtcttgaaaa 1980
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<210> 581

<211> 312

<212> PRT

<213> Homo Sapiens

<400> 581

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Leu Gln Pro Gln Arg Ser Ile Gln Lys Leu Ala Ser Lys Glu Glu Ser
20     25     30
Ser Asn Ser Ser Asp Ser Lys Ser Gln Ser Arg Arg His Leu Ser Ala
35     40     45
Lys Glu Arg Arg Glu Met Lys Lys Lys Lys Leu Pro Ser Asp Ser Gly
50     55     60
Asp Leu Glu Ala Leu Glu Gly Lys Asp Lys Glu Lys Glu Ser Thr Val
65     70     75     80
His Ile Glu Thr His Gln Asn Thr Ser Lys Asn Val Ala Ala Val Gln
85     90     95
Pro Met Lys Arg Gly Gln Lys Ser Lys Met Lys Lys Met Lys Glu Lys
100    105    110
Tyr Lys Asp Gln Asp Glu Glu Asp Arg Glu Leu Ile Met Lys Leu Leu
115    120    125
Gly Ser Ala Gly Ser Asn Lys Glu Glu Lys Gly Lys Lys Gly Lys Lys
130    135    140
Gly Lys Thr Lys Asp Glu Pro Val Lys Lys Gln Pro Gln Lys Pro Arg
145    150    155    160
Gly Gly Gln Arg Val Ser Asp Asn Ile Lys Lys Glu Thr Pro Phe Leu
165    170    175
Glu Val Ile Thr His Glu Leu Gln Asp Phe Ala Val Asp Asp Pro His
180    185    190
Asp Asp Lys Glu Glu Gln Asp Leu Asp Gln Gln Gly Asn Glu Glu Asn
195    200    205
Leu Phe Asp Ser Leu Thr Gly Gln Pro His Pro Glu Asp Val Leu Leu
210    215    220
Phe Ala Ile Pro Ile Cys Ala Pro Tyr Thr Thr Met Thr Asn Tyr Lys
225    230    235    240
Tyr Lys Val Lys Leu Thr Pro Gly Val Gln Lys Lys Gly Lys Ala Ala
245    250    255
Lys Thr Ala Leu Asn Ser Phe Met His Ser Lys Glu Ala Thr Ala Arg
260    265    270
Glu Lys Asp Leu Phe Arg Ser Val Lys Asp Thr Asp Leu Ser Arg Asn
275    280    285
Ile Pro Gly Lys Val Lys Ser Val Cys Thr Gln Ser Ser Glu Arg Lys
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Lys Glu Ile Ala Glu Met Lys Phe
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<210> 582
 <211> 3309
 <212> DNA
 <213> Homo Sapiens

<400> 582

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acaatcgag	ttgcagccaa	aaatcagcaa	atcactcatg	caaacaatac	ggtgtctaac	240
ttcaaaagat	ttcatggccg	agcattcaat	gaccccttca	ttcaaaagga	gaaggaaaac	300
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ggtgaagaac	atctatttag	tgtggagcag	ataacagcca	tgttgttgac	taagctgaag	420
gaaactgctg	aaaacagcct	caagaaacca	gtaacagatt	gtgttatttc	agtccccctcc	480
ttctttacag	atgctgagag	gcgatctgtg	ttagatgctg	cacagattgt	tggcctaaac	540
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gaaatgaaaa	aagtggagaa	gtctgttaat	gaagtgatgg	aatggatgaa	taatgtcatg	2340
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ttcctgtgga	attgtgaatt	cataactaagc	tttctgtgca	gtctcaccat	ttgcatcact	2880
gaggatgaaa	ctgacttttg	tcttttgag	aaaaaaaact	gtactgcttg	ttcaagaggg	2940

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ctgtgattaa aatctttaag catttgttcc tgccaaggta gttttcttgc attttgctct 3000
ccattcagca tgtgtgtggg tgtggatgtt tataaacaag actaagtctg acttcataag 3060
ggcttttctaa aaccatttct gtccaagaga aaatgacttt ttgctttgat attaaaaatt 3120
caatgagtaa aacaaaagct agtcaaagtgt gtttagcagca tgcagaacaa aaactttaaa 3180
ctttctctct cactatacag tatattgtca tgtgaaagtgt tggaatggaa gaaatgtcga 3240
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<210> 583

<211> 872

<212> PRT

<213> Homo Sapiens

<400> 583

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 20          25          30
Arg Ala Gly Gly Ile Glu Thr Ile Ala Asn Glu Phe Ser Asp Arg Cys
 35          40          45
Thr Pro Ser Val Ile Ser Phe Gly Ser Lys Asn Arg Thr Ile Gly Val
 50          55          60
Ala Ala Lys Asn Gln Gln Ile Thr His Ala Asn Asn Thr Val Ser Asn
 65          70          75          80
Phe Lys Arg Phe His Gly Arg Ala Phe Asn Asp Pro Phe Ile Gln Lys
 85          90          95
Glu Lys Glu Asn Leu Ser Tyr Asp Leu Val Pro Leu Lys Asn Gly Gly
100          105          110
Val Gly Ile Lys Val Met Tyr Met Gly Glu Glu His Leu Phe Ser Val
115          120          125
Glu Gln Ile Thr Ala Met Leu Leu Thr Lys Leu Lys Glu Thr Ala Glu
130          135          140
Asn Ser Leu Lys Lys Pro Val Thr Asp Cys Val Ile Ser Val Pro Ser
145          150          155          160
Phe Phe Thr Asp Ala Glu Arg Arg Ser Val Leu Asp Ala Ala Gln Ile
165          170          175
Val Gly Leu Asn Cys Leu Arg Leu Met Asn Asp Met Thr Ala Val Ala
180          185          190
Leu Asn Tyr Gly Ile Tyr Lys Gln Asp Leu Pro Ser Leu Asp Glu Lys
195          200          205
Pro Arg Ile Val Val Phe Val Asp Met Gly His Ser Ala Phe Gln Val
210          215          220
Ser Ala Cys Ala Phe Asn Lys Gly Lys Leu Lys Val Leu Gly Thr Ala
225          230          235          240
Phe Asp Pro Phe Leu Gly Gly Lys Asn Phe Asp Glu Lys Leu Val Glu
245          250          255
His Phe Cys Ala Glu Phe Lys Thr Lys Tyr Lys Leu Asp Ala Lys Ser
260          265          270
Lys Ile Arg Ala Leu Leu Arg Leu Tyr Gln Glu Cys Glu Lys Leu Lys
275          280          285
Lys Leu Met Ser Ser Asn Ser Thr Asp Leu Pro Leu Asn Ile Glu Cys
290          295          300
Phe Met Asn Asp Lys Asp Val Ser Gly Lys Met Asn Arg Ser Gln Phe
305          310          315          320
Glu Glu Leu Cys Ala Glu Leu Leu Gln Lys Ile Glu Val Pro Leu Tyr

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325 330 335
 Ser Leu Leu Glu Gln Thr His Leu Lys Val Glu Asp Val Ser Ala Val
 340 345 350
 Glu Ile Val Gly Gly Ala Thr Arg Ile Pro Ala Val Lys Glu Arg Ile
 355 360 365
 Ala Lys Phe Phe Gly Lys Asp Ile Ser Thr Thr Leu Asn Ala Asp Glu
 370 375 380
 Ala Val Ala Arg Gly Cys Ala Leu Gln Cys Ala Ile Leu Ser Pro Ala
 385 390 395 400
 Phe Lys Val Arg Glu Phe Ser Val Thr Asp Ala Val Pro Phe Pro Ile
 405 410 415
 Ser Leu Ile Trp Asn His Asp Ser Glu Asp Thr Glu Gly Val His Glu
 420 425 430
 Val Phe Ser Arg Asn His Ala Ala Pro Phe Ser Lys Val Leu Thr Phe
 435 440 445
 Leu Arg Arg Gly Pro Phe Glu Leu Glu Ala Phe Tyr Ser Asp Pro Gln
 450 455 460
 Gly Val Pro Tyr Pro Glu Ala Lys Ile Gly Arg Phe Val Val Gln Asn
 465 470 475 480
 Val Ser Ala Gln Lys Asp Gly Glu Lys Ser Arg Val Lys Val Lys Val
 485 490 495
 Arg Val Asn Thr His Gly Ile Phe Thr Ile Ser Thr Ala Ser Met Val
 500 505 510
 Glu Lys Val Pro Thr Glu Glu Asn Glu Met Ser Ser Glu Ala Asp Met
 515 520 525
 Glu Cys Leu Asn Gln Arg Pro Pro Glu Asn Pro Asp Thr Asp Lys Asn
 530 535 540
 Val Gln Gln Asp Asn Ser Glu Ala Gly Thr Gln Pro Gln Val Gln Thr
 545 550 555 560
 Asp Ala Gln Gln Thr Ser Gln Ser Pro Pro Ser Pro Glu Leu Thr Ser
 565 570 575
 Glu Glu Asn Lys Ile Pro Asp Ala Asp Lys Ala Asn Glu Lys Lys Val
 580 585 590
 Asp Gln Pro Pro Glu Ala Lys Lys Pro Lys Ile Lys Val Val Asn Val
 595 600 605
 Glu Leu Pro Ile Glu Ala Asn Leu Val Trp Gln Leu Gly Lys Asp Leu
 610 615 620
 Leu Asn Met Tyr Ile Glu Thr Glu Gly Lys Met Ile Met Gln Asp Lys
 625 630 635 640
 Leu Glu Lys Glu Arg Asn Asp Ala Lys Asn Ala Val Glu Glu Tyr Val
 645 650 655
 Tyr Glu Phe Arg Asp Lys Leu Cys Gly Pro Tyr Glu Lys Phe Ile Cys
 660 665 670
 Glu Gln Asp His Gln Asn Phe Leu Arg Leu Leu Thr Glu Thr Glu Asp
 675 680 685
 Trp Leu Tyr Glu Glu Gly Glu Asp Gln Ala Lys Gln Ala Tyr Val Asp
 690 695 700
 Lys Leu Glu Glu Leu Met Lys Ile Gly Thr Pro Val Lys Val Arg Phe
 705 710 715 720
 Gln Glu Ala Glu Glu Arg Pro Lys Met Phe Glu Glu Leu Gly Gln Arg
 725 730 735
 Leu Gln His Tyr Ala Lys Ile Ala Ala Asp Phe Arg Asn Lys Asp Glu
 740 745 750
 Lys Tyr Asn His Ile Asp Glu Ser Glu Met Lys Lys Val Glu Lys Ser
 755 760 765

Val	Asn	Glu	Val	Met	Glu	Trp	Met	Asn	Asn	Val	Met	Asn	Ala	Gln	Ala
770						775					780				
Lys	Lys	Ser	Leu	Asp	Gln	Asp	Pro	Val	Val	Arg	Ala	Gln	Glu	Ile	Lys
785					790					795					800
Thr	Lys	Ile	Lys	Glu	Leu	Asn	Asn	Thr	Cys	Glu	Pro	Val	Val	Thr	Gln
				805					810					815	
Pro	Lys	Pro	Lys	Ile	Glu	Ser	Pro	Lys	Leu	Glu	Arg	Thr	Pro	Asn	Gly
				820				825					830		
Pro	Asn	Ile	Asp	Lys	Lys	Glu	Glu	Asp	Leu	Glu	Asp	Lys	Asn	Asn	Phe
		835				840						845			
Gly	Ala	Glu	Pro	Pro	His	Gln	Asn	Gly	Glu	Cys	Tyr	Pro	Asn	Glu	Lys
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Asn	Ser	Val	Asn	Met	Asp	Leu	Asp								
865					870										

<210> 584

<211> 2918

<212> DNA

<213> Homo Sapiens

<400> 584

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gctccctgat	ggagatggag	gggaaggagg	atgcccttta	aggtgctgaa	gtgcatgtac	180
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<210> 585

<211> 687

<212> PRT

<213> Homo Sapiens

<400> 585

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Ala Asn Pro Tyr Val Thr Pro Asn Asn Arg Tyr Gly Tyr Gln Asn Gly
  20          25          30
Ala Ser Tyr Thr Trp Gln Phe Glu Ala Arg Lys Ala Gln Ile Leu Lys
  35          40          45
Cys Met Glu Cys Gly Ser Ser His Asp Thr Leu Gln Gln Leu Thr Ala
  50          55          60
His Met Met Val Thr Gly His Phe Leu Lys Val Thr Thr Ser Ala Ser
  65          70          75          80
Lys Lys Gly Lys Gln Leu Val Leu Asp Pro Val Val Glu Glu Lys Ile
  85          90          95
Gln Ser Ile Pro Leu Pro Pro Thr Thr His Thr Arg Leu Pro Ala Ser
  100          105          110
Ser Ile Lys Lys Gln Pro Asp Ser Pro Ala Gly Ser Thr Thr Ser Glu
  115          120          125
Glu Lys Lys Glu Pro Glu Lys Glu Lys Pro Pro Val Ala Gly Asp Ala
  130          135          140
Glu Lys Ile Lys Glu Glu Ser Glu Asp Ser Leu Glu Lys Phe Glu Pro
  145          150          155          160
Ser Thr Leu Tyr Pro Tyr Leu Arg Glu Glu Asp Leu Asp Asp Ser Pro
  165          170          175
Lys Gly Gly Leu Asp Ile Leu Lys Ser Leu Glu Asn Thr Val Ser Thr
  180          185          190
Ala Ile Ser Lys Ala Gln Asn Gly Ala Pro Ser Trp Gly Gly Tyr Pro
  195          200          205
Ser Ile His Ala Ala Tyr Gln Leu Pro Gly Thr Val Lys Pro Leu Pro
  210          215          220
Ala Ala Val Gln Ser Val Gln Val Gln Pro Ser Tyr Ala Gly Gly Val
  225          230          235          240
Lys Ser Leu Ser Ser Ala Glu His Asn Ala Leu Leu His Ser Pro Gly
  245          250          255
Ser Leu Thr Pro Pro Pro His Lys Ser Asn Val Ser Ala Met Glu Glu

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260 265 270
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 Pro Pro Glu Lys Glu Lys Ser Ser Leu Ala Lys Ala Ala Ser Pro Ile
 290 295 300
 Ala Lys Glu Asn Lys Asp Phe Pro Lys Thr Glu Glu Val Ser Gly Lys
 305 310 315 320
 Pro Gln Lys Lys Gly Pro Glu Ala Glu Thr Trp Glu Ala Lys Lys Glu
 325 330 335
 Gly Pro Leu Asp Val His Thr Pro Asn Gly Thr Glu Pro Leu Lys Ala
 340 345 350
 Lys Val Thr Asn Gly Cys Asn Asn Leu Gly Ile Ile Met Asp His Ser
 355 360 365
 Pro Glu Pro Ser Phe Ile Asn Pro Leu Ser Ala Leu Gln Ser Ile Met
 370 375 380
 Asn Thr His Leu Gly Lys Val Ser Lys Pro Val Ser Pro Ser Leu Asp
 385 390 395 400
 Pro Leu Ala Met Leu Tyr Lys Ile Ser Asn Ser Met Leu Asp Lys Pro
 405 410 415
 Val Tyr Pro Ala Thr Pro Val Lys Gln Ala Asp Ala Ile Asp Arg Tyr
 420 425 430
 Tyr Tyr Glu Asn Ser Asp Gln Pro Ile Asp Leu Thr Lys Ser Lys Asn
 435 440 445
 Lys Pro Leu Val Ser Ser Val Ala Asp Ser Val Ala Ser Pro Leu Arg
 450 455 460
 Glu Ser Ala Leu Met Asp Ile Ser Asp Met Val Lys Asn Leu Thr Gly
 465 470 475 480
 Arg Leu Thr Pro Lys Ser Ser Thr Pro Ser Thr Val Ser Glu Lys Ser
 485 490 495
 Asp Ala Asp Gly Ser Ser Phe Glu Glu Ala Leu Asp Glu Leu Ser Pro
 500 505 510
 Val His Lys Arg Lys Gly Arg Gln Ser Asn Trp Asn Pro Gln His Leu
 515 520 525
 Leu Ile Leu Gln Ala Gln Phe Ala Ser Ser Leu Arg Glu Thr Thr Glu
 530 535 540
 Gly Lys Tyr Ile Met Ser Asp Leu Gly Pro Gln Glu Arg Val His Ile
 545 550 555 560
 Ser Lys Phe Thr Gly Leu Ser Met Thr Thr Ile Ser His Trp Leu Ala
 565 570 575
 Asn Val Lys Tyr Gln Leu Arg Arg Thr Gly Gly Thr Lys Phe Leu Lys
 580 585 590
 Asn Leu Asp Thr Gly His Pro Val Phe Phe Cys Asn Asp Cys Ala Ser
 595 600 605
 Gln Phe Arg Thr Ala Ser Thr Tyr Ile Ser His Leu Glu Thr His Leu
 610 615 620
 Gly Phe Ser Leu Lys Asp Leu Ser Lys Leu Pro Leu Asn Gln Ile Gln
 625 630 635 640
 Glu Gln Gln Asn Val Ser Lys Val Leu Thr Asn Lys Thr Leu Gly Pro
 645 650 655
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<210> 586

<211> 1898

<212> DNA

<213> Homo Sapiens

<400> 586

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gcctggacga naagctgcgg actctgctct accaggagca cgtgcccacc tctcagcct      240
cagctgggac ccctgtggag gtgggcgaca ganacttcac cctggagccc ctgagagggg      300
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cgggtctcagg gcgtgtccag ctgccccagc ccttgggtgga gaagtcagaa ctggccccca      420
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gtatgctagg ctatgacaga gatggaaggc aggtggcctc agactcccat gtgggtcccca      540
gcgtcccccga ggatgtacct gcttttgtga gacctgcacg tgtgganccc acanacaggg      600
atgggtggana agctgganaa agctcggcan agcccccgcc gagtgcacatg ggcanngtgg      660
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gtccagatca ccaggtggtc agctcaccag ccaagactgt gggccgtttc tcggtggtca      780
gcactcagga cgagtggacc ctggcctccc cccacagcct gagatactct gccccaccgc      840
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<210> 587

<211> 399

<212> PRT

<213> Homo Sapiens

<400> 587

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Ser Leu Ala Thr Ser Gln Leu Pro Ser Pro Pro Leu Gly Pro Thr Val
 20             25             30
Pro Pro Gln Pro Pro Ser Ala Leu Glu Ser Asp Gly Glu Gly Pro Pro
 35             40             45
Pro Arg Val Gly Phe Val Asp Ser Thr Ile Lys Ser Leu Asp Lys Leu
 50             55             60
Arg Thr Leu Leu Tyr Gln Glu His Val Pro Thr Ser Ser Ala Ser Ala
 65             70             75             80
Gly Thr Pro Val Glu Val Gly Asp Arg Phe Thr Leu Glu Pro Leu Arg

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85 90 95
 Gly Asp Gln Pro Arg Ser Val Cys Gly Gly Asp Leu Ala Leu Pro Pro
 100 105 110
 Val Pro Lys Glu Ala Val Ser Gly Arg Val Gln Leu Pro Gln Pro Leu
 115 120 125
 Val Glu Lys Ser Glu Leu Ala Pro Thr Arg Gly Ala Val Met Glu Gln
 130 135 140
 Gly Thr Ser Ser Ser Met Thr Glu Ser Ser Pro Arg Ser Met Leu Gly
 145 150 155 160
 Tyr Asp Arg Asp Gly Arg Gln Val Ala Ser Asp Ser His Val Val Pro
 165 170 175
 Ser Val Pro Gln Asp Val Pro Ala Phe Val Arg Pro Ala Arg Val Pro
 180 185 190
 Thr Arg Asp Gly Gly Ala Gly Ser Ser Ala Pro Pro Ser Asp Met
 195 200 205
 Gly Val Gly Gly Gln Ala Ser His Pro Gln Thr Leu Gly Arg Ala Leu
 210 215 220
 Gly Ser Pro Arg Arg Pro Asp His Gln Asp Val Ser Ser Pro Ala Lys
 225 230 235 240
 Thr Val Gly Arg Phe Ser Val Val Ser Thr Gln Asp Glu Trp Thr Leu
 245 250 255
 Ala Ser Pro His Ser Leu Arg Tyr Ser Ala Pro Pro Asp Val Tyr Leu
 260 265 270
 Asp Glu Ala Pro Ser Ser Pro Asp Val Lys Leu Ala Val Arg Arg Ala
 275 280 285
 Gln Thr Ala Ser Ser Ile Glu Val Gly Val Gly Glu Pro Val Ser Ser
 290 295 300
 Asp Ser Gly Asp Glu Gly Pro Arg Ala Arg Pro Pro Val Gln Lys Gln
 305 310 315 320
 Ala Ser Leu Pro Val Ser Gly Ser Val Ala Gly Asp Phe Val Lys Lys
 325 330 335
 Ala Thr Ala Ser Cys Arg Gly Leu Leu Gly Pro Ala Ser Leu Gly Pro
 340 345 350
 Glu Thr Pro Ser Arg Val Gly Met Lys Val Pro Thr Ile Ser Val Thr
 355 360 365
 Ser Phe His Ser Gln Ser Ser Tyr Ile Ser Ser Asp Asn Asp Ser Glu
 370 375 380
 Leu Glu Asp Ala Asp Ile Lys Lys Glu Leu Ser Leu Arg Glu Lys
 385 390 395

<210> 588

<211> 707

<212> DNA

<213> Homo Sapiens

<400> 588

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caaaagttgc acagaagtca tatggaaatg aaanaaggtt tttttgcca cctccttggtg      180
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ctgaacaaaa gtctcaaccg tgtgcattta ttgggatagg aaatagtgac caaaaaatgc      300
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attgaaaaat gctgacttat gcattgcctc angaacaaa gtggctctgt ttaatcgact      540

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acnatcccan	acagttagta	ccagatactt	gcatgttana	aggaggtnat	tttcatgcca	600
gttcacagcn	gtggggagcc	ttttttattc	anctcttgga	tgatgatgan	tcnaaggag	660
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<210> 589

<211> 551

<212> DNA

<213> Homo Sapiens

<400> 589

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<210> 590

<211> 478

<212> DNA

<213> Homo Sapiens

<400> 590

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ttttgttaac	ttttngccac	actcaantca	gtttaagtcc	tagcaaaaan	acggtagtta	180
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<210> 591

<211> 707

<212> DNA

<213> Homo Sapiens

<400> 591

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<210> 592
 <211> 541
 <212> DNA
 <213> Homo Sapiens

<400> 592
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 attaaaatcc tntcctgtaa ttccaagcat ggctacttcc ccaccgccat tcaactnaag 480
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<210> 593
 <211> 605
 <212> DNA
 <213> Homo Sapiens

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 gaaag 605

<210> 594
 <211> 666
 <212> DNA
 <213> Homo Sapiens

<400> 594
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 acttattctt catgcaaaaag ttgcacagaa gtcatatgga aatgaaaaaa ggtttttttg 180
 cccacctcct tgtgtatatc ttatgggcag tggatggaag aaaaaaaaag aacaaatgga 240
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 tgaatc 666

<210> 595

<211> 600
 <212> DNA
 <213> Homo Sapiens

<400> 595
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<210> 596
 <211> 835
 <212> DNA
 <213> Homo Sapiens

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 ggataccact gtggctgtaa atnatgtgac actggttgaa tttgtgctgg cgtttgtgta 240
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 gattgctcct gctgcactgc aatgtggccg cggccctggt tctggtgtgt aggtaaagg 360
 aaggctggtg gaataaatga ttccatcatt tcggaccaa gttactggaa cctggactgg 420
 ttgccggacc catctccaac cttctcggaa tgcagaaatg tctgggacga cacanancat 480
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 tggagtgaat ttctgtcctg taagttcaag cattgctacg tccccaccgc cattcaactg 600
 aaggcctcta cacaggcaca ggaatgactg gggcaaggan agggccatt cctcataaa 660
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 tcnttattgg ttcttttggg antggaatgg cctgaaattg aaatattctt ccttgaaaaa 780
 aggccaaata cntcttctgt ttctttnaag ggtaaaatgc ccatttttgg aattg 835

<210> 597
 <211> 443
 <212> DNA
 <213> Homo Sapiens

<400> 597
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 tggatgctcg atttctctg cctctctctt tgccgagctt tccgcnacgg ccgctccgag 180
 gacttcnncn ggacccgcaa cagcgcanag gctattattc atggactatc cagtctaaca 240
 gcttgccagt gagaacgata tacatatgtc agtttttgac aagaattgca gcaggaaaaa 300
 cccttgatgc ncagtttgaa aatgatgaac gaattacacc cttggaatcn gccctgatga 360
 tttgggggtc aattgaaaag gaacatgacn aacttcntga agaaatacag aatttaatta 420
 aaattcangc tatngctgtt tgt 443

<210> 598
 <211> 491
 <212> DNA

<213> Homo Sapiens

<400> 598

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gaggattcag ttaccgcaga ctgtttgtca ctaacacttt ttcttgatc caaattagct      180
tcagtttcca tttcaacatc attaccacta gggttatctt gagaagttat tgttcttgct      240
cttttgcttt ctactacttt tgcgcgtgcc ttcattagaa aggttgatga ttttccactt      300
agcacataat tcacataact cttaattttc tccatcatgt ggttgtagct gaagtgttga      360
aaaaaggaat gaaatgtatc tttctgagan attatcataa gcaatttgct tttgaaaggc      420
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<210> 599

<211> 802

<212> DNA

<213> Homo Sapiens

<400> 599

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gaggattcag ttaccgcaga ctgtttgtca ctaacacttt ttcttgatc caaattagct      180
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attcggtcat cattttcaaa ctgtgcatca aggggttttc ctgctgcaat tcttgtaaaa      660
aactgacata tgtntatcgt tctcaactgg cnagcctggt aaactggaaa atccatgaat      720
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<210> 600

<211> 523

<212> DNA

<213> Homo Sapiens

<400> 600

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gccaggaggc gtggaggggc ccagggatgg cccccccac agggagtcag ggagggcctg      180
gggcgacagc ggaaagggtta agcgtcnaaa aggtcaagtg ctaccgtgga naaatcatct      240
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gggctttcct gtcacaaana ttaaaaaacc cnaaatgca tttgaacaac atnatacacn      360
ataacaaatt taaaccttgc tctctgttcc cactgggttna accctggccc atccccatc      420
cctggtccca tcccaggggc ccagcctccg atnactcctc anaaacacng ccttnntgct      480
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<210> 601

<211> 530

<212> DNA

<213> Homo Sapiens

<400> 601

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ccaaaaangct	tnaaggggcc	cagggatngc	cncccccnca	gggattcngg	gagggcctgg	180
ggcaanancg	naaagggttaa	ccntcnaaaa	ggtcaattnc	taccgtgnaa	aaatnatctn	240
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tnncaatttt	naaccttgcn	cctctntccc	actgggtnaa	ccctggccca	tcccccatcc	420
ctgggcccnt	ccnnggggcc	caccccccnca	taacttcctc	aaaaaacngc	cttnttntctg	480
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<210> 602

<211> 311

<212> DNA

<213> Homo Sapiens

<400> 602

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gganccgctg	cggntnccgn	tgtgccnctt	ggtgcncgga	anancanggc	tacngnttct	180
acctntacgt	gtganannng	ccgccgcggg	cacttctntcc	ggcgcgtgna	ncctctgttc	240
ccccgccgag	gcngccgcgc	tgtgctctgg	ggatctnctg	ntcnaggtea	acntgcntca	300
acgtgnaggg	c					311

<210> 603

<211> 289

<212> DNA

<213> Homo Sapiens

<400> 603

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tatnangaan	anaaccatca	ncnncntcc	ctttcantca	tctggcncct	gcanaccatc	180
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<210> 604

<211> 356

<212> DNA

<213> Homo Sapiens

<400> 604

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tgtgccgctt	ggtgcgcgga	nagcanggct	acggcttcca	cctgcacggg	gagaangggc	180
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gcgctgggga	ccgcntgntc	naggtcnacn	gcgtcaacnt	ggagggcgat	accaccnct	300
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<210> 605

<211> 290

<212> DNA

<213> Homo Sapiens

<400> 605

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nnantcgact	nccaccaact	gtnnntcttc	cttcccttcc	cnangtcctt	anntaccncc	180
tnttgccctt	ctnccccctn	tttccccctn	cgctttccct	nactctttat	ctntcttntc	240
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<210> 606

<211> 714

<212> DNA

<213> Homo Sapiens

<400> 606

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atgcagataa	ttaaactttac	atgaaaaagg	aaaattataa	caaaggactg	agaacgttat	180
aaattgaaat	gagattataa	tttgaaaact	gcactctgaa	gcaaacttta	ttgttcaatt	240
atncttaatg	atggtgtttt	atgactaata	cactgatttt	tcaagaagga	aacctatggt	300
aaaaatat	ttattttaaa	aataagcctg	tgttcaagct	ctgatcatat	ttcttttatt	360
ttgatttggg	aanaaaatac	tgtttctgat	agcatgaaat	gcaaaat	tagattttta	420
atctcactaa	ttttaanaac	tattgagaaa	ttgattaatg	acatgaagtg	cacaacacta	480
attactggcc	agctgttggc	attgtgttcc	ttacttagtt	ctccaagg	aaaactctta	540
aattgaatct	tcagcagaat	aatccttaaa	tatactttgt	aagcaaaaca	aaagcttttt	600
tgtttacata	gttctttggg	attttaactgt	tcctaatttt	attctgaaac	tcaattttac	660
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<210> 607

<211> 687

<212> DNA

<213> Homo Sapiens

<400> 607

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acttacatga	aaaaggaaaa	ttataacaaa	ggactgagaa	cgttataaat	tgaaatgaga	180
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aaatactgtt	tctgatagca	tgaaatgcaa	aattttttaga	tttttaattct	cnctaatttt	420
aagaactatt	gagaaattga	ttaatgacat	gaagtgcaca	acactaatta	ctggccagct	480
gttggcattg	tgtttcttac	ttagtctctc	caaggaaaac	tcttaaaactg	aatcttcagc	540
ngaataacct	taaatatact	ttgttagcca	aacaaaactt	ttttgtttac	atagttcttt	600
ggattttact	gttcctaatt	ttattctgaa	actccatttt	tccccagacc	ataattaccc	660
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<210> 608

<211> 994

<212> DNA

<213> Homo Sapiens

<400> 608

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accgcatttc	ccagttccaa	gatgaatata	gtttagatga	agtgatggca	tctaaagaag	180
tttttgattt	tttgactatc	ttacaatggt	gtcccacttc	agatggtgct	gcagcagcaa	240
ttttggccag	tgaagcattt	gtacagaagt	atggcctgca	atccaaagct	gtggaaattt	300

tggcacaaga	aatgatgact	gatttgccaa	gctcgtttga	agaaaaaagc	attattaaaa	360
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caccaaata	tattgacgta	atagaacttc	acgattgctt	ttctaccaac	gaactcctta	480
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<210> 609

<211> 843

<212> DNA

<213> Homo Sapiens

<400> 609

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tngcaaatan	ttaaccttnc	ttgaaaangg	aaatttntac	caanggaacng	aaancnttnt	180
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tggattgggg	aaaaaaatnc	ngttccnnat	accnngaann	gcaaantttt	taaattttta	420
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<210> 610

<211> 707

<212> DNA

<213> Homo Sapiens

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<211> 663
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 <213> Homo Sapiens

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 tga 663

<210> 612
 <211> 621
 <212> DNA
 <213> Homo Sapiens

<400> 612
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 aagtaatctc anaaaaaaaaa ggttttttga aattaaactt gactttttaa aaatcatacg 180
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<210> 613
 <211> 637
 <212> DNA
 <213> Homo Sapiens

<400> 613
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 tantntnctn aaaaaaaaga ggtttganga aattaaactt gactttttaa anatcatgng 180
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 aanacttct tgtcccaggc cctnctnaaa aaaacctctt gtggaaaccn agcnaaaaat 300
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<210> 614

<211> 673
 <212> DNA
 <213> Homo Sapiens

<400> 614
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 cttgaaggct acaagtggca aggaagattc tttttcaaat atagccacag aaataaagga 180
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<210> 615
 <211> 714
 <212> DNA
 <213> Homo Sapiens

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 tccttttatt tntgttanc atatcnaagc aaaatctggt ttgtcccttg ttacctttg 660
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 <213> Homo Sapiens

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<210> 617
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 <212> DNA
 <213> Homo Sapiens

<400> 617
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<210> 618
 <211> 461
 <212> DNA
 <213> Homo Sapiens

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 <212> DNA
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 aactgaaggc ccccgggcc ggaccattac ggaacaagtg ctgtcccttg naggagaaaa 660
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 <211> 556
 <212> DNA
 <213> Homo Sapiens

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<210> 621
 <211> 708
 <212> DNA
 <213> Homo Sapiens

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 caacaaaaac ttgtttaaat ngttccttna atttnnacta cttaaaanca taggtntaaa 180
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 aaaaactnat atattccaaa ttcncggcat ntggnaatnt tnccatggac nctgnatctt 300
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 tggatnanaa cctttttcta catnactatt gaaaaaacct gtggtttctt gctttttaac 660
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<210> 622
 <211> 675
 <212> DNA
 <213> Homo Sapiens

<400> 622
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 gattctcaaa acttaaatc aagaaggagc cctgtcccag ctcaaatagc tataactgta 180
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<210> 623
 <211> 713
 <212> DNA
 <213> Homo Sapiens

<400> 623
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 gtgaaacttt ttaaaaaaat acttaaattg tttcttttgt ttcattttgt gtatttgaag 300
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 cagtgtccac tctgaaggta naagaatcng gttattatag cttgctttaa caaacagcng 660
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<210> 624
 <211> 554
 <212> DNA
 <213> Homo Sapiens

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 tggctatctt cnaggatttg gttggtaaat gtgaccctcg agaanaagca gcgaaagaca 180
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 aattaaagct gaattagcta aaaccaatgg agaattaatc tcnaccncnc acnanttcnc 300
 ccagaganaa natgaatccg attcattgat tcaagagctt gagacatctg ntaaganaat 360
 aattnacana aatctggaga attnnagaat tgatnaatat nattgatcnn tcgaagatac 420
 tatcanogaa tttcagaacc tnangtctca tatggaaaac tcnttttaaat gcnatgacaa 480
 ggctgataca tcttctttaa taataaacia taaattgatt tgttatgaaa cagttgaagt 540
 acctaaggga cagc 554

<210> 625
 <211> 551
 <212> DNA
 <213> Homo Sapiens

<400> 625
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 tggggatggt taatgggtac aaaaacaaat aagatnaaaa gaatgattta atatctgata 180
 gcacaatana ntgactataa tcaataataa cttacttgta tttttttaa tgatctaaaa 240
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 ctccatgata cacgtntttc acattgatgc ctgtgtcaaa acatctcaca taccctgtaa 360
 atatatacat gtactatgta ccacaaaatg tttacaaaat aagtganaca ttctaattaa 420
 agactgaaat ctttttctaa ataattgata tacatgtttt gtgatctgta cacacttatt 480
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 aaaaaaatcc t 551

<210> 626
 <211> 680

<212> DNA

<213> Homo Sapiens

<400> 626

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tgccaaactgt	tgtgctttcc	agtgtatcag	tggttgctac	attctccttc	ttgtcttcgg	240
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cgactcgatc	aatgcccatg	ccccagccag	ctgtgggggg	cagcccatat	tccagggcag	360
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<211> 753

<212> DNA

<213> Homo Sapiens

<400> 627

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gtncaaaaca	atggttaggat	ccaagttgac	cnaactcctt	atggtgactc	ccatggtggt	720
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<210> 628

<211> 675

<212> DNA

<213> Homo Sapiens

<400> 628

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gttaaancca	ccttaacata	aaccttatng	caattntaca	cntcttttga	acncaatcta	180
taaaaaaaaa	aataactncc	anggcattac	aacttttnct	ctggcatntt	aaaaaacaac	240
tctnactaat	ggctaattgca	ttataaaaatt	ncctatctna	caaactctnc	taaattatgc	300
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tatnggccca	taacaaaant	tcctnccagg	ttattttta	ntnttaacnt	aaaaaaacnc	420
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 <212> DNA
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<210> 630
 <211> 665
 <212> DNA
 <213> Homo Sapiens

<400> 630
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<210> 631
 <211> 698
 <212> DNA
 <213> Homo Sapiens

<400> 631
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 tgatgttact ggtcaatggc agtaatcctg aagggtgaaga tcttgagagg gaacctgtan 180
 aaaatgaaga ttatagagaa aagtcttcag atgatgatga aatggattct tcttgggtct 240
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698

<210> 632

<211> 466

<212> DNA

<213> Homo Sapiens

<400> 632

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gacctgtnc	ttatcatata	acttcaaaaa	ggaaagctcc	ttantccaaa	aagcctanat	420
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<210> 633

<211> 734

<212> DNA

<213> Homo Sapiens

<400> 633

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ncacctatgg	tatgtctgat	attaaattta	acattttcaag	taacatatat	atagcaaaca	600
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<210> 634

<211> 822

<212> DNA

<213> Homo Sapiens

<400> 634

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tctaatacaa	gtacttccat	tgtaaacaga	atacatccaa	gtactgccag	cacggtagt	660
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<210> 635

<211> 819

<212> DNA

<213> Homo Sapiens

<400> 635

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<210> 636

<211> 704

<212> DNA

<213> Homo Sapiens

<400> 636

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<210> 637

<211> 693

<212> DNA

<213> Homo Sapiens

<400> 637

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<210> 638

<211> 619

<212> DNA

<213> Homo Sapiens

<400> 638

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<210> 639

<211> 694

<212> DNA

<213> Homo Sapiens

<400> 639

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<210> 640

<211> 728

<212> DNA

<213> Homo Sapiens

<400> 640

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<210> 641

<211> 732

<212> DNA

<213> Homo Sapiens

<400> 641

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<210> 642

<211> 582

<212> DNA

<213> Homo Sapiens

<400> 642

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<210> 643

<211> 784

<212> DNA

<213> Homo Sapiens

<400> 643

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aaaaaacagt	agttttgcc	ccattgttg	ccagcagagg	acaatcagag	gagcctgcag	420
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<210> 644

<211> 749

<212> DNA

<213> Homo Sapiens

<400> 644

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<210> 645

<211> 751

<212> DNA

<213> Homo Sapiens

<400> 645

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<210> 646

<211> 760

<212> DNA

<213> Homo Sapiens

<400> 646

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<210> 647

<211> 1041

<212> DNA

<213> Homo Sapiens

<400> 647

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<210> 648

<211> 810

<212> DNA

<213> Homo Sapiens

<400> 648

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<211> 656

<212> DNA

<213> Homo Sapiens

<400> 649

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<210> 650

<211> 645

<212> DNA

<213> Homo Sapiens

<400> 650

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aantggtnca	aatantgcgn	aacncaaaaac	tttnactaat	acaattgctt	taaatntaaa	120
ncaaaanttat	tttttataaaa	acaaaaaaa	taaaaaatnt	ttccaaangg	gacctgaaan	180
ctntaaccta	atccccaaaa	caaaataatt	aaaaannccn	nggtnaancc	tnaacntnct	240
nccnctnctt	tgnaaaaggg	ctatcanaca	acntncattc	ncctaaaaat	gnatnggtaa	300
aggtttttct	anacataaac	ttcattcatt	ttggcttntn	caaaaancacc	ccaanctncc	360
caaaactnaa	tgggcnncc	ntggcttnt	ccttttccca	tnntcccaac	aagggtactt	420
naattncaac	ncttnataac	ccccttacia	caccattncc	ttagnacca	cataacaggt	480
gggtcaaat	ncccnataaa	aaacaaanct	ggccccncc	ccaaaatncc	caaagggta	540
ttcctnccn	ccctcccccc	ngnatatata	caacatntcc	cctttcanaa	atatattccc	600
ccacgcttat	tcnccccaaa	nntaancctt	gaagttattt	aagga		645

<210> 651

<211> 780

<212> DNA

<213> Homo Sapiens

<400> 651

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ctcttttctc	cgacattttt	atgtttctaa	cattgaactc	taaggaagct	ggtgaacaaa	120
cacgccatat	gtatgcagaa	cacttaacag	aattatgcta	tgttgtctgt	ttttgtttgt	180
atttcttgtc	cttgctgaag	attgacttga	aatcttaaac	taagttctcc	ctctttatag	240
gcggtgacag	tgatcctcca	ttaaagcgta	gcctggcaca	gaggctaggg	aagaaagttg	300

aagctccaga	aactaacatt	gacaaaacac	caaagaaagc	tcaagtttcc	aagtctctta	360
aggagcgatt	aggcatgtca	gctgatccag	ataatgagga	tgcaacagat	aaagttaata	420
aagttgggtga	gatccatgtg	aagacattag	aagaaattct	tcttgaaaga	gccagtcaga	480
aacgtggaga	attgcaaact	aaactcaaga	cagaaggacc	ttcaaaaact	gatgattcta	540
cttcaggagc	aagaagctcc	tccactatcc	gtatcaaaac	cttctctgag	gtcctggctg	600
aaaaaaaaaca	tcngcagcag	ggaactgaag	agacaaaaaa	gccnaaagga	tacaacttgc	660
atcaagctaa	agattgatag	tgaaattaaa	aaaaacagta	attttngcca	cccattgttg	720
ccngcagaag	acaatcanaa	gaacctgcag	gtaaaacaaa	ntctatgcag	ggaggtgccc	780

<210> 652

<211> 518

<212> DNA

<213> Homo Sapiens

<400> 652

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aatgggttca	aataatgagg	aacacaaaac	nttnactaat	acaattgctt	taaatntnaa	120
acaaaattat	tttttaaaaa	ancaaaaaaa	taaaaaatnt	ttncaaaang	gacctgaaat	180
ctntaanctn	atnccaaaaa	caaaataatt	naaaaaatcca	nggtgaaacc	tnaacntnct	240
nccnctgctt	tggaagagg	ctntcatata	acnttcattc	ncctaaaaat	ggattggtaa	300
angttttnt	atacataaac	tncattcatt	tttgcttntg	caaaatcanc	ccaanctncc	360
caaaactnaa	tgggcantcc	tntggctttc	tncctttccc	anatncccaa	caaggctact	420
tnaatattca	oncttnataa	nccgcttaca	acancatttc	cttaggancc	aacatnacgg	480
tggtgtcaaat	cccctataaa	aaacaaaact	ggcncct			518

<210> 653

<211> 490

<212> DNA

<213> Homo Sapiens

<400> 653

gttaataaaag	ttggtgagat	ccatgtgaag	acattagaag	aaattcttct	tgaaagagcc	60
agtcagaaac	gtggagaatt	gcaaaactaaa	ctcaagacag	aaggaccttc	aaaaactgat	120
gattctactt	caggagcaag	aagctcctcc	actatccgta	tcaaaacctt	ctctgaggtc	180
ctggctgaaa	aaaaacatcg	gcagcaggaa	gcagagagac	aaaaaagcaa	aaaggataca	240
acttgcatca	agctaaagat	tgatagtga	attaaaaaaa	cagtagtttt	gccaccatt	300
gttgccagca	gaggacaatc	agaggagcct	gcaggtaaaa	caaagtctat	gcaggagggt	360
gcacatcaag	acgctggaag	aaattaaact	ggagaaggca	ctgaggggtgc	agcagagctc	420
tgagagcagc	accagctccc	cgtctcaaca	cnaggccact	ccaagggcaa	ggcggctgct	480
gnaatcccc						490

<210> 654

<211> 359

<212> DNA

<213> Homo Sapiens

<400> 654

cccantccn	ttttanttna	aancccaacc	aatntttccc	cttccgntan	gggcaatngn	60
tccaattatn	ncgaacncca	aaccttnaan	natnccaatt	ncttaaatnt	taaaccaaat	120
tnntttttta	aaaagccaaa	naattaagaa	ttttttccaa	agggaaacng	aatecnntag	180
ggtaatccca	aaaccaaatt	agttaaaaat	ccctggntaa	accnnaacnt	tcnccnccn	240
ccttggaaaa	agggmnnccn	ncnaccttcc	atnccnntaa	aatgaatgg	ntaaagnttt	300
ttcnnnccct	aacntccatc	ctttttgnct	nttccaaanc	ctccccance	tecccaaaa	359

<210> 655

<211> 611
 <212> DNA
 <213> Homo Sapiens

<400> 655
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 catcangcta angattgata gtgaaattaa aaaaacagta tttttgccac ccattgttgc 120
 cancagagga caatcanagg agcctgcagg taaaannaag tctatgcagg aggtgcacat 180
 caagacgctg gaagaaatta aactggagaa ggcactgagg gtgcagcana gctctgagag 240
 cagcaccagc tccccgtctc aacacnaagc cactccatgg gcnangcggc tgctgcgant 300
 cncnaaaga ncagggatga angaagagaa gaaccttcag gaaggaaatg aatttgattc 360
 tcagancatt attataactg aagctnnana ngcttcnggt gagaccacng ganttgacat 420
 cactaaaatt ccagtcgaaga gatgtgagac catgagagag aagcacatgc acaaaacanc 480
 nngagaggga aaaatcagtc ttgacacctc ttgggggaga tgtagcatct tgcggnaccc 540
 aantggcaga gaaaccagtg ctactgctg tgccaggaat cacncggcac ctgaccaagc 600
 ggcttccac a 611

<210> 656
 <211> 634
 <212> DNA
 <213> Homo Sapiens

<400> 656
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 tcaaataatg cggaacacna aacattgact aatacaantn ctttaaatat gaaacaaaat 120
 tatttttttaa aaaancnaaa naataaagaa tatntncaaa agggacctgg aatctgt nag 180
 ctgattccaa aaacnaaata anttnaaaat ccntgggtgaa acctgaacat tctacctctg 240
 ctttggaataa gggntatcat acaacattca gtcngctgaa aatggattgg taaaagtntn 300
 tctatacata aacttcagtc atttttgctt gtncaaaatc atcccaatct tcccaaaant 360
 gaatgggcag tcctgtggct ttcttccttt tccatattcc caacaaggnt acntnaantt 420
 caactcttga nnanccgctt acaacagcag ttccttagga nccccatgac aggtgggtcn 480
 aatttcccta tnaaaaacaa aactggggcc tacagcaaaa tatccaaatg ggtnagtctt 540
 tccttcctct tccccgtant atatacacat atctcctttc aanaatanta tttcccatg 600
 cttattcctt ccnaatcta aaccttgaag tgat 634

<210> 657
 <211> 958
 <212> DNA
 <213> Homo Sapiens

<400> 657
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 tgaaattcta cctcctaaga aaatgaaagt ttctaacaac aaaaagaagc cagaggaaga 120
 aggcagtgt catcaagata ctgctgaaaa gaatgcatct tccccagaga aagccaaggg 180
 tagacatact gtgccttgta tgccacctgc aaagcagaag tttctaaaaa gtactgagga 240
 gcaagagctg gagaagagta tgaaaatgca gcaagagggt gtggagatgc ggaaaaagaa 300
 tgaagaattc aagaaacttg ctctggctgg aatagggcaa cctgtgaaga aatcagtgag 360
 ccaggtcacc aaatcagttg acttccactt ccgcacagat gagcgaatca aacaacatcc 420
 taagaaccag gaggaatata aggaagtga ctttacatct gaactacgaa agcatccttc 480
 atctcctgcc cgagtgaacta agggatgtac cattgttaag cctttcaacc tgtcccaagg 540
 aaagaaaaga acatttgatg aaacagtttc tacatatgtg ccccttgac agcaagttga 600
 agacttccat aaacgaacc ctaacagata tcatttgagg agcaagaagg atgatattaa 660
 cctgttacc tccaaatct ctgtgaccaa gatttgacga gaccacagg actcctgtac 720
 tgcaacaan acaccgtgca cgggctgtga cctgcaaaaa gtacagcaga gctggaggct 780
 gaggagctnc gagaaattgc aaccantaca anttccaaag cacgtngaac cttgattccc 840

agaataactt	ganggggtggg	cccaaccttg	cccaagaaaa	ccaccngtga	aancaancca	900
acggagccct	antnggcttt	gatttgggaa	tttgggaaan	gaatncaagg	gaggngag	958

<210> 658

<211> 816

<212> DNA

<213> Homo Sapiens

<400> 658

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tccctgttgt	tatcagcacc	agtaaggaaa	gaactgtgct	taacggcagc	cccacccaga	120
gectgtctgcg	tggctgtctgt	gaggtcctcc	atgaatccac	gcagtcttct	tctcactggg	180
tgcagttgggt	gaggtttttct	accctcacag	caaagggatc	cttaactata	aattcacggt	240
atgcagagaa	gaggacagaa	tctgattttac	tgattgttcc	tcattttaaac	catgacttaa	300
tctctatctt	aggatttaac	tatcttttatt	ttctggttaa	aattttttaa	aaaagtgggg	360
agaggggtgag	agtcgtaagg	ggcaatagca	atagagatta	cactgtgctg	acacagagac	420
taaattctag	tcagagtga	gaccatataa	aaggccggct	gatggtttta	aggaagtaac	480
tacatggagt	ctaactcgaga	cattcatgan	ttacatctca	ttattagcct	tagtaatgta	540
agaaaaaact	tctcaacaaa	actgggagtc	cacagttgtc	aagtatgctt	tctcangcac	600
gggtaggttaa	aagtctggan	aaatgggttc	tctccatgcc	caatgacaaa	gcaagacggt	660
cctaggtttg	aagttaaaaa	caggtcccaa	ttgcccggtc	ggtatccgcc	agctcacagc	720
tgaatttaan	catggaaatc	caatggaaaa	attggganat	acnggcacat	tcanaaggct	780
ggtcctttga	cttatctcca	naaccgggt	actggc			816

<210> 659

<211> 726

<212> DNA

<213> Homo Sapiens

<400> 659

tgagaaaagt	ggtacaaata	ctgggaaaaa	cctgctcttc	tgcgttaagt	gggagacaat	60
gtcacaagtt	aaaagctctt	attcctatga	tgccccctcg	gatttcatca	atttttcatc	120
cttggatgat	gaaggagata	ctcaaaacat	agattcatgg	tttgaggaga	aggccaattt	180
ggagaataag	ttactgggga	agaatggaac	tggagggtct	tttcagggca	aaactccttt	240
gagaaaaggct	aatcttcagc	aagctattgt	cacacctttg	aaaccagttg	acaacactta	300
ctacaaaagag	gcagaaaaag	aaaatcttgt	ggaacaatcc	attccgtcaa	atgcttgctc	360
ttccctggaa	gttgaggcag	ccatatcaag	aaaaactcca	gcccagcctc	agagaagatc	420
tcttaggctt	tctgctcaga	aggatttggg	acagaaagaa	aagcatcatg	taaaaatgaa	480
agccaagaga	tgtgccactc	ctgtaatcat	cgatgaaatt	ctaccctcta	agaaaatgaa	540
agtttctaac	ancacaaaga	agccagagga	agaaggcagt	gctcatcaag	atactgctga	600
aaagaatgca	tcttccccaa	gagaaagcca	agggtagaca	tactgtgcct	tgtatgccac	660
ctgcanagca	gaagtttcna	aaangtactg	angagcaang	aatctggaga	agagtatgaa	720
aaatgc						726

<210> 660

<211> 824

<212> DNA

<213> Homo Sapiens

<400> 660

aggatttaac	tatcttttatt	ttctggttaa	aattttttaa	aaaagtgggg	agaggggtgag	60
agtcgtaagg	ggcaatagca	atagagatta	cactgtgctg	acacagagac	taaattctag	120
tcagagtga	nacccatata	aaaggccggc	tgatggttta	aaggaagtaa	ctacatggag	180
tctaactcgag	acattcatga	gttacatctc	attattagcc	ttagtaatgt	aagaaaacaa	240
ttctcaacaa	aactggagtc	cacagttgtc	aagtatgctt	tctcaggcac	gggtaggttaa	300

aagtctggan	aaatgggttc	tctccatgcc	caatgacaaa	gcaagacggt	cctaggtttg	360
aggttaagan	caggtcccat	tgcggggcgg	tatccgcage	tcacagctga	ntttagcagt	420
ggaatcgagt	ggagaatttg	gggagatata	ggcncagtc	gaggtcgttc	acttgacttt	480
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ctggccanct	cctctttttt	ctgctcttcc	tctgtagtc	tggcctcctc	caactgctgg	600
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ctctcagtag	cccactgaaa	angtccctga	acnaaaaaaa	ccanaaanng	gccctcacia	720
ctgatttcnt	ctctttcttg	gggaaccaag	ggccccctga	aaaanaaacg	gtgtttggaa	780
caaaccntga	aacaagcngc	ctcctttctgc	ctgtcccaat	tcct		824

<210> 661

<211> 399

<212> DNA

<213> Homo Sapiens

<400> 661

ggtttgnagg	gaaaaanaaa	actttttttt	cccagnccag	ttcttaaant	nccccnngcn	60
nggtccctn	tnnttttctc	ccccattaag	gaaaaaactt	gcntnancgg	nagccccccc	120
caaaacctnc	tgcttggttg	ctttaaggnc	cccataannc	ccccatnnt	cctccccac	180
tggtncattg	gtnagggttc	ctcccccccn	ccaaaggmnt	ccttacntat	aatccccngg	240
tttncaaaaa	aaaanaaaaa	accaatttct	gatntcccc	cttnaancca	gnacttaatc	300
cctntctnag	gattnaacaa	cctttttttt	cgggttaaaa	tttttaaaaa	aattngggaa	360
anggttaa	at	aatnccnata	aaaattacc			399

<210> 662

<211> 826

<212> DNA

<213> Homo Sapiens

<400> 662

gtcaaatgct	tgttcttccc	tggaagttga	ggcagccata	tcaagaaaaa	ctccagccca	60
gcctcagaga	agatctctta	ggctttctgc	tcagaaggat	ttggaacaga	aagaaaagca	120
tcattgtaaaa	atgaaagcca	agagatgtgc	cactcctgta	atcatcgatg	aaattctacc	180
ctctaagaaa	atgaaagttt	ctaacaacaa	aaagaagcca	gaggaagaag	gcagtgtctc	240
tcaagatact	gctgaaaaga	atgcattctc	tctaaaaagt	cccagagaaa	gccaagggtg	300
gccttgatg	ccacctgcaa	agcagaagtt	actgaggagc	aagagctgga		360
gaagagtatg	aaaatgcagc	aagaggtggt	ggagatgcgg	aaaaagaatg	aagaattcaa	420
gaaacttgct	ctggctggaa	tagggcaacc	tgtgaagaaa	tcagtgagcc	aggtcaccaa	480
atcagttgac	ttccacttcc	gcacagatga	gcgaatcnaa	caacatccta	ngaaccagga	540
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gaantgacta	aggggatgtt	ccattgttaa	gcctttcaac	ctgtcccngg	gaaagaanag	660
aacntttgat	gaaacagttt	ctacatatgt	gccccttgcc	cngcaagttg	aagacttccn	720
taanccaacc	ctnactgatt	tcttttgang	aaccagaang	gntgattttt	ccctgtttcc	780
ctccaatctt	ctgtgaacaa	gatttggcgg	aanacccccg	aacccc		826

<210> 663

<211> 770

<212> DNA

<213> Homo Sapiens

<400> 663

gggaaagaca	aaacgtat	attccaggcc	aggtcttaaa	atgcacactg	cacggttccc	60
tggtgttata	agcaccagta	aggaaagaac	gtgccttaac	ggcagcccca	cccanagcct	120
gctgcgtggc	tgctgtgagg	ctccccatga	atccacgcag	tcttcttcc	cactggtgca	180
gttggtgagg	ttttctaccc	tcacagcaaa	gggatcccta	actataaatt	cacggtatgc	240

anagaanagg	acagaatctg	atttactgat	tggttcctcat	ttaaaccatg	acttaatctc	300
tatcttagga	tttaactatc	tttattttct	ggttaaaatt	tttaaaaaaa	gtggggagag	360
ggtagagatc	gtaaggggca	atagcaatag	agattacact	gtgctgacac	agagactaaa	420
ttctagtcag	agtgaagacc	catataaaaag	gccggctgat	ggtttaaagg	aagtaactac	480
atggagtcta	atcgagacat	tcatgagttt	catctcatta	ttagccttag	taatgtaaga	540
aaacnattct	caacaaaact	ggagtccaca	gttgtcaant	ntgctttctc	aggcacgggt	600
aggtnaaaat	ctgganaaat	gggttctctc	catgcccaat	gacaanacan	anggtcctag	660
gtttgaagtt	aaaaaacangt	cccattgccg	goggtatccg	cagctcacag	ctgaattttac	720
cngtggaatc	aantggaaaa	tttgggaaaa	tacnggccca	atcaaaaagg		770

<210> 664

<211> 593

<212> DNA

<213> Homo Sapiens

<400> 664

gaaganctga	gcagcacagc	actggtgaag	aagagctgcc	tggcggagct	cctccggctt	60
tacacaaaaa	gcagcagctc	tgatgaggag	tacatttata	tgaacaaagt	gaccatcaac	120
aagcaacaga	atgcagagtc	tcaaggcaaa	gcgcctgagg	agcagggcct	gctaccaaat	180
ggggagccca	gccagcactc	ctcgccccct	cagaagagcc	ttccagacct	cccgccacce	240
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tcctacgagt	cctacgatga	anaggacggc	agcaagggca	agtccggccc	ttaccantgg	420
ncctcgccgg	aggccggcat	cgantgatg	cgtgacgccc	gentctgcgc	cttctgtggg	480
cgcaagaaag	tggctgggac	agtgggccaa	gcagctctgt	gtcatcnagg	acaacaggct	540
tctgtgctnc	naatcctcca	aggaccccng	ccctcagctg	gacgtgaacc	tac	593

<210> 665

<211> 1024

<212> DNA

<213> Homo Sapiens

<400> 665

aagagattga	agcaaatgaa	tggaagaaga	aatacgaaga	gacccggcaa	gaagttttgg	60
agatgaggaa	aattgtagct	gaatatgaaa	agactattgc	tcaaatgatt	gaagatgaac	120
aaaggacaag	tatgacctct	cagaagagct	tccagcaact	gaccatggag	aaggaacagg	180
ccctggctga	ccttaactct	gtggaaagg	ccctttctga	tctcttcagg	agatatgaga	240
acctgaaaag	tggtctggaa	gggttcaaga	agaatgaaga	agccttgaag	aaatgtgctc	300
aggattactt	agccagagtt	aaacaagagg	agcagcgata	ccaggccctg	aaaatccacg	360
cagaagagaa	actggacaaa	gccaatgaag	agattgctca	ggttcgaaca	aaagcaaagg	420
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aaagggccct	gcagcagaag	aaccaagaaa	ttgaaggaac	tgacaaaaat	ctgtgatgag	540
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catttggtctg	cttctcttgt	gaccacaatt	atcttgccct	atccaggaat	aattgcccct	660
ttgcaganga	aaaaaatata	cttaanaaaa	gcacatgcct	actgctgcct	gtcccgcctt	720
gctgccaatg	caacagccct	ggaagaaaao	cctatanggn	tgcatagtct	aaaaagggag	780
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cccaaattgt	gtttaaaatt	tgtaacnccc	cctttgggg	cttcccaaca	accggtccga	960
tttttttggg	gatcgggtta	acccttttaa	tttttttagta	nccagtgggg	tttaatttag	1020
ggga						1024

<210> 666

<211> 734

<212> DNA

<213> Homo Sapiens

<400> 666

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gccttgacct	cccaggctcc	cacctcagcc	tcccaagtag	ctgggaccac	aggcacgtgc	120
caccatgccc	agctaatttt	tatttttgga	nanacaaggt	ttcaccatgt	tgcttaggta	180
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tagctagcag	gttatattggc	cctcacatgt	gttgaggcaa	actctatact	atattcttac	360
tctccanagt	tccaaaatcc	tttattttta	aanaaaaata	aacaaacata	cttcattctg	420
cccagtatat	tctcttgatc	tgtacaagct	acgattttta	ttctctttgg	gagaggaagc	480
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aattatcact	taacgaaggt	cctttgggtgc	tccctgtgca	tcagcttcat	tcactggggg	600
caggttctta	aggggtctct	tccaccaatg	tgctagggaa	gggctgccat	cacctctgtt	660
taacacatag	ctactttctt	aaaccnataa	gcttaaaaaa	gangactatg	gaattaccaa	720
tggaaggcnt	ataa					734

<210> 667

<211> 592

<212> DNA

<213> Homo Sapiens

<400> 667

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<212> DNA

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<210> 678

<211> 1771

<212> DNA

<213> Homo Sapiens

<400> 678

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<210> 679

<211> 1367

<212> DNA

<213> Homo Sapiens

<400> 679

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<210> 680

<211> 2545

<212> DNA

<213> Homo Sapiens

<400> 680

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<210> 681

<211> 1745

<212> DNA

<213> Homo Sapiens

<400> 681

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<211> 1745

<212> DNA

<213> Homo Sapiens

<400> 682

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<211> 3127

<212> DNA

<213> Homo Sapiens

<400> 683

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<210> 684
 <211> 803
 <212> PRT
 <213> Homo Sapiens

<400> 684

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Met Asn Lys Phe Lys Val Leu Met Glu Ile Gln Asp Leu Met Phe Glu
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          20          25          30
Lys Ala Thr Ile Pro Glu Val Lys Asn Ser Glu Asn Ser Ser Ser Arg
          35          40          45
Gln Val Ser Ala Asn Asn Gln Phe Ser Ile Thr Lys Asn Arg Asp Gly
 50          55          60
Arg Glu Asn Arg Arg Arg Asn Ser Lys Ile Gly Asp Asp Asn Glu Asn
 65          70          75          80
Leu Thr Phe Lys Leu Glu Val Asn Glu Leu Ser Gly Lys Leu Asp Asn
          85          90          95
Thr Asn Glu Tyr Asn Ser Asn Asp Gly Lys Lys Leu Pro Gln Gly Glu
          100          105          110
Ser Arg Ser Tyr Glu Val Met Gly Ser Met Glu Glu Thr Leu Cys Asn
          115          120          125
Ile Asp Asp Arg Asp Gly Asn Arg Asn Val His Leu Glu Phe Thr Glu
          130          135          140
Arg Glu Ser Arg Lys Asp Gly Glu Asp Glu Phe Val Lys Glu Met Arg
          145          150          155          160
Glu Glu Arg Lys Phe Gln Lys Leu Lys Asn Lys Glu Glu Val Leu Lys
          165          170          175
Ala Ser Arg Glu Glu Lys Val Leu Met Asp Glu Gly Ala Val Leu Thr
          180          185          190
Leu Ala Ala Asp Leu Ser Ser Ala Thr Leu Asp Ile Ser Lys Gln Trp
          195          200          205
Ser Asn Val Phe Asn Ile Leu Arg Glu Asn Asp Phe Glu Pro Lys Phe
          210          215          220
Leu Cys Glu Val Lys Leu Ala Phe Lys Cys Asp Gly Glu Ile Lys Thr
          225          230          235          240
Phe Ser Asp Leu Gln Ser Leu Arg Lys Phe Ala Ser Gln Lys Ser Ser
          245          250          255
Met Xaa Xaa Leu Leu Xaa Asp Val Leu Pro Gln Lys Glu Glu Ile Asn
          260          265          270
Gln Gly Gly Arg Lys Tyr Gly Ile Gln Glu Lys Arg Asp Lys Thr Leu
          275          280          285
Ile Asp Ser Xaa His Arg Ala Gly Glu Ile Thr Ser Asp Gly Leu Ser
          290          295          300
Phe Leu Phe Leu Lys Glu Val Lys Val Ala Lys Pro Glu Glu Met Lys
          305          310          315          320
Asn Leu Glu Thr Gln Glu Glu Glu Phe Ser Glu Leu Glu Glu Leu Asp
          325          330          335
Glu Glu Ala Ser Gly Met Glu Asp Asp Glu Asp Thr Ser Gly Leu Glu
          340          345          350
Glu Glu Glu Glu Glu Glu Ala Ser Gly Leu Glu Glu Asp Xaa Ser Ser
          355          360          365
Xaa Leu Glu Glu Glu Glu Glu Gln Thr Ser Glu Gln Asp Ser Thr Phe
          370          375          380
Xaa Gly His Thr Leu Val Asp Ala Lys His Glu Val Glu Ile Thr Ser

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385 390 395 400
 Xaa Gly Met Glu Thr Thr Phe Ile Asp Ser Val Glu Asp Ser Glu Ser
 405 410 415
 Glu Glu Glu Glu Glu Gly Lys Ser Ser Glu Thr Gly Lys Val Lys Thr
 420 425 430
 Thr Ser Leu Thr Glu Lys Lys Ala Ser Arg Arg Gln Lys Glu Ile Pro
 435 440 445
 Phe Ser Tyr Leu Val Gly Asp Ser Gly Lys Lys Lys Leu Val Lys His
 450 455 460
 Gln Val Val His Lys Thr Gln Glu Glu Glu Glu Thr Ala Val Pro Thr
 465 470 475 480
 Ser Gln Gly Thr Gly Thr Thr Cys Leu Thr Leu Cys Leu Ala Ser Pro
 485 490 495
 Ser Lys Ser Leu Glu Met Ser His Asp Glu His Lys Lys His Ser His
 500 505 510
 Thr Asn Leu Ser Ile Ser Thr Gly Val Thr Lys Leu Lys Lys Thr Glu
 515 520 525
 Glu Lys Lys His Arg Thr Leu His Thr Glu Glu Leu Thr Ser Lys Glu
 530 535 540
 Ala Asp Leu Thr Glu Glu Thr Glu Glu Asn Leu Arg Ser Ser Val Ile
 545 550 555 560
 Asn Ser Ile Arg Glu Ile Lys Glu Glu Ile Gly Asn Leu Lys Ser Ser
 565 570 575
 His Ser Gly Val Leu Glu Ile Glu Asn Ser Val Asp Asp Leu Ser Ser
 580 585 590
 Arg Met Asp Ile Leu Glu Glu Arg Ile Asp Ser Leu Glu Asp Gln Ile
 595 600 605
 Glu Glu Phe Ser Lys Asp Thr Met Gln Met Thr Lys Gln Ile Ile Ser
 610 615 620
 Lys Glu Gly Pro Arg Asp Ile Glu Glu Arg Ser Arg Ser Cys Asn Ile
 625 630 635 640
 Arg Leu Ile Gly Ile Pro Glu Lys Glu Ser Tyr Glu Asn Arg Ala Glu
 645 650 655
 Asp Ile Ile Lys Glu Ile Ile Asp Glu Asn Phe Ala Glu Leu Lys Lys
 660 665 670
 Gly Ser Ser Leu Glu Ile Val Ser Ala Cys Arg Val Pro Ser Lys Ile
 675 680 685
 Asp Glu Lys Arg Leu Thr Pro Arg His Ile Leu Val Lys Phe Trp Asn
 690 695 700
 Ser Ser Asp Lys Glu Lys Ile Ile Arg Pro Ser Arg Glu Arg Arg Glu
 705 710 715 720
 Ile Thr Tyr Gln Gly Thr Arg Ile Arg Leu Thr Ala Asp Leu Ser Leu
 725 730 735
 Asp Thr Leu Asp Ala Arg Ser Lys Trp Ser Asn Val Phe Lys Val Leu
 740 745 750
 Leu Glu Lys Gly Phe Asn Pro Arg Thr Leu Tyr Pro Ala Lys Met Ala
 755 760 765
 Phe Asp Phe Arg Gly Lys Thr Lys Val Phe Leu Ser Ile Glu Glu Phe
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 Arg Asp Tyr Val Leu His Met Pro Thr Leu Arg Glu Leu Leu Gly Asn
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 Asn Ile Pro

<210> 685

<211> 947
 <212> PRT
 <213> Homo Sapiens

<400> 685
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 Gln Tyr Leu Gln Lys Val Val Leu Lys Asp Leu Trp Lys His Ser Phe
 35 40 45
 Ser Trp Pro Phe Gln Arg Pro Val Asp Ala Val Lys Leu Lys Leu Pro
 50 55 60
 Asp Tyr Tyr Thr Ile Ile Lys Asn Pro Met Asp Leu Asn Thr Ile Lys
 65 70 75 80
 Lys Arg Leu Glu Asn Lys Tyr Tyr Ala Lys Ala Ser Glu Cys Ile Glu
 85 90 95
 Asp Phe Asn Thr Met Phe Ser Asn Cys Tyr Leu Tyr Asn Lys Pro Gly
 100 105 110
 Asp Asp Ile Val Leu Met Ala Gln Ala Leu Glu Lys Leu Phe Met Gln
 115 120 125
 Lys Leu Ser Gln Met Pro Gln Glu Glu Gln Val Val Gly Val Lys Glu
 130 135 140
 Arg Ile Lys Lys Gly Thr Gln Gln Asn Ile Ala Val Ser Ser Ala Lys
 145 150 155 160
 Glu Lys Ser Ser Pro Ser Ala Thr Glu Lys Val Phe Lys Gln Gln Glu
 165 170 175
 Ile Pro Ser Val Phe Pro Lys Thr Ser Ile Ser Pro Leu Asn Val Val
 180 185 190
 Gln Gly Ala Ser Val Asn Ser Ser Ser Gln Thr Ala Ala Gln Val Thr
 195 200 205
 Lys Gly Val Lys Arg Lys Ala Asp Thr Thr Thr Pro Ala Thr Ser Ala
 210 215 220
 Val Lys Ala Ser Ser Glu Phe Ser Pro Thr Phe Thr Glu Lys Ser Val
 225 230 235 240
 Ala Leu Pro Pro Ile Lys Glu Asn Met Pro Lys Asn Val Leu Pro Asp
 245 250 255
 Ser Gln Gln Gln Tyr Asn Val Val Glu Thr Val Lys Val Thr Glu Gln
 260 265 270
 Leu Arg His Cys Ser Glu Ile Leu Lys Glu Met Leu Ala Lys Lys His
 275 280 285
 Phe Ser Tyr Ala Trp Pro Phe Tyr Asn Pro Val Asp Val Asn Ala Leu
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 Gly Leu His Asn Tyr Tyr Asp Val Val Lys Asn Pro Met Asp Leu Gly
 305 310 315 320
 Thr Ile Lys Glu Lys Met Asp Asn Gln Glu Tyr Lys Asp Ala Tyr Ser
 325 330 335
 Phe Ala Ala Asp Val Arg Leu Met Phe Met Asn Cys Tyr Lys Tyr Asn
 340 345 350
 Pro Pro Asp His Glu Val Val Thr Met Ala Arg Met Leu Gln Asp Val
 355 360 365
 Phe Glu Thr His Phe Ser Lys Ile Pro Ile Glu Pro Val Glu Ser Met
 370 375 380
 Pro Leu Cys Tyr Ile Lys Thr Asp Ile Thr Glu Thr Thr Gly Arg Glu
 385 390 395 400

Asn Thr Asn Glu Ala Ser Ser Glu Gly Asn Ser Ser Asp Asp Ser Glu
 405 410 415
 Asp Glu Arg Val Lys Arg Leu Ala Lys Leu Gln Glu Gln Leu Lys Ala
 420 425 430
 Val His Gln Gln Leu Gln Val Leu Ser Gln Val Pro Phe Arg Lys Leu
 435 440 445
 Asn Lys Lys Lys Glu Lys Ser Lys Lys Glu Lys Lys Lys Glu Lys Val
 450 455 460
 Asn Asn Ser Asn Glu Asn Pro Arg Lys Met Cys Glu Gln Met Arg Leu
 465 470 475 480
 Lys Glu Lys Ser Lys Arg Asn Gln Pro Lys Lys Arg Lys Gln Gln Phe
 485 490 495
 Ile Gly Leu Lys Ser Glu Asp Glu Asp Asn Ala Lys Pro Met Asn Tyr
 500 505 510
 Asp Glu Lys Arg Gln Leu Ser Leu Asn Ile Asn Lys Leu Pro Gly Asp
 515 520 525
 Lys Leu Gly Arg Val Val His Ile Ile Gln Ser Arg Glu Pro Ser Leu
 530 535 540
 Ser Asn Ser Asn Pro Asp Glu Ile Glu Ile Asp Phe Glu Thr Leu Lys
 545 550 555 560
 Ala Ser Thr Leu Arg Glu Leu Glu Lys Tyr Val Ser Ala Cys Leu Arg
 565 570 575
 Lys Arg Pro Leu Lys Pro Pro Ala Lys Lys Ile Met Met Ser Lys Glu
 580 585 590
 Glu Leu His Ser Gln Lys Lys Gln Glu Leu Glu Lys Arg Leu Leu Asp
 595 600 605
 Val Asn Asn Gln Leu Asn Ser Arg Lys Arg Gln Thr Lys Ser Asp Lys
 610 615 620
 Thr Gln Pro Ser Lys Ala Val Glu Asn Val Ser Arg Leu Ser Glu Ser
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 Ser Ser Ser Ser Ser Ser Ser Ser Glu Ser Glu Ser Ser Ser Ser Asp
 645 650 655
 Leu Ser Ser Ser Asp Ser Ser Asp Ser Glu Ser Glu Met Phe Pro Lys
 660 665 670
 Phe Thr Glu Val Lys Pro Asn Asp Ser Pro Ser Lys Glu His Val Lys
 675 680 685
 Lys Met Lys Asn Glu Cys Ile Leu Pro Glu Gly Arg Thr Gly Val Thr
 690 695 700
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 705 710 715 720
 Val His Gln Thr Thr Pro Ser His Val Met Pro Pro Asn His His Gln
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 Leu Ala Phe Asn Tyr Gln Glu Leu Glu His Leu Gln Thr Val Lys Asn
 740 745 750
 Ile Ser Pro Leu Gln Ile Leu Pro Pro Ser Gly Asp Ser Glu Gln Leu
 755 760 765
 Ser Asn Gly Ile Thr Val Met His Pro Ser Gly Asp Ser Asp Thr Thr
 770 775 780
 Met Leu Glu Ser Glu Cys Gln Ala Pro Val Gln Lys Asp Ile Lys Ile
 785 790 795 800
 Lys Asn Ala Asp Ser Trp Lys Ser Leu Gly Lys Pro Val Lys Pro Ser
 805 810 815
 Gly Val Met Lys Ser Ser Asp Glu Leu Phe Asn Gln Phe Arg Lys Ala
 820 825 830
 Ala Ile Glu Lys Glu Val Lys Ala Arg Thr Gln Glu Leu Ile Arg Lys

835	840	845
His Leu Glu Gln Asn Thr Lys Glu Leu Lys Ala Ser Gln Glu Asn Gln		
850	855	860
Arg Asp Leu Gly Asn Gly Leu Thr Val Glu Ser Phe Ser Asn Lys Ile		
865	870	875
Gln Asn Lys Cys Ser Gly Glu Glu Gln Lys Glu His Pro Gln Ser Ser		880
	885	890
		895
Glu Ala Gln Asp Lys Ser Lys Leu Trp Leu Leu Lys Asp Arg Asp Leu		
	900	905
		910
Ala Arg Pro Lys Glu Gln Glu Arg Arg Arg Arg Glu Ala Met Val Gly		
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Asn Phe Asp		
945		

<210> 686

<211> 3106

<212> DNA

<213> Homo Sapiens

<400> 686

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gtcgacaaac	agctattatt	gttaaccctc	ctccaccaga	atatataaat	actaagaaaa	180
atgggcgatt	gacaaatcaa	cttcagtatc	tacaaaaagt	tgtcctaaag	gatttatgga	240
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attattatac	cattataaaa	aacccaatgg	atttaaatac	aattaagaag	cgcttgga	360
ataaatatta	tgcaaggcct	tcagaatgta	tagaagactt	caatacaatg	ttctcaaatt	420
gttatttata	taacaagcct	ggagatgaca	ttgttcttat	ggcacaagct	ctagagaagc	480
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gaatcaagaa	aggcactcaa	cagaatatag	ctgtttcttc	tgctaaagaa	aaatcatcac	600
ccagcgcaac	agaaaaagta	tttaagcagc	aagaaattcc	ttctgtattt	cctaagacat	660
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caaagaaaca	tttttcatat	gcatggccct	tttataatcc	tgttgacgtt	aatgcttttg	1020
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aaatggataa	ccaagaatat	aaggatgcat	actcatttgc	ggcagatgtt	agattaatgt	1140
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agaaaataat	gatgtccaaa	gaagaacttc	actcacagaa	aaaacaggaa	ttggaaaagc	1920
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<210> 687

<211> 1759

<212> DNA

<213> Homo Sapiens

<400> 687

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tggaagacca	ctctgaagag	atgaaataag	tcttctgcc	aagattactt	attaatttac	180
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gaatagtttt	ggcatccagg	gtcatttttc	attaaaaaga	gaaaagtcat	gtcaaataatg	300
aatttccgca	gattattcag	cactagaccc	tgggagattc	tgtaaagagg	ggttttgtta	360
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1759

<210> 688
 <211> 207
 <212> PRT
 <213> Homo Sapiens

<400> 688
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 Ile Ser Ala Ser Arg Lys Val Pro Asn Leu Ser Val Ser Lys Leu Ile
 35 40 45
 Thr Glu Ala Leu Ser Val Ser Gln Glu Arg Val Gly Met Ser Leu Val
 50 55 60
 Ala Leu Lys Lys Ala Leu Ala Ala Ala Gly Tyr Asp Val Glu Lys Asn
 65 70 75 80
 Asn Ser Arg Ile Lys Leu Ser Leu Lys Ser Leu Val Asn Lys Gly Ile
 85 90 95
 Leu Val Gln Thr Arg Gly Thr Gly Ala Ser Gly Ser Phe Lys Leu Ser
 100 105 110
 Lys Lys Val Ile Pro Lys Ser Thr Arg Ser Lys Ala Lys Lys Ser Val
 115 120 125
 Ser Ala Lys Thr Lys Lys Leu Val Leu Ser Arg Asp Ser Lys Ser Pro
 130 135 140
 Lys Thr Ala Lys Thr Asn Lys Arg Ala Lys Lys Pro Arg Ala Thr Thr
 145 150 155 160
 Pro Lys Thr Val Arg Ser Gly Arg Lys Ala Lys Gly Ala Lys Gly Lys
 165 170 175
 Gln Gln Gln Lys Ser Pro Val Lys Ala Arg Ala Ser Lys Ser Lys Leu
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 Thr Gln His Glu Val Asn Val Arg Lys Ala Thr Ser Lys Lys
 195 200 205

<210> 689
 <211> 1464
 <212> DNA
 <213> Homo Sapiens

<400> 689
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 tggaaaatgc caatgttctg gcccgttatg ccagtatctg ccagcagaat ggcattgtgc 720
 ccatcgtgga gcctgagatc ctccctgatg gggaccatga cttgaagcgc tgccagtatg 780
 tgaccgagaa ggtgctggct gctgtctaca aggcctctgag tgaccaccac atctacctgg 840

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tactgggat caccttcctg tctggaggcc agagtgagga ggaggcgtcc atcaacctca 1020
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aagcggaggt gttcccaggc tgcccccaac aactccaggc cctgccccct cccactcttg 1320
aagaggaggc cgcctcctcg gggctccagg ctggcttgcc cgcgctcttt cttccctcgt 1380
gacagtgggtg tgtggtgtcg tctgtgaatg ctaagtccat caccctttcc ggcacactgc 1440
caaataaaca gctatttaag gggg 1464

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<210> 690
 <211> 363
 <212> PRT
 <213> Homo Sapiens

<400> 690

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Asp Glu Ser Thr Gly Ser Ile Ala Lys Arg Leu Gln Ser Ile Gly Thr
35     40     45
Glu Asn Thr Glu Glu Asn Arg Arg Phe Tyr Arg Gln Leu Leu Leu Thr
50     55     60
Ala Asp Asp Arg Val Asn Pro Cys Ile Gly Gly Val Ile Leu Phe His
65     70     75     80
Glu Thr Leu Tyr Gln Lys Ala Asp Asp Gly Arg Pro Phe Pro Gln Val
85     90     95
Ile Lys Ser Lys Gly Gly Val Val Gly Ile Lys Val Asp Lys Gly Val
100    105    110
Val Pro Leu Ala Gly Thr Asn Gly Glu Thr Thr Thr Gln Gly Leu Asp
115    120    125
Gly Leu Ser Glu Arg Cys Ala Gln Tyr Lys Lys Asp Gly Ala Asp Phe
130    135    140
Ala Lys Trp Arg Cys Val Leu Lys Ile Gly Glu His Thr Pro Ser Ala
145    150    155    160
Leu Ala Ile Met Glu Asn Ala Asn Val Leu Ala Arg Tyr Ala Ser Ile
165    170    175
Cys Gln Gln Asn Gly Ile Val Pro Ile Val Glu Pro Glu Ile Leu Pro
180    185    190
Asp Gly Asp His Asp Leu Lys Arg Cys Gln Tyr Val Thr Glu Lys Val
195    200    205
Leu Ala Ala Val Tyr Lys Ala Leu Ser Asp His His Ile Tyr Leu Glu
210    215    220
Gly Thr Leu Leu Lys Pro Asn Met Val Thr Pro Gly His Ala Cys Thr
225    230    235    240
Gln Lys Phe Ser His Glu Glu Ile Ala Met Ala Thr Val Thr Ala Leu
245    250    255
Arg Arg Thr Val Pro Pro Ala Val Thr Gly Ile Thr Phe Leu Ser Gly
260    265    270
Gly Gln Ser Glu Glu Glu Ala Ser Ile Asn Leu Asn Ala Ile Asn Lys
275    280    285
Cys Pro Leu Leu Lys Pro Trp Ala Leu Thr Phe Ser Tyr Gly Arg Ala

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290	295	300
Leu Gln Ala Ser Ala Leu Lys Ala Trp Gly Gly Lys Lys Glu Asn Leu		
305	310	315
Lys Ala Ala Gln Glu Glu Tyr Val Lys Arg Ala Leu Ala Asn Ser Leu		320
	325	330
Ala Cys Gln Gly Lys Tyr Thr Pro Ser Gly Gln Ala Gly Ala Ala Ala		335
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Ser Glu Ser Leu Phe Val Ser Asn His Ala Tyr		350
355	360	

<210> 691
 <211> 1216
 <212> DNA
 <213> Homo Sapiens

<400> 691

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cacaacatct	cagatgcttt	tgaccagaag	ttctcaaagg	tgctaccac	ggtaaaggc	240
tatgacaacc	tctttgctat	ggagattgac	cccagcctgg	gcgtggcgga	cgtgcctgac	300
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ctcaacttcc	ccaccatcgt	ggagcggggc	ctgggcgggc	ttatgcagat	caagaaccag	540
atcagccctt	tcatctcaca	gatgtgcaac	atgctgggcc	tgggggacat	gaacgcagac	600
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ctcctcctgg	agccctacaa	gccccccagt	gcccagtagc	acagctgcca	gccccaaccc	1020
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tcccccccat	aatacagggg	gagccacttg	ggcaggaggc	agggaggggg	ccattccccc	1140
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aaatgatctt	aaactg					1216

<210> 692
 <211> 1958
 <212> DNA
 <213> Homo Sapiens

<400> 692

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tcccgccac	gtcccatctt	gcccctcg	tccggagtcc	ccgtggccag	atctaaccat	180
gagctaccct	ggctatcccc	cgccccag	tggctacca	ccagctgcac	caggtggtgg	240
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cgtggccacc	tatgcggggc	agttcaacca	ggactatctc	tcgggaatgg	cggccaacat	360
gtctgggaca	tttgaggag	ccaacatgcc	caacctgtac	cctggggccc	ctggggctgg	420
ctaccacca	gtgccccctg	gcggctttg	gcagccccc	tctgcccagc	agcctgttcc	480
tccctatggg	atgtatccac	cccaggagg	aaaccaccc	tccaggatgc	cctcatatcc	540
gccataccca	ggggccctcg	tgccgggcca	gccatgccca	ccccccggac	agcagcccc	600
aggggcctac	cctgggcagc	caccagtgc	ctaccctggt	cagcctccag	tgccaactcc	660

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tgggcagcag cagccagtgc cgagctaccc aggatacccg gggctctggga ctgtcacccc 720
cgctgtgccc ccaacccagt ttggaagccg aggcaccatc actgatgctc ccggctttga 780
ccccctgcga gatgccgagg tccctgoggaa ggccatgaaa ggcttcggga cggatgagca 840
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tgggtggcaat gactgaacag tgactggtgg ctcaactctg cccacctgcc ggcaacacca 1740
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tcaccgtcct agagcttagg cctgtcttcc acccctcctg acccgatatag tgtgccacag 1860
gacctgggtc ggtctagaac tctctcagga tgccctttct accccatccc tcacagcctc 1920
ttgtctgctaa aatagatggt tcatttttct gaaaaaaa 1958

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<210> 693

<211> 505

<212> PRT

<213> Homo Sapiens

<400> 693

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20      25      30
Ser Met Pro Pro Ile Gly Leu Asp Asn Val Ala Thr Tyr Ala Gly Gln
35      40      45
Phe Asn Gln Asp Tyr Leu Ser Gly Met Ala Ala Asn Met Ser Gly Thr
50      55      60
Phe Gly Gly Ala Asn Met Pro Asn Leu Tyr Pro Gly Ala Pro Gly Ala
65      70      75      80
Gly Tyr Pro Pro Val Pro Pro Gly Gly Phe Gly Gln Pro Pro Ser Ala
85      90      95
Gln Gln Pro Val Pro Pro Tyr Gly Met Tyr Pro Pro Pro Gly Gly Asn
100     105     110
Pro Pro Ser Arg Met Pro Ser Tyr Pro Pro Tyr Pro Gly Ala Pro Val
115     120     125
Pro Gly Gln Pro Met Pro Pro Pro Gly Gln Gln Pro Pro Gly Ala Tyr
130     135     140
Pro Gly Gln Pro Pro Val Thr Tyr Pro Gly Gln Pro Pro Val Pro Leu
145     150     155     160
Pro Gly Gln Gln Gln Pro Val Pro Ser Tyr Pro Gly Tyr Pro Gly Ser
165     170     175
Gly Thr Val Thr Pro Ala Val Pro Pro Thr Gln Phe Gly Ser Arg Gly
180     185     190
Thr Ile Thr Asp Ala Pro Gly Phe Asp Pro Leu Arg Asp Ala Glu Val
195     200     205

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Leu Arg Lys Ala Met Lys Gly Phe Gly Thr Asp Glu Gln Ala Ile Ile
 210 215 220
 Asp Cys Leu Gly Ser Arg Ser Asn Lys Gln Arg Gln Gln Ile Leu Leu
 225 230 235 240
 Ser Phe Lys Thr Ala Tyr Gly Lys Asp Leu Ile Lys Asp Leu Lys Ser
 245 250 255
 Glu Leu Ser Gly Asn Phe Glu Lys Thr Ile Leu Ala Leu Met Lys Thr
 260 265 270
 Pro Val Leu Phe Asp Ile Tyr Glu Ile Lys Glu Ala Ile Lys Gly Val
 275 280 285
 Gly Thr Asp Glu Ala Cys Leu Ile Glu Ile Leu Ala Ser Arg Ser Asn
 290 295 300
 Glu His Ile Arg Glu Leu Asn Arg Ala Tyr Lys Ala Glu Phe Lys Lys
 305 310 315 320
 Thr Leu Glu Glu Ala Ile Arg Ser Asp Thr Ser Gly His Phe Gln Arg
 325 330 335
 Leu Leu Ile Ser Leu Ser Gln Gly Asn Arg Asp Glu Ser Thr Asn Val
 340 345 350
 Asp Met Ser Leu Ala Gln Arg Asp Ala Gln Glu Leu Tyr Ala Ala Gly
 355 360 365
 Glu Asn Arg Leu Gly Thr Asp Glu Ser Lys Phe Asn Ala Val Leu Cys
 370 375 380
 Ser Arg Ser Arg Ala His Leu Val Ala Val Phe Asn Glu Tyr Gln Arg
 385 390 395 400
 Met Thr Gly Arg Asp Ile Glu Lys Ser Ile Cys Arg Glu Met Ser Gly
 405 410 415
 Asp Leu Glu Glu Gly Met Leu Ala Val Val Lys Cys Leu Lys Asn Thr
 420 425 430
 Pro Ala Phe Phe Ala Glu Arg Leu Asn Lys Ala Met Arg Gly Ala Gly
 435 440 445
 Thr Lys Asp Arg Thr Leu Ile Arg Ile Met Val Ser Arg Ser Glu Thr
 450 455 460
 Asp Leu Leu Asp Ile Arg Ser Glu Tyr Lys Arg Met Tyr Gly Lys Ser
 465 470 475 480
 Leu Tyr His Asp Ile Ser Gly Asp Thr Ser Gly Asp Tyr Arg Lys Ile
 485 490 495
 Leu Leu Lys Ile Cys Gly Gly Asn Asp
 500 505

<210> 694

<211> 1141

<212> DNA

<213> Homo Sapiens

<400> 694

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gaatttcgta	accagaagcc	gaagccggag	aaccaagatg	aatcagaact	ccttacggtt	120
cctgatgggt	ggaaggaacc	agctttttcc	aaagaggaca	atcccagagg	acttttggag	180
gagagcagtt	tcgcaacttt	gttcccaaaa	tacaggggaag	cttacttgaa	agagtgttgg	240
ccattgggtgc	agaaagcctt	aaatgaacat	catgttaatg	caaccctgga	cctgatcgaa	300
ggcagcatga	ctgtttgtac	tacaaagaag	acttttgate	catatatcat	cattagggcc	360
agagatctga	taaaactggt	agcaaggagt	gtttcatttg	aacaggcagt	acgaattctt	420
caggatgatg	ttgcatgtga	catcattaaa	ataggttctt	tagtaaggaa	taaagagaga	480
tttgtaaaac	gaagacaacg	gcttattggt	cccaaaggat	ctacattgaa	ggcattggaa	540
ctcttaacta	attgttacat	tatggttcag	ggaaacacag	tttcagccat	tggacctttt	600

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agtggccttaa aagaggttag aaaagtagtc cttgatacta tgaagaatat tcatccaatt      660
tataacatta aaagcttaat gattaagaga gagttggcaa aagattctga attacgatca      720
caaagttggg agagattttt gccacagttc aaacacaaaa atgtgaataa acgcaaggaa      780
ccaaagaaaa aaactgttaa gaaagatata cgccattccc accaccacaa ccagaaaagtc      840
agatcgataa agaattggct agtgggtgaat actttttgaa ggcaaatcag aagaagcggc      900
agaaaatgaa gcaataaagg ctaaacaagc agaagccatc agtaagagac aagaggaaaag      960
aaacaaagca tttattccac ctaaggaaaa accaattgtg aaacctaagg aagctttctac     1020
tgaaactaaa attgatgtgg ccagcatcaa ggaaaagggt aagaaagcaa agaataagaa     1080
actgggagct cttacagctg aagaaattgc acttaagatg gaggcagatg aaaaaaaaaa     1140
a                                                                                   1141

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<210> 695
 <211> 288
 <212> PRT
 <213> Homo Sapiens

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<400> 695
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                20                    25                    30
Leu Leu Thr Val Pro Asp Gly Trp Lys Glu Pro Ala Phe Ser Lys Glu
                35                    40                    45
Asp Asn Pro Arg Gly Leu Leu Glu Glu Ser Ser Phe Ala Thr Leu Phe
                50                    55                    60
Pro Lys Tyr Arg Glu Ala Tyr Leu Lys Glu Cys Trp Pro Leu Val Gln
 65                    70                    75                    80
Lys Ala Leu Asn Glu His His Val Asn Ala Thr Leu Asp Leu Ile Glu
                85                    90                    95
Gly Ser Met Thr Val Cys Thr Thr Lys Lys Thr Phe Asp Pro Tyr Ile
                100                    105                    110
Ile Ile Arg Ala Arg Asp Leu Ile Lys Leu Leu Ala Arg Ser Val Ser
                115                    120                    125
Phe Glu Gln Ala Val Arg Ile Leu Gln Asp Asp Val Ala Cys Asp Ile
                130                    135                    140
Ile Lys Ile Gly Ser Leu Val Arg Asn Lys Glu Arg Phe Val Lys Arg
 145                    150                    155                    160
Arg Gln Arg Leu Ile Gly Pro Lys Gly Ser Thr Leu Lys Ala Leu Glu
                165                    170                    175
Leu Leu Thr Asn Cys Tyr Ile Met Val Gln Gly Asn Thr Val Ser Ala
                180                    185                    190
Ile Gly Pro Phe Ser Gly Leu Lys Glu Val Arg Lys Val Val Leu Asp
                195                    200                    205
Thr Met Lys Asn Ile His Pro Ile Tyr Asn Ile Lys Ser Leu Met Ile
                210                    215                    220
Lys Arg Glu Leu Ala Lys Asp Ser Glu Leu Arg Ser Gln Ser Trp Glu
 225                    230                    235                    240
Arg Phe Leu Pro Gln Phe Lys His Lys Asn Val Asn Lys Arg Lys Glu
                245                    250                    255
Pro Lys Lys Lys Thr Val Lys Lys Asp Ile Arg His Ser His His His
                260                    265                    270
Asn Gln Lys Val Arg Ser Ile Lys Asn Trp Leu Val Val Asn Thr Phe
                275                    280                    285

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<210> 696

<211> 1008
 <212> DNA
 <213> Homo Sapiens

<400> 696

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atactacagt	gaagaaacct	gaatcaaaga	aggaacagac	cccagagcat	gggaagaaaa	120
aacgtggcag	aggaaaagcc	caagttaaag	caacaaatga	atccgaagac	gaaatccac	180
agctggtacc	aataggaag	aagactccag	ctaataaaaa	agtagagatt	caaaaacatg	240
ccacagggaa	gaagtctcca	gcaaagagtc	ctaataccag	cacacctcgt	gggaagaaaa	300
agaaaggctt	tgccagcatc	tgagacccca	aaagctgcag	agtctgagac	cccagggaaa	360
agcccagaga	agaagcctaa	aatcaaagaa	gaggcagtg	aggaaaaaag	tccttcgctg	420
gggaaaaaag	atgcgagaca	gactcccaaa	aaagccagag	gccaagtttt	tcaccattcc	480
tagtaaatct	gtgagaaaag	cttcccacac	ccccaaaaaa	tggcccaaaa	aaccctaaagt	540
accccgatcg	acctaagtc	agtgattcaa	ctggaaggaa	acctcaatgc	tgctccaga	600
gctttttgga	aatactcaga	tcctggccgc	ctttgtaacc	ttctctaaac	gtcaggcctg	660
gacttaaaag	atTTTTTtaa	acctccataa	gtagtccagg	ggcgggtggc	cacgcctgta	720
atcccagcac	tttgggaggg	cgaggcaggc	ggatcacaag	gtcaacgaga	tcgagaccat	780
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ggtggacacc	tgtaatccca	gctactaggg	aggctgaggc	aggagaattg	cttgaacctg	900
ggaggcgagg	gttgcagtg	gccactgcac	tcagcctgta	tgacagagca	agactcagtc	960
tcaaaaataa	ataaaaataa	taaaacctcc	ataagtaatc	ctgaaaaa		1008

<210> 697
 <211> 685
 <212> DNA
 <213> Homo Sapiens

<400> 697

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aaaaanaaaa	aagaaaaaag	anaatgccca	gcgcgggtgg	taatgcctgt	aaccctagtg	120
agacagccaa	gtaaaaacgg	ctcccaagac	aatctacaag	cactgggagg	atgggggtgca	180
gcaccaaaat	gttcacacca	tttgcagagg	ggaacagcct	ggccctgct	gttccaggat	240
agtaaccagg	aattcagttg	gtgagatgga	cagcctgtta	gcaggactcc	atctcacttt	300
gctgtgtgt	tctttttccc	ttttgcccac	ttaattngta	acccctcacc	tttcaaagt	360
tctgcgtgcc	taatctttcc	ctgccatgtg	accagaacct	ggttttgttt	acaacaccag	420
cactttggga	ggcgaagatg	ggctgattgc	ttgagctcag	gggtttaaga	acagcctggg	480
caacatagtg	aaaccctagt	ttttaccaaa	aatacgaaaa	ttaaccaggc	atgcctgtta	540
tcccagctga	ggcacaagaa	tcccttgaac	ccaggaggcn	gaanncta	tnnaaccgga	600
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ccctgagac	gctgtntcaa	aaaaa				685

<210> 698
 <211> 1205
 <212> DNA
 <213> Homo Sapiens

<400> 698

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ggatgtgctt	ttacatggaa	ctcctgacca	aaaacgaaaa	ctcatcagag	aatgtcttac	180
cggagaaaag	gaatcatcta	gtgaagatga	atTTTgaaaag	gagatggaa	ctgaattaaa	240
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aaatggaaaa	gttgcacacg	ctccgacaag	gtactacgat	gatatatatt	ttgattctga	360
ttccgaggat	gaagacagag	cagtacaggt	gaccaagaaa	aaaaagaaga	aacaacacaa	420

gattccaaca	aatgacgaat	tactgtntga	tcctgaaaaa	gataacagag	atcaggcctg	480
ggttgatgca	cagagaagg	gttaccatgg	tttgggacca	cagagatcac	gtcaacaaca	540
gcctgttcca	aatagtgatg	ctgtcttgan	ttgtcctgcc	tgcattgacca	cactttgcct	600
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ggtccataag	aagatgaggt	ctaaccggga	agatgctgcc	gagaaggcag	agacagatgt	780
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tgttcatatc	cttcagtgac	attgaggaag	cagtgtttct	cttttttaaag	gagaatagtt	1020
gtcaaccttc	attcatctct	tacatctctc	accctctcct	tttttttttc	tttgattttc	1080
ccccattattg	atgggactga	tattcattct	gtttttgatg	aacatttgga	aactgtcggg	1140
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aaaaa						1205

<210> 699

<211> 1427

<212> DNA

<213> Homo Sapiens

<400> 699

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gatgttgcca	caagctgcat	tggagactca	ttgcagtaat	atttccaatg	tgccacctac	180
aagagagata	cttcaagtct	ttcttactga	tgtacacatg	aaggaagtaa	ttcagcagtt	240
cattgatgtc	ctgagtgtag	cagtcaagaa	acgtgtcttg	tgtttacctt	gggatgaaaa	300
cctgacagca	aatgaagttt	tgaaaacgtg	tgataggaaa	gcaaattgtg	caatcctggt	360
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tcgtgtccgc	tttcagtcgc	atgggctgga	aggattgaat	aaggaaataa	tgatggaact	960
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agaagcaaga	tttcttttcc	tggatgaaaa	tgttgtctcc	tttctaaatt	ctctgccgat	1080
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gctccaaatc	atgtccttag	aaaatctttc	tattgaaaag	gagactaaat	tgtaatgtga	1320
ttcacaatgt	aacaatataa	aaataagttt	ttatataatt	atataaaagt	aagatactct	1380
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<210> 700

<211> 1967

<212> DNA

<213> Homo Sapiens

<400> 700

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cagacttcaa	tataaaaaaa	aagtaaatcc	agatttgcaa	gtagaagtaa	agcctagtat	180

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<210> 701

<211> 3423

<212> DNA

<213> Homo Sapiens

<400> 701

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<210> 702

<211> 1106

<212> DNA

<213> Homo Sapiens

<400> 702

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<211> 1095

<212> DNA

<213> Homo Sapiens

<400> 703

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<210> 704

<211> 1968

<212> DNA

<213> Homo Sapiens

<400> 704

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<210> 705

<211> 800

<212> DNA

<213> Homo Sapiens

<400> 705

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<210> 706

<211> 487

<212> DNA

<213> Homo Sapiens

<400> 706

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<210> 707

<211> 3599

<212> DNA

<213> Homo Sapiens

<400> 707

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<210> 708

<211> 1123

<212> PRT

<213> Homo Sapiens

<400> 708

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Gly Arg Asp Ser Leu Pro Phe Asp Phe Gln Gly His Ser Gly Pro Pro
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Phe Ala Asn Val Glu Glu His Ser Phe Ser Tyr Gly Ala Arg Asp Gly
          65          70          75          80
Pro His Gly Asp Tyr Arg Gly Gly Glu Gly Pro Gly His Asp Phe Arg
          85          90          95
Gly Gly Asp Phe Ser Ser Ser Asp Phe Gln Ser Arg Asp Ser Ser Gln
          100          105          110
Leu Asp Phe Arg Gly Arg Asp Ile His Ser Gly Asp Phe Arg Asp Arg
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Glu Gly Pro Pro Met Asp Tyr Arg Gly Gly Asp Gly Thr Ser Met Asp
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Tyr Arg Gly Arg Glu Ala Pro His Met Asn Tyr Arg Asp Arg Asp Ala
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His Ala Val Asp Phe Arg Gly Arg Asp Ala Pro Pro Ser Asp Phe Arg
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Gly Arg Gly Thr Tyr Asp Leu Asp Phe Arg Gly Arg Asp Gly Ser His
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Ala Asp Phe Arg Gly Arg Asp Leu Ser Asp Leu Asp Phe Arg Ala Arg
          195          200          205
Glu Gln Ser Arg Ser Asp Phe Arg Asn Arg Asp Val Ser Asp Leu Asp
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Phe Arg Asp Lys Asp Gly Thr Gln Val Asp Phe Arg Gly Arg Gly Ser
          225          230          235          240
Gly Thr Thr Asp Leu Asp Phe Arg Asp Arg Asp Thr Pro His Ser Asp
          245          250          255

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 Phe Lys Glu Glu Gly Gly Leu Asp Phe Leu Gly Arg Gln Asp Thr Asp
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 Tyr Arg Ser Met Glu Tyr Arg Asp Val Asp His Arg Leu Pro Gly Ser
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 Glu Gly Gln Glu Ser Arg Leu Gly His Gln Lys Arg Glu Ala Glu Arg
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 Ile Ile Lys Asn Arg Thr Gly Pro Met Gly His Thr Tyr Gly Phe Ile

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 Gly Arg Asn Ser Asp Trp Ser Ser Asp Thr Asn Arg Gln Gly Gln Gln
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 Tyr Val Pro Gln Asp Pro Gly Leu Pro Glu Glu Glu Glu Ile Lys Glu
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<210> 709
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 <212> DNA
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<400> 709

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<210> 710

<211> 1177

<212> PRT

<213> Homo Sapiens

<400> 710

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Asn Arg Asp Tyr Pro Pro Pro Leu Lys Ser His Ala Gln Glu Arg
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 Ser Thr Gln Asp Arg Glu His Ser Gly Met Asn Val Asn Arg Arg Glu
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 Lys Gly Glu Phe Glu His Ser Glu Thr Arg Glu Gly Glu Thr Gln Gly
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 Met Ile Gln Asp Lys Glu Val Thr Leu Glu Tyr Val Ser Ser Leu Asp
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His	Thr	Tyr	Gly	Phe	Ile	Asp	Leu	Asp	Ser	His	Val	Glu	Ala	Leu	Arg
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<400> 711

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<212> PRT

<213> Homo Sapiens

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 35 40 45
 Pro Pro Thr Tyr Pro Thr Lys Tyr Phe Gly Cys Glu Leu Gly Ala Gln
 50 55 60
 Thr Gln Phe Asp Val Lys Asn Asp Arg Tyr Ile Val Asn Gly Ser His
 65 70 75 80
 Glu Ala Asn Lys Leu Gln Asp Met Leu Asp Gly Phe Ile Lys Lys Phe
 85 90 95
 Val Leu Cys Pro Glu Cys Glu Asn Pro Glu Thr Asp Leu His Val Asn
 100 105 110
 Pro Lys Lys Gln Thr Ile Gly Asn Ser Cys Lys Ala Cys Gly Tyr Arg
 115 120 125
 Gly Met Leu Asp Thr His His Lys Leu Cys Thr Phe Ile Leu Lys Asn
 130 135 140
 Pro Pro Glu Asn Ser Asp Ile Gly Thr Gly Lys Lys Glu Lys Glu Lys
 145 150 155 160
 Lys Asn Arg Lys Gly Lys Asp Lys Glu Asn Gly Ser Val Ser Thr Ser

165 170 175
 Glu Thr Pro Pro Pro Pro Pro Pro Asn Glu Ile Ser Pro Pro His Ala
 180 185 190
 Val Glu Glu Glu Glu Asp Asp Asp Trp Gly Glu Asp Thr Thr Glu Glu
 195 200 205
 Ala Gln Arg Arg Arg Met Asp Glu Ile Ser Asp His Ala Lys Gly Leu
 210 215 220
 Thr Leu Ser Asp Asp Leu Glu Arg Thr Val Glu Glu Arg Val Asn Ile
 225 230 235 240
 Leu Phe Asp Phe Val Lys Lys Lys Lys Glu Glu Gly Ile Ile Asp Ser
 245 250 255
 Ser Asp Lys Asp Ile Val Ala Glu Ala Glu Arg Leu Asp Val Lys Ala
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 Met Gly Pro Leu Val Leu Thr Glu Val Leu Phe Asp Glu Lys Ile Arg
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 Glu Gln Ile Lys Lys Tyr Arg Arg His Phe Leu Arg Phe Cys His Asn
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 Asn Lys Lys Ala Gln Arg Tyr Leu Leu His Gly Leu Glu Cys Val Val
 305 310 315 320
 Ala Met His Gln Ala Gln Leu Ile Ser Lys Ile Pro His Ile Leu Lys
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 Glu Met Tyr Asp Ala Asp Leu Leu Glu Glu Glu Val Ile Ile Ser Trp
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 Ser Glu Lys Ala Ser Lys Lys Tyr Val Ser Lys Glu Leu Ala Lys Glu
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His Arg Phe Lys Asp Leu Gly Glu Asn Phe Lys Ala Leu Val Leu
35 40 45
Ile Ala Phe Ala Gln Tyr Leu Gln Gln Cys Pro Phe Glu Asp His Val
50 55 60
Lys Leu Val Asn Glu Val Thr Glu Phe Ala Lys Thr Cys Val Ala Asp
65 70 75 80
Glu Ser Ala Glu Asn Cys Asp Lys Ser Leu His Thr Leu Phe Gly Asp
85 90 95
Lys Leu Cys Thr Val Ala Thr Leu Arg Glu Thr Tyr Gly Glu Met Ala
100 105 110
Asp Cys Cys Ala Lys Gln Glu Pro Glu Arg Asn Glu Cys Phe Leu Gln
115 120 125
His Lys Asp Asp Asn Pro Asn Leu Pro Arg Leu Val Arg Pro Glu Val
130 135 140
Asp Val Met Cys Thr Ala Phe His Asp Asn Glu Glu Thr Phe Leu Lys
145 150 155 160
Lys Tyr Leu Tyr Glu Ile Ala Arg Arg His Pro Tyr Phe Tyr Ala Pro
165 170 175
Glu Leu Leu Phe Phe Ala Lys Arg Tyr Lys Ala Ala Phe Thr Glu Cys
180 185 190
Cys Gln Ala Ala Asp Lys Ala Ala Cys Leu Leu Pro Lys Leu Asp Glu

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195 200 205
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 210 215 220
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 260 265 270
 Asp Leu Leu Glu Cys Ala Asp Asp Arg Ala Asp Leu Ala Lys Tyr Ile
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 Cys Glu Asn Gln Asp Ser Ile Ser Ser Lys Leu Lys Glu Cys Cys Glu
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 Lys Pro Leu Leu Glu Lys Ser His Cys Ile Ala Glu Val Glu Asn Asp
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 Glu Met Pro Ala Asp Leu Pro Ser Leu Ala Ala Asp Phe Val Glu Ser
 325 330 335
 Lys Asp Val Cys Lys Asn Tyr Ala Glu Ala Lys Asp Val Phe Leu Gly
 340 345 350
 Met Phe Leu Tyr Glu Tyr Ala Arg Arg His Pro Asp Tyr Ser Val Val
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 370 375 380
 Cys Ala Ala Ala Asp Pro His Glu Cys Tyr Ala Lys Val Phe Asp Glu
 385 390 395 400
 Phe Lys Pro Leu Val Glu Glu Pro Gln Asn Leu Ile Lys Gln Asn Cys
 405 410 415
 Glu Leu Phe Lys Gln Leu Gly Glu Tyr Lys Phe Gln Asn Ala Leu Leu
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 Pro Glu Ala Lys Arg Met Pro Cys Ala Glu Asp Tyr Leu Ser Val Val
 465 470 475 480
 Leu Asn Gln Leu Cys Val Leu His Glu Lys Thr Pro Val Ser Asp Arg
 485 490 495
 Val Thr Lys Cys Cys Thr Glu Ser Leu Val Asn Arg Arg Pro Cys Phe
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 Ser Ala Leu Glu Val Asp Glu Thr Tyr Val Pro Lys Glu Phe Asn Ala
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 Glu Thr Phe Thr Phe His Ala Asp Ile Cys Thr Leu Ser Glu Lys Glu
 530 535 540
 Arg Gln Ile Lys Lys Gln Thr Ala Leu Val Glu Leu Val Lys His Lys
 545 550 555 560
 Pro Lys Ala Thr Lys Glu Gln Leu Lys Ala Val Met Asp Asp Phe Ala
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Asp Ile Pro Ala Lys Lys Val Cys Arg Trp Asp Ser Phe Thr Lys Gln
          35          40          45
Val Gln Arg Val Thr Met Asp Ala Pro Val Ser Ser Val Ala Leu Arg
          50          55          60
Gln Ser Gly Gly Tyr Val Ala Thr Ile Gly Thr Lys Phe Cys Ala Leu
65          70          75          80
Asn Trp Lys Glu Gln Ser Ala Val Val Leu Ala Thr Val Asp Asn Asp
          85          90          95
Lys Lys Asn Asn Arg Phe Asn Asp Gly Lys Val Asp Pro Ala Gly Arg
          100          105          110
Tyr Phe Ala Gly Thr Met Ala Glu Thr Ala Pro Ala Val Leu Glu
          115          120          125
Arg His Gln Gly Ala Leu Tyr Ser Leu Phe Pro Asp His His Val Lys
          130          135          140
Lys Tyr Phe Asp Gln Val Asp Ile Ser Asn Gly Leu Asp Trp Ser Leu
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Val	Tyr	Lys	Leu	Glu	Lys	Glu	Glu	Gln	Ile	Pro	Asp	Gly	Met	Cys	Ile
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Asp	Ala	Glu	Gly	Lys	Leu	Trp	Val	Ala	Cys	Tyr	Asn	Gly	Gly	Arg	Val
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Ile	Arg	Leu	Asp	Pro	Val	Thr	Gly	Lys	Arg	Leu	Gln	Thr	Val	Lys	Leu
225						230					235				240
Pro	Val	Asp	Lys	Thr	Thr	Ser	Cys	Cys	Phe	Gly	Gly	Lys	Asn	Tyr	Ser
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Glu	Met	Tyr	Val	Thr	Cys	Ala	Arg	Asp	Gly	Met	Asp	Pro	Glu	Gly	Leu
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Leu	Arg	Gln	Pro	Glu	Ala	Gly	Gly	Ile	Phe	Lys	Ile	Thr	Gly	Leu	Gly
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									280					285	
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<212> DNA
<213> Homo Sapiens
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<210> 808

<211> 659

<212> PRT

<213> Homo Sapiens

<400> 808

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 Val Glu Lys Val Ser Ser Ile Leu Ala Lys Lys Gly Ile Asn Pro Gly
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 Gly Asn Leu Glu Cys Leu Asn Ala Ile Leu Ile His Gly Val Asp Ile
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 Tyr Gly His Ala Leu Cys Leu Gln Lys Leu Leu Gln Tyr Asn Cys Pro
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 Thr Glu His Ala Asp Leu Gln Gly Arg Thr Ala Leu His Asp Ala Ala
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 Thr Gln Met Cys Arg Pro Ala Ile Cys Gln Leu Leu Ile Asp Arg Gly
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 Ala Glu Ile Asn Ser Arg Asp Lys Gln Asn Arg Thr Ala Leu Met Leu
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 Gly Cys Glu Tyr Gly Cys Lys Asp Ala Val Glu Val Leu Leu Lys Asn
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 Gly Ala Asp Val Ser Leu Leu Asp Ala Leu Gly His Asp Ser Ser Tyr
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 Asn Glu Asp Leu Lys Asp Arg Leu Arg Lys Ile Gln Gln Glu Gln Arg
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 Ile Leu Leu Asp Lys Val Asn Gly Leu Gln Leu Gln Leu Asn Glu Glu
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 Ala Lys Leu Thr Leu Ser Val Pro Thr Glu Lys Phe Glu Ser Met Lys
 595 600 605
 Ser Leu Leu Ser Ser Glu Val Asn Glu Lys Val Lys Lys Ile Gly Glu
 610 615 620
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<210> 809
 <211> 1725
 <212> DNA
 <213> Homo Sapiens

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<210> 810

<211> 355

<212> PRT

<213> Homo Sapiens

<400> 810

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Phe Gln Thr Gly Phe Ser Gly Asn Asp Ile Ala Phe His Phe Asn Pro
50          55          60
Arg Phe Glu Asp Gly Gly Tyr Val Val Cys Asn Thr Arg Gln Asn Gly
65          70          75          80
Ser Trp Gly Pro Glu Glu Arg Lys Thr His Met Pro Phe Gln Lys Gly
85          90          95
Met Pro Phe Asp Leu Cys Phe Leu Val Gln Ser Ser Asp Phe Lys Val
100          105          110
Met Val Asn Gly Ile Leu Phe Val Gln Tyr Phe His Arg Val Pro Phe
115          120          125
His Arg Val Asp Thr Ile Ser Val Asn Gly Ser Val Gln Leu Ser Tyr
130          135          140
Ile Ser Phe Gln Asn Pro Arg Thr Val Pro Val Gln Pro Ala Phe Ser
145          150          155          160
Thr Val Pro Phe Ser Gln Pro Val Cys Phe Pro Pro Arg Pro Arg Gly
165          170          175
Arg Arg Gln Lys Pro Pro Gly Val Trp Pro Ala Asn Pro Ala Pro Ile
180          185          190
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195          200          205
Ser Thr Pro Ala Ile Pro Pro Met Met Tyr Pro His Pro Ala Tyr Pro
210          215          220

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 Asn Leu Cys Ser Gly Asn His Ile Ala Phe His Leu Asn Pro Arg Phe
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 Asp Glu Asn Ala Val Val Arg Asn Thr Gln Ile Asp Asn Ser Trp Gly
 275 280 285
 Ser Glu Glu Arg Ser Leu Pro Arg Lys Met Pro Phe Val Arg Gly Gln
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 Ser Phe Ser Val Trp Ile Leu Cys Glu Ala His Cys Leu Lys Val Ala
 305 310 315 320
 Val Asp Gly Gln His Leu Phe Glu Tyr Tyr His Arg Leu Arg Asn Leu
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 Val Gln Thr
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 <211> 1022
 <212> DNA
 <213> Homo Sapiens

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<210> 812
 <211> 317
 <212> PRT
 <213> Homo Sapiens

<400> 812
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35 40 45
 Gly Thr Leu Glu Lys Val Pro Ala Ala Glu Ser Ala Asp Pro Pro Gln
 50 55 60
 Ser Pro Gln Gly Ala Ser Ala Leu Pro Thr Thr Ile Ser Phe Thr Cys
 65 70 75 80
 Trp Arg Gln Pro Asn Glu Gly Ser Ser Ser Gln Glu Glu Glu Glu Ala
 85 90 95
 Ser Thr Ser Pro Asp Ala Glu Ser Leu Phe Arg Glu Ala Leu Ser Asn
 100 105 110
 Lys Val Asp Glu Leu Ala His Phe Leu Leu Arg Lys Tyr Arg Ala Lys
 115 120 125
 Glu Leu Val Thr Lys Ala Glu Met Leu Glu Arg Val Ile Lys Asn Tyr
 130 135 140
 Lys Arg Cys Phe Pro Val Ile Phe Gly Lys Ala Ser Glu Ser Leu Lys
 145 150 155 160
 Met Ile Phe Gly Ile Asp Val Lys Glu Val Asp Pro Ala Ser Asn Thr
 165 170 175
 Tyr Thr Leu Val Thr Cys Leu Gly Leu Ser Tyr Asp Gly Leu Leu Gly
 180 185 190
 Asn Asn Gln Ile Phe Pro Lys Thr Gly Leu Leu Ile Ile Val Leu Gly
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 Thr Ile Ala Met Glu Gly Asp Ser Ala Ser Glu Glu Glu Ile Trp Glu
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 Glu Leu Gly Val Met Gly Val Tyr Asp Gly Arg Glu His Thr Val Tyr
 225 230 235 240
 Gly Glu Pro Arg Lys Leu Leu Thr Gln Asp Trp Val Gln Glu Asn Tyr
 245 250 255
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 260 265 270
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<210> 813

<211> 5175

<212> DNA

<213> Homo Sapiens

<400> 813

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Trp Val Asn Gly Asn Lys Pro Gly Phe Ile Gln Phe Leu Gly Glu Thr
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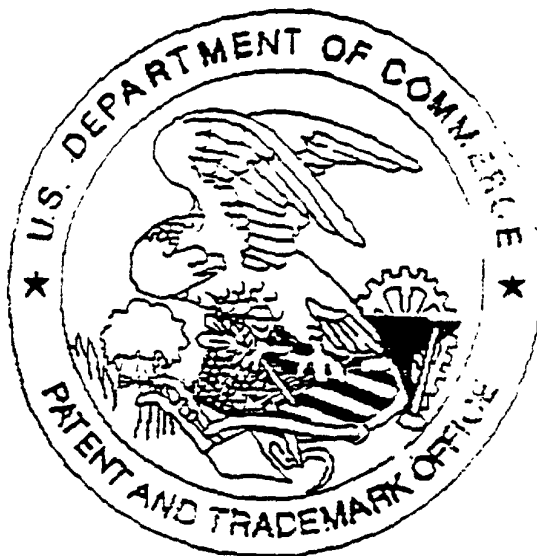
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 100 105 110
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 Cys Ala His Asp Trp Val Tyr Glu
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Drawings

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